

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 116716

TO: Vanessa L Ford

Location: REM/3B25/3C18

Art Unit: 1645

Friday, March 12, 2004

Case Serial Number: 09/543407

From: Barb O'Bryen

**Location: Biotech-Chem Library** 

Remsen E01A69

Phone: 571-272-2518

POB

barbara.obryen@uspto.gov

### Search Notes

# RUSH



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### STIC-Biotech/ChemLib

116716

From:

Chan, Christina

Sent:

Thursday, March 11, 2004 12:51 PM

To:

Ford, Vanessa; STIC-Biotech/ChemLib

Subject:

RE: In re: 09543407 sequence search

### Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

-----Original Message-----

From:

Ford, Vanessa

Sent:

Thursday, March 11, 2004 11:40 AM

Chan, Christina

Subject:

In re: 09543407 sequence search

Please search SEQ ID NO: 12, 14, 16, 18, 20, 22, 24, 26, 28 and 30. Please include interference searches. Please

rush.

Vanessa L. Ford

Biotechnology Patent Examiner

Office: REM 3B25 Mailbox: REM 3C18 Phone: 571.272.0857 Art Unit: 1645



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Searcher: Phone: Location: Date Picked Up: Date Completed: Searcher Prep/Review:\_ Clerical: Online time:

TYPE OF SEARCH: NA Sequences: AA Sequences: Structures: Bibliographic:\_ Litigation:\_ Full text: Patent Family:\_ Other:\_

VENDOR/COST (where applic.) STN: DIALOG: Questel/Orbit: DRLink: Lexis/Nexis: Sequence Sys.: WWW/Internet: Other (specify):\_

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seq length: 2000000000
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1: geneseqp1980s.*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                        1586107 seqs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALA.....VTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-543-407-12
                                                                                                                                                                                       Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyright
                                                                     geneseqp1980s:*
geneseqp1990s:*
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geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	ω U	32	31	30	29	28	27	26
92	92	92	92	92	92	93	94.5	94.5	95	98	98.5	98.5	100.5	109	109	109	113	115	115
11.8	11.8	11.8	11.8	11.8	11.8	11.9	12.1	12.1	12.2	12.6	12.6	12.6	12.9	14.0	14.0	14.0	14.5	14.8	14.8
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AAY44402	AAU79539	AAY44404	AAU79538	AAY44403	AAB36331	AAE36890	ABP74039	ABU36649	ABR82647	ABR82645	ABB62708	ABB65764	AAB36342	AAB36319	AAB36324	AAB36340	ABR82644	AAB36320	AAB36339
Aay44402	Aau79539	Aay44404	Aau79538	Aay44403	Aab36331	Aae36890	Abp74039	Abu36649	Abr82647	Abr82645	Abb62708	Abb65764	Aab36342	Aab36319	Aab36324	Aab36340	. Abr82644	Aab36320	Aab36339
Human tan	Truncated	Human tru	Truncated	Human tru	Escherich	Plectreur	Candida a		B. coli c		Drosophil	Drosophil	Salmonell	Salmonell	Salmonell	Salmonell	E. coli c	Salmonell	Salmonell

# ALIGNMENTS

RESULT 1

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AAB36346
                                                                                                               WPI; 2000-672631/65.
N-PSDB; AAC64622.
                                                                                                                                                                                                                          Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                   White AP, Doran JL,
                                                                                                                                                              05-APR-1999;
                                                                                                                                                                           05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                      WO200060102-A2
                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                26-FEB-2001
                                                                                                                                                                                                                                                                                             AAB36346;
                                                                                                                                                                                                                                                                                                          AAB36346 standard; protein; 151
                                                                                                                                                                                        12-OCT-2000.
                                                                                                                                                                                                                                                                 AgfA::PT3#1 amino acid sequence SEQ ID NO:12
                                                                                                                                                  (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                              99US-0127888P
                                                                                                                                    Collison SK,
                                                                                                                                                                                                                                                                                                           ጅ
                                                                                                                                    Kay WW;
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 135; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native

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comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid polymer comprising a recombinant AgfA acid sequence or sequences grown on a Salmonella, E. coli or conjumer into the animal in conjunction with a carrier or diluent. (I) is cuseful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for conjunction with a carrier or diluent. (I) is cuseful for the expression animal. In a fimbrial presentation conjunction with a carrier or diluent for conjunction with a carrier or diluent. (I) is conjunction with a carrier or diluent. (I) is conjunction with a carrier or diluent for combinant animal. In a fimbrial presentation conjunction conjunction with a carrier function properties research the to conjunct and animal. In a fimbrial presentation conjunction possesses both the conjunctive and adhesion properties relevant for an efficient live immunogenic, the carrier fimbrial subunit proteins are usually strong conjunctions. Which may be important for directing an immune response conjunction of the present invention.
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Best Local !
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                               N-PSDB; AAC64623.
                                                                                                                                           White AP, Doran JL,
                                                                                                              WPI; 2000-672631/65.
                                                                                                                                                                                                                       05-APR-1999;
                                                                                                                                                                                  (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36347 standard; protein; 151
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                                                                                                                                             Collison
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                                                                                                                                         Kay WW
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Disclosure; Page 136; 139pp; English.

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RESULT 3
AAR74625
ID AAR7
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                                                                     26-APR-1993;
    (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J.
                                                                                                               26-APR-1994;
                                                                                                                                                    10-NOV-1994.
                                                                                                                                                                                               WO9425598-A2
                                                                                                                                                                                                                                       Salmonella
                                                                                                                                                                                                                                                                       Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                 AgfA sequence.
                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                       AAR74625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR74625 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
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                                                                   93US-00054452
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Pred. No. 1.7e-58;
0; Mismatches 0;
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RESULT 4
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Best Local Similarity 90.3
Matches 136; Conservative
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                   Disclosure; Page 135; 139pp; English
                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                               05-APR-1999;
                                                                                                                                                                                                                                                        05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                               Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36341 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Salmonella AgfA protein and DNA are used in vaccine and genetic immunitation compositions, respectively, to elicit an immune respons Salmonella in animals (e.g. food producing animals) and humans. (Upon 25-MAR-2003 to correct PN field.)
                                                                                                                                                                           White AP,
                                                                                                                                                                                                                                                                                    12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
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N-PSDB; AAQ87467.
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                                                                                                                                                                                                                                                                                                                                                                 immune response; immunogen
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                                                                                                                                                                          Doran JL,
                                                                                                                                                                                                                                                                                                                                                                            agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 7B;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                               99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95pp; English.
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                                                                                                                                                                           Collison SK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 695; DB 2;
Pred. No. 2.2e-58;
4; Mismatches 11
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                                                                                                                                                                          Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doran
                                                                                                                                                                             £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                                                                                                                             fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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ns. (Updated
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POWER TO SEE TO 
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Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant Agfa; CsgA and Agfa-homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
Collinson SK,
                                                                                                                                                                                                   26-APR-1994;
                                                                                                                                                                                                                                                                  03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
29-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW23570 standard; protein; 151 AA
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                                                                                                                                 26-APR-1993;
                                                                                                                                                                                                                                                                                                                                US5635617-A
                                                              (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enteritidis 27655-3b agfA
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(first entry)
Kay
                                                                                                                                    93US-00054452
                                                                                                                                                                                               94US-00233788
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by GCC"
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90.1%;
   Doran JL;
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Pred. No. 2.2e-58;
4; Mismatches 11
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AAB36352
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Best Local !
Recombinant agfA gene which encodes foreign
                                                                                     N-PSDB; AAC64628.
                                                                                                            WPI; 2000-672631/65
                                                                                                                                                                                                                                                                         05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                  White AP,
                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                            05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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DB; AAT74142.
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135; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Fig 7; 85pp; English.
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                                                                                                                                                         Doran JL,
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                                                                                                                                                                                                                                                                   99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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                                                                                                                                                            Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunogen
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Pred. No. 6.5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene replacement; fimbrin; epitope;
                                                                                                                                                            SK,
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                                                                                                                                                         Kay WW
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having a segment replaced by a foreign DNA sequence epitope or antigen, expresses recombinant AgfA

05-APR-2000; 2000WO-CA000356

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Righ, CsgA and Agfa-homologue fimbrin subunits, respectively; (2) C directing recombination of a recombination of the comprising appears of the homologous species, replacing the native comprising a replacement segment or response in an animal, and complete of the response of the response of a recombinant Agfa composition of a recombinant Agfa composition of recombination of the superior of directing the composition of recombination of the superior of directing the composition of recombination and superior or diluent. (I) is composition of the expression of recombination and protein which is useful for composition of the host cell and introducing the composition of the properties are usually extrong composition of the protein are usually extrong commonogens, which may be important for directing an immune response composition of the protein and introducing the inserted epitope, and hybrid fimbriae are easy and composition of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 134; Conservative
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                                                                 12-OCT-2000
                                                                                                                                                                       Escherichia
                                                                                                                                                                                              Salmonella enteritidis.
                                                                                                                                                                                                                                   vaccine; immune response; immunogen
                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal
                                                                                                                                                                                                                                                                                                                                                                                               AAB36353;
                                                                                                        WO200060102-A2
                                                                                                                                                                                                                                                                                                         AgfA::PT3#8
                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36353 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                       COLI
                                                                                                                                                                                                                                                                                                  amino acid sequence SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - NYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.1%;
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Pred. No. 1.4e-54;
0; Mismatches 0;
                                                                                                                                                                                                                                                        gene replacement;
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                                                                                                                                                                                                                                                        fimbrin;
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RESULT 8
AAB36349
ID AAB3
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AC AAB3
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DT 26-F
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DE AgfA
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KW Salm
KW Vacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid sequence or sequences grown on a Salmonella, E. coli or Enterobacterlaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                    Salmonella;
                                                          AgfA::PT3#4 amino acid sequence SEQ ID NO:18
                                                                                                   26-FEB-2001
                                                                                                                                                                              AAB36349 standard; protein; 151 AA.
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                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                     121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                            LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 AA
                                                                                                                                                                                                                                                                              NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                    agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention
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Pred. No. 1.2e-50;
6; Mismatches 23;
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                                                                                                                                                                                                                                               Matches
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Best Local &
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Escherichia coli.
                                                                                                                                                                                                                                                                                                                            Sequence 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 136; 139pp; English.
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                                    121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                    Similarity
NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                              MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                               SDARKSETTITOSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doran JL,
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                              A,
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                                                                                                                                                                                                                                          Score 613; DB 3;
Pred. No. 1.5e-50;
7; Mismatches 22
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                                                                                                                                                                           CC Agfa, CsgA and Agfa, homologue fimbrin subunits, respectively; (2) CC homologous species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologous species; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant Agfa ccid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the useful for the expression of recombinant Agfa protein which is useful for cellifor the expression of recombinant Agfa protein which is useful for cystem the heterologous antigens are presented in high numbers (up to immunogens, which may be important for directing an immune response conjunction with a carrier or diluent. (I) is conjunction an animal. In a fimbrial presentation conjunction with a carrier or diluent. (I) is conjunction with a carrier or diluent. (I) is conjunction with a carrier or diluent. (I) is conjunction an animal in conjunction with a carrier or diluent. (I) is conjunction and the carrier of recombinant Agfa protein which is useful for conjunction and the presented in high numbers (up to immunogens/cell), the hybrid fimbrian protein possesses both the conjunction of the proteins are usually strong immunogens, which may be important for directing an immune response conjunction of the present invention. The present sequence is given in the exemplification of the present invention.
                                                                                                          Query Match
Best Local
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative finbriae (SERF1/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1999;
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                                                                                                        Similarity
                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
151
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                                                                                                                                                               ₹,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                    78.4%;
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                                                                            Score 611; DB 3; I
Pred. No. 2.3e-50;
7; Mismatches 22;
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                                                                                                                Length 151;
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CC Regment of the gene has been replaced by a segment of a foreign DNA CC (1) use of thin aggregative fimbriae (SERI7/TNAP) nucleation described are: (2) use of thin aggregative fimbriae (SERI7/TNAP) nucleation depended CC assembly system of strains of salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) (2) (2) (3) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant of protein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein main a immune response in an immune response in an enterobacteriaceae host cell, from the host cell and introducing the cuseful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to companion), the carrier fimbrial subunit protein possesses both the communogenicity and adhesion properties relevant for an efficient live immunogenicity and the hybrid fimbrin protein are usually strong immunogens. which may be immortant for directing an immune response
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immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White AP,
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Escherichia coli.
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RESULT 11
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Best Local Similarity
        The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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N-PSDB; AAC64627.
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                                                                                                                                                                                                                                                                                                                                              White AP,
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                                                                                                                                                                                                                                                                                                                                           Doran JL,
                                                                                                                                                                                                               Page 137; 139pp; English.
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Best Local Similarity
Matches 122; Conserv
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Pred. No. 1.1e-49;
6; Mismatches 23
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described

Recombinant agfA gene having a segment replaced by a foreign which encodes foreign epitope or antigen, expresses recombina protein useful for eliciting immune response in animal.

expresses recombinant use in animal.

DNA sequence ant AgfA

Disclosure; Page 139; 139pp; English.

WPI; 2000-672631/65. N-PSDB; AAC64631.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

N-PSDB; AAC64624.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended CC Enterobacteriaceae for the production of fimbriae conjugated and AgfA. Homologue fimbria subunits, respectively, (2) and AgfA. Homologue fimbria subunits, respectively, (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, cc copy of that gene; and (4) eliciting an immune response in an animal, respecies, replacing the native CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC acid sequence of sequences grown on a Salmonella, E. coli or CC useful for the expression of recombinant AgfA protein which is useful for CC useful for the expression of recombinant AgfA protein which is useful for CC system the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens are presented in high numbers (up to CC immunogenicity and adhesion properties relevant for an efficient live compensate the inserted spitope, and hybrid fimbria are usually strong CC against the inserted apitope, and hybrid fimbriae are easy and consequence in an animal. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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WPI; 2000-672631/65
                                                                                                                             05-APR-2000; 2000WO-CA000356
                                                               (UYVI-) UNIV VICTORIA
                                                                                                 05-APR-1999;
                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                    12-OCT-2000
                                                                                                                                                                                                  WO200060102-A2
                                                                                                                                                                                                                                                  Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#3 amino acid sequence SEQ ID NO:16
                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36348;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36348 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVFOWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATYDOLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKILKVAAFAAI VVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYOYGSANAALALO
                              Doran JL,
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                             99US-0127888P
                                                                                                                                                                                                                                                                                              response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.4%;
80.8%;
                              Collison
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Pred. No. 1.3e-49;
                            SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
                            Kay WW,
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CC directing recombination of a recombinant gene into the chromosome of the CR homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of back into the chromosome of the homologous species, replacing the native CR pack into the chromosome of the homologous species, replacing the native CR protein containing an amino acid polymer comprising a recombinant AgfA CR comprising separating an amino acid polymer comprising a recombinant CR protein containing a replacement segment or segments of foreign amino CR containing a replacement segment or segments of foreign amino CR enterobacteriaceae host cell, from the host cell and introducing the CR polymer into the animal in conjunction with a carrier or diluent. (I) is CR contained the expression of recombinant AgfA protein which is useful for CR eliciting an immune response in an animal. In a fimbrial presentation CR system the heterologous antigens are presented in high numbers (up to CR immunogenicity and adhesion properties relevant for an efficient live immunogens, which may be important for directing an immune response CR immunogens, which may be important for directing an immune response CR immunogens, which may be important for directing an immune response CR immunogens, which may be important for directing an immune response CR immunogens, which may be important for directing an immune response CR immunogens, and hybrid fimbriae are easy and CR inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
Query Match
Best Local S
Matches 121
                                                                                                                 Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 136, 139pp; English.
                         Similarity
                      74.5%;
80.1%;
               Score 580; DB 3;
Pred. No. 2.1e-47;
                                            Length 151;
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RESULT 14
AAR62761
ID AAR62
27-AUG-2003
25-MAR-2003
26-JUN-1995
            WO9425598-A2
                                       Salmonella; AgfA; vaccine
                          Salmonella enteritidis.
                                                      AgfA sequence.
                                                                                                  AAR62761;
                                                                                                             AAR62761 standard; protein; 120 AA
                                                                                                                                                 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                            (revised)
                                                                    (first entry)
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10-NOV-1994

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> 61 61

121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151

SDARKSETTÍT ÓSGYGNGADVGOGADNSTÍELTONG FRANKATIDOWNÁKNSDÍT VGOYGG SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ MKLLKVAAFAAIVVSGSALAGYVPQWGGGGNHNGGGNSGFDSTLSIYQYGSANAALALQ

120 120 60 6 0

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121;

Conservative

Mismatches

Indels

0,

Gaps

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RESULT 15
AAW23569
ID AAW23
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Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents the Salmonella enteritis 27655-3b TaphoA mutant strain AgfA protein. The encoding DNA and isolated AgfA protein are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals and humans. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
        Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                               WPI; 1997-309886/28.
N-PSDB; AAT74141.
                                                                                                                                                                                           03-JUN-1997.
                                                                                                                                                                                                                                             Salmonella enteritidis.
                                                                                                                                                                                                                                                                      Enteropathogenic bacteria;
                                                                                                                                                                                                                                                                                               Salmonella enteritidis 27655-3b TnphoA mutant agfA fragment.
                                                                                                                                                                                                                                                                                                                           25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                         AAW23569 standard; protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and humans. (Updated on 25-MAR AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 7A;
                                                                                    Collinson SK,
                                                                                                             (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                       26-APR-1993;
                                                                                                                                                                 26-APR-1994;
                                                                                                                                                                                                                     US5635617-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 GOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGGNNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95pp; English.
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                                                                                    Doran JL;
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                                                                                                                                                                                                                                                                      enterobacteria; S.enteritidis; antibody.
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Pred. No. 1.2e-45;
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Search completed: March 11, Job time : 46.9 secs

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&XSSSSSSSSSXXX
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Best Local Sim:
Matches 106;
                                                                                                                                                                                                                                                                                        strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                       Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents an agfA fragment encoded by an agfA gene
fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Fig 7; 85pp; English
51
                          82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
                                                                                                           22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                     -
                                                                                                                                                                                          Similarity
GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
                                                                                   VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                      Conservative
                                                                                                                                                             71.9%; out
100.0%; Pr
                                                                                                                                                                    Score 560; DB 2;
Pred. No. 1.2e-45;
0; Mismatches 0;
                                                                                                                                                                                                           Length 120;
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Minimum DB
Maximum DB
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Maximum Match
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Perfect score:
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779
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1: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                                          Maximum Match 100%
Listing first 45 summaries
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    9
 US-09-841-835-8
US-09-196-387-10
US-09-841-835-2
US-09-196-387-2
US-09-196-387-2
US-09-972-115A-8
US-09-972-115A-8
US-09-072-566-109
US-09-072-567-204
US-09-072-567-204
US-09-136-447A-5
US-09-136-447A-13
US-09-316-447A-13
US-09-316-447A-30263
US-09-540-236-3739
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US-09-328-336-4764
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US-08-233-788A-57
US-09-196-387-8
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                                                                                                                                                              Sequence 59, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appl
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Sequence 6, Appli
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5, Appli
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<b>.</b> 4.	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28
75.5	76.5	76.5	76.5	77	77	77	77	77.5	77.5	77.5	78	78	78	78	78	78.5	79
9.7	9.8	9.8	9.8	9.9	9.9	9.9	9.9	9.9	9.9	9.9	10.0	10.0	10.0	10.0	10.0	10.1	10.1
624	605	186	159	2315	1690	528	415	878	714	702	906	906	906	906	906	2123	941
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US-09-336-447A-7	US-09-489-039A-13002	US-09-382-276-2	US-08-856-253-2	US-09-543-681A-5434	US-09-595-684B-39	US-09-490-291-8	US-09-025-769B-280	US-09-540-236-3401	US-09-841-786-4	US-09-252-991A-22119	US-08-216-326-2	US-08-172-332-1	US-08-687-379-4	US-08-687-379-2	US-08-254-573-2	US-08-968-685A-10	US-09-336-447A-9
Sequence 7, Appli	Sequence 13002, A	Sequence 2, Appli	Sequence 2, Appli	Sequence 5434, Ap	Sequence 39, Appl	Sequence 8, Appli	Sequence 280, App	Sequence 3401, Ap	Sequence 4, Appli	Sequence 22119, A	Sequence 2, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 9, Appli

# ALIGNMENTS

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COUNTRY: U.S.A.

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Ploppy DC 505/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 920043.403C2
REFERENCE/DOCKET NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-490
TELEFAX: (206) 622-693
TELEFAX: 3723836 SEEDANBERRY
INFORMATION FOR SEG ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-08-233-788A-59
Query Match 88.6%;
Best Local Similarity 89.4%;
Matches 135; Conservative
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GENERAL INFORMATION:
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APPLICANT: I
APPLICANT: C
APPLICANT: C
                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acid
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                        H: 151 amino acids amino acid
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KAY, William W.
COllinson, Karen S.
Clouthier, Sharon C.

VENTION: METHODS AND COMPOSITIONS FOR DETECTION

VENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center,
Score 690; DB 1; Length 151; Pred. No. 7.1e-62; Mismatches 12; Indels
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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                                                            RESULT 3
US-09-196-387-8
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-233-788A-57
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          Sequence 8, Application US/09196387 Patent No. 6277613 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                     Matches 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
                                                                                                                                  61
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                                                                                                                                                    GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
                                                                                                                                                                                                                        VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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                                                                                                                           GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
                                                                                                                                                                                           VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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                                                                                                                                                                                                                                                                                                                                                                                                    120 amino acids
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                                                                                                                                                                                                                                                            71.9%; Score 560; DB 1; Length 120; ilarity 100.0%; Pred. No. 6e-49; Conservative 0; Mismatches 0; Indels
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Kay, William W.
Collinson, Karen S.
Clouthier, Sharon C.
Clouthier, Sharon C.
VENTION: METHODS AND COMPOSITIONS FOR DETECTION
VENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seed and Berry
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                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                      STREET:
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GENERAL INFORMATION:
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                                                                                                                        TITLE OF INVENTION: A PROTEIN THAT TITLE OF INVENTION: OF USE THEREOF NUMBER OF SEQUENCES: 12
                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                 APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201.487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 673 amino acids
               CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 11.8%; Score 92; DB: Local Similarity 30.4%; Pred. No. 0.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Hackensack
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                               158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                     65 KSETTIT----OSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
07601
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                                                                      411 Hackensack Avenue,
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                                                                                                                                                                           A PROTEIN THAT BINDS TO TRF1
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                                                                        4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 673;
                                                                                                                                                                             AND METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-841-835-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: de Lange, Titia
APPLICANT: Smith, Susar
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-230 CIP1
                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                       APPLICATION NUMBER: US/09/196,387 FILING DATE:
                                                                                                                                                                                                                                                                                                                           COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                             CITY: Hackensack
STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
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6277613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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Pred. No. 0.6;
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; MOLECULE TYPE: protein US-09-841-835-10
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              Query Match
Best Local Similarity
Matches
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GENERAL INFORMATION:
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Best Local (
                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 949 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTE
TITLE OF INVENTION: OF USE
                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
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                                                                                                                                                                           TELEFAX: 201
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                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                  TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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Similarity 30.4%;
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 Conservative
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                11.8%;
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Pred. No. 0.94
15; Mismatches
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                Score 92;
Pred. No.
Mismatches
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                              DB 4;
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6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64

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US-09-841-835-2
; Sequence 2, Application US/09841835
; Patent No. 6506587
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                                                                  RESULT 8
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US-09-196-387-2
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Best Local !
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: de Lan
APPLICANT: Smith,
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REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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TELEPHONE: 201-1
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                               158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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    Application US/09196387
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Smith, Susan
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NO
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RESULT 9
US-09-972-115A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                         APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Piatyszek A.
APPLICANT: Mieczyslaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
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PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                  APPLICANT: Geron Corporation
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0:
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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STRANDEDNESS: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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mino acid
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Pred. No. 1
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RESULT 11
US-08-864-038A-3
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US-09-336-115C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06132/055002
CURRENT FILING NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-19
PRIOR APPLICATION NUMBER: US 09/100,258
PRIOR FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09336115C
Patent No. 6576244
GENERAL INFORMATION:
APPLICANT: Weltzin, Richard A.
APPLICANT: Guy, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Sequence 3, Application US/08864038A
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LOCATION: 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa = Any Amino Acid
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LOCATION: (1)...(20)
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                                                                                        271 NNAEQLLNQAAN
                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                 38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNG-----
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                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                          HEMAHANNATAN 149
                                                                                                                                                                                          G-----ADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVT 137
                                                                                                                                                                                                                                                                                                    AYQAVFLAINAAVGL---WNTIGYAVMCGNGNGTESGPGSVIFNDQPGQDSTQITCNRFE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                             GVYQFCKAKNGS-SSSSNGGNGSSTQTTATTTQDGVTITTTYNNNKATVKFD--
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                        282
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RESULT 12
US-09-056-556-204
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APPLICANT: KUNIO NAK
TITLE OF INVENTION:
               Patent No. 6350456
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
                                                                                                                               Patent No. 6350456
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/864,038A FILING DATE: May 28, 1997
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: UP 8-184459
PILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 2.389
REFERENCE/DOCKET NUMBER: F-5610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212)986-23-
TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Pin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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LOCATION:
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SOFTWARE: Word Perfect 6.1
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GY: linear
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CONTAINING SAID CDNA, HOST CELTS TRANSFORMED WITH SAID
VECTOR, POLYPEPTIDE PRODUCED THERBBY, METHOD OF PRODUCING
SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
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Pred. No. 1
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US-09-072-596-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               equence 199, Application US/09072596
Litent No. 6458366
             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                    APPLICANT:
                                                                                                                                       NUMBER OF SEQUENCES: 3
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LENGTH: 943 amino acids
                                                                                                                                                                   FITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/056,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                        STREET:
                                                               COUNTRY:
                                                                                                                         ADDRESSEE:
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TOPOLOGY: 1:
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                                                                                             Seattle
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Hendrickson, Ronald C.
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Vedvick, Thomas S.
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Dillon, Davin C.
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IBM PC compatible
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US-09-477-135A-131
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CURRENT FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08990823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 657286
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                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 1:
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             LENGTH: 943
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 05-MAY CLASSIFICATION:
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159 IGLTGSGLLGF-----
                                                                                     12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR----KSET 68
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33; Conserva
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; Pred. No. 1.9;
15; Mismatches 5
                                                                                                                       Score 89; DB 4;
Pred. No. 1.9;
5; Mismatches 5
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TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 204:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 amino acids
; TYPE: amino acid
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-072-967-204
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US-09-072-967-204
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Best Local Similarity 25.6%;
Matches 33; Conservative 1
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/072,967
FILING DATE: 05-WAY-1998
CCLASSIFICATION:
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APPLICANT: Hendricks
TITLE OF INVENTION:
TITLE OF INVENTION: I
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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APPLICANT: Reed, Steven G.
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                                       119 GGNNAALVN 127
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                                                                                                                 69 TITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNAKNSD---ITVGQY----- 118
                                                                                                                                                                                                12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
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5. 6592877
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Hendrickson, Ronald C.
JENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
JENTION: AND DIAGNOSIS OF TUBERCULOSIS
QUENCES: 355
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Vedvick, Thomas S.
Twardzik, Daniel R.
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Dillon, Davin C.
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; Pred. No. 1.9;
15; Mismatches 5
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Search completed: March 11, 2004, 18:44:23

Job time: 13.4 secs

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Result
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Maximum
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Maximum Match 100%
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*

7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/prodata/1/pubpaa/US09E_PUBCOMB.pep:*

10: /cgn2_6/prodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*

13: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*

14: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/prodata/1/pubpaa/US10E_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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     10 US-09-972-115A-8

14 US-10-199-937-4

18 US-08-834-666A-6

18 US-10-238-075-749

15 US-10-369-493-20619

9 US-09-996-634-131

10 US-09-997-182-131

10 US-09-997-182-131

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US-09-841-835-10
US-09-841-835-2
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US-10-032-585-7876
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Sequence 20638, A
Sequence 7776, Ap
Sequence 8, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 79, App
Sequence 791, App
Sequence 131, App
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US-09-880-748-1281	US-09-880-748-1153	US-10-080-170-348	US-09-712-363-156	US-10-156-761-13168	US-09-880-748-1554	US-09-880-748-1122	US-10-322-673-48	US-10-369-493-9134	US-10-156-761-11222	US-10-394-575-61	US-09-996-194-16	US-09-801-368-126	US-10-156-761-9343	US-10-050-704-100	US-09-880-748-1226	US-09-880-748-2098	US-09-952-267-13	US-10-156-761-13039	US-09-880-748-1165	US-09-880-748-1136	09-793-306-1	-09-880-748-	-1	-10	-10	US-09-880-748-1494	-10	-05	US-09-820-843A-21
128	Sequence 1153, Ap	e 348	156,	131		1122	48,	9134	11	e 61	16,	126, A		O		Sequence 2098, Ap				æ		Sequence 1850, Ap					Sequence 8763, Ap		Sequence 21, Appl

# ALIGNMENTS

US-10-369-493-20638

Sequence 20638, Application US/10369493 Publication No. US20030233675A1

GENERAL INFORMATION:

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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/360,039
PRIOR APPLICATION NUMBER: US/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEO. ID NOS: 47374
SEO. ID NO 20638
LENGTH: 445
                                                                                                                                                       Query Match
Best Local S
Matches 47
                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Rhodopseudomonas palustris FEATURE:
19 AAFAADSNTVYLNOTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
                                                                                                                7 AAFAA-----GNSSGPDSTLSIYQY
                                                                                                                                                                                 Similarity
                                                                                                                                                            Conservative
                                                                                                                                                       12.8%; Score 100; DB: 26.6%; Pred. No. 0.11; ive 20; Mismatches
                                                                                                                                                                                                    DB 15; Length 445;
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Gaps

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US-09-841-835-8
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US-10-032-585-7876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
---- tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7876, Application US/10032585 Publication No. US20030180953A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQ ID NO 7876
LENGTH: 688
TYPE: PRT
                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Terry,
                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                STREET: 411
STREET: 411
CITY: Hackensack
Tersey
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
             NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                               FILING DATE:
                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 TGLTNN---NNSKSPAKSKKKSNFD----NNSNSALNNLDKSKLKINTNEITNISETTSN 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30. GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST 89
                                                                                                                                                                                                                                                                                                  07601
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                                                                                                                                                                                                                                                                                                                              New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPGVFNKITQDSSSNGSKVSVIQDGKNN---
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                                                                                                                                                                                                                                                                                                                                                               411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                USA
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Smith, Susan
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                                                                                                                                                                                                                                                     Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%; Score 94.5; DB 14; 25.8%; Pred. No. 0.67; tive 24; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SDITVGQYGGNNAALVNYDQLVTRVVTHEMAHANNATA-NQ 150
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                                                        US-09-841-835-10
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                   Query Match
 Best Local Similarity
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GENERAL INFORMATION:
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Patent No. US20020076795A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
--- Tocal Similarity
                                                                                                                                                     TELEFAX: 201-343-1504
TELEX: 133521
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                                      NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION: 201-487-5800
                                                                                            TOPOLOGY:
                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 673 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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                                                                    TYPE: protein
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Smith, Susan
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                                                                                            linear
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 11.8%;
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92;
No.
DB 9;
1.8;
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               Length 949;
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                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                 Query Match
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                  TYPE: amino
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  Local
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                                                                     158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                     65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                          99 VAAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLÄESPEÄA 157
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linear
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                                                                                                                                                                                                                15; Mismatches
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                                                                                                                                                                                                                              Score 92; DB
Pred. No. 2.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Applicat Publication No. US20 GENERAL INFORMATION:
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Best Local S
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SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Christenson, Erik
APPLICANT: DeMaggio, Anthon
APPLICANT: Goldman, Phyllis
APPLICANT: MCBlligott, David
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PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 27866/36559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 64
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CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
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TYPE: PRT
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158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                        65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                  99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                       35;
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                                                                                                                                                                                           Similarity
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Similarity 30.4%;
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No. US20030190739A1
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                                                                                                                                                                       Conservative
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                                                                                                                                                                                         11.8%; Score 92; 30.4%; Pred. No.
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06
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APPLICANT: Al-Garawi
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FREEEEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,666A
FILING DATE: 01-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-428-0200
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ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                             NAME/KEY: Signal Sequence LOCATION: 1...20
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                            138 HEMAHANNATAN 149
271 NNAEQLLNQAAN
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                                                                                                                                                                      102 AYQAVFLAINAAVGL---WNTIGYAVMCGNCNGTESGPGSVIFNDQPGQDSTQITCNRFE 158
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                                                   GVYQFCKAKNGS-SSSSNGGNGSSTQTTATTTQDGVTITTTYNNNKATVKFD-----IT 270
                                                                            G-----ADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVT 137
                                                                                                           STGPGKSMSIDEFKKLNEAYQIIQQALKNQSGFPELG-GNGTKVSVNYNYECRQTADING 217
                                                                                                                                         SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNG------ADVGQ 83
                                                                                                                                                                                                    AFAAIVVSGSALAGVVPQW------GGGGNHNGGGN-----
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internal
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                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20619
LENGTH: 486
                                                                                        Matches
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                                                                                                                           Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chen, XianTeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 749
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                                                                                                                                                                              FEATURE:
NAME/KEY: unsure
LOCATION: (1).. (486)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolar TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1024 -----
86 SVVVAGTDYRDIVÁGVLÞSLGGVKKAYAIGDGSGÞFAPFKDLASDTPFSAPEFGAADGFV 145
                                   11 AIVVSGS----ALAGVVPQWCGGGNHNGGGNSSGP-----DSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 DOWNAKUSDITVGQYGGNNAALVNYDQLVT 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             906 KISSNSTDAINGSQLYGVADSFTSYLGGGADISDTGVLSGPTYTIGGTDYTNVGDALAAI
                                                                                      l Similarity
35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn version 3.1
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                                                                                      Conservative
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DS20030148324A1
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                                                                                                      11.5%;
                                                                                                    Score 89.5;
Pred. No. 1.
                                                                                 Mismatches
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                                                                                                                     DB 15;
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                                                                                 Indels
                                                                                                                   Length 486;
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                                                                               49;
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US-09-997-182-131
; Sequence 131, Application US/09997182
; Publication No. US20030049263A1
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; ORGANISM: Mycobacterium tuberculosis
US-09-996-634-131
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US-09-996-634-131
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CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR APPLICATION NUMBER: 60/000,254
                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 131
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                                                                                                           FILE REFERENCE: 61258
CURRENT APPLICATION NUMBER: US/09/997,182
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nano, Prancis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIH-----AAVGGRPRGALISQG--NLLI-----AQSSLVDAWRLTEADVNLGM 188
                                                                                                                                                                                                                                                                                                                                                                                                   GNYNTGLAN
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Pred. No. 3
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                                     RESULT 14
US-10-193-002-199
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US-09-997-181-131
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   Sequence 199, Appropriate Publication No.
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                             Matches
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Similarity 25.6%;
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                                                                                                                 GNYNTGLAN 381
   Application US/10193002
5. US20030135026A1
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25.6%;
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; LENGTH: 943
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-997-182-131
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CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR FILING TION NUMBER: 08/990,823
PRIOR APPLICATION NUMBER: US/96/10375
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US/96/10375
PRIOR APPLICATION NUMBER: US/96/10375
PRIOR APPLICATION NUMBER: US/96/10375
PRIOR APPLICATION NUMBER: US/96/10375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61257
                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium tuberculosis
313 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNS
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                                                      69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY-----
                                                                                                                                                                    12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR----KSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY-----
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                                                                                                                                                                                                                           15; Mismatches
                                                                                                                                                                                                                                                     Score 89; DB
Pred. No. 3.5;
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Pred. No. 3.5;
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                                                                                                             ---IGLFNSGTGNVGIGNSGTGNWGIGNSG 312
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                                                                                                                                                                                                                           55; Indels
                                                                                                                                                                                                                                                                            Length 943;
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RESULT 15
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                                                       Sequence 204, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 199: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 11.4%; Score 89; DB Local Similarity 25.6%; Pred. No. 3.5; Mismatches 33; Conservative 15; Mismatches
                                       APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,392
REFORENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/193,002

FILING DATE: 10-Jul-2002

FILING DATE: (Unknown)

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: U$/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                  266 GNYNTGLAN 274
                                                                                                                                                                                                                                                                 206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNNGQYNTGYLNS 265
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ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lodes, Michael J.

TITLE OF INVENTION: COMPONING AND METHODS FOR DIAGNOSIS OF

TUBERGULOSIS

NUMBER OF CECUTATION TUBERGULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 350
                                                                                                                                                                                                                                                                                                                       69
                                                                                                                                                                                                                                                                                                                                                                                 12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
                                                                                                                                                                                                                                                                                                       TITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSD---ITVGQY-----
                                                                                                                                                                                                                                                                                                                                                        IGLTGSGLLGF-
                                                                                                                                                                                                                                         GGNNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Washington
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Skeiky, Yasir A.W.
Dillon, Davin C.
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Vedvick, Thomas S.
Twardzik, Daniel R.
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Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 943;
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Search completed: March 11, 2004, 19:18:34 Job time : 25.6 secs
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                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER IBM DC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION ADTA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 62-4900
TELEPHONE: (206) 62-400
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Vedrick, Thomas S.
Twardzik, Daniel R.
Todes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                              206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNS 265
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD----ITVGQY-----
                                                                                                                                                                                                                                                                12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR----KSET 68
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                11.4%; Score 89; DB 14; ilarity 25.6%; Pred. No. 3.5; Conservative 15; Mismatches 55
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Scoring table:
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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779
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Copyright (c) 1993 - 2004 Compugen Ltd.
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# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Regult No.

89.5 11.5 343 2 T05221	89.5 11.5 262 2 500275	<b>.</b> .	s i	11 6 409 2	745 2	91 11.7 1250 2 F85862	1250 2	7 770 2	7 256 2	11.7 151 2	7		11.9 573 2	12.0 1238 2	5 12.1 678 2	12.3 145 2	12.3 145 2	12.6 1213 2	12.6 1028 2	N	13.0 151 2	104 13.4 2174 2 E95965	13.6 1748 2	64.4 152 2	152 2	66.8 151 2	69.2 131 2	99.2	3 1 1	Score Match Length Do In	Query	
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hemolysin [importe CREB-binding prote	class 3 outer memb probable sugar ABC	probable PPB prote protein F3308.1b [ hypothetical prote			merozoite 45K surf probable PPE prote hypothetical prote

## ALIGNMENTS

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A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augun
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; R.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate names: csgA protein; major curlin protein (,Species: Bscherichia coli (,Species: Bscherichia coli (,Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01 (,Accession: $70788; G64846; $31202; $34560; $344559 R; Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995 A; Title: Expression of two csg operons is required for production A; Reference number: $70783; MUID:96414468; PMID:8817489 A; Accession: $70788 A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                        A; Molecule type: DNA
A; Residues: 1-151 <BLAT>
                                                                                                                                                        A;Status: nucleic
                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-151 < HAM>
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S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Barry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A; A; Aither: Complete genome sequence of a multiple drug resistant A; Title: Complete genome sequence of a multiple drug resistant A; Title: Complete genome sequence of a multiple drug resistant A; Title: Complete genome sequence of a multiple drug resistant ABO502; MUID:21534947; PMID:11677608
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A; Residues: 1-151 < PAR>
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th, T.; Connerton, P.; Cronin, A.;
       (Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; Experimental source: strain K-12, substrain Mg1655; Olsen, A.; Arnqvist, A., Hammar, M.; Sukupolvi, S.; Normark, S. ol. Microbiol. 7, 523-536, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references:
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C;Accession: AI0635
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                              acid sequence not shown; translation not
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Pred. No. 1.8e-50;
4; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K.D.; Thomson, N.R.;
Davis, P.; Davies, R.
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                                                                        PID:g1787279
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A;Title: The RpoS sigma factor rel
A;Reference number: S31202; MUID:9
A;Accession: S31202
A;Molecule type: DNA
A;Residues: 1-6,'V',8-151 <OLS1>
A;Cross-references: EMBL:L04979
                                                                                                                                                                                          A; Status, Processing A; Molecule type: DNA
A; Molecule type: DNA
A; Mesidues: 1-152 <HAY>
A; Kesidues: 1-152 <HAY>
A; Cross-references: GB: BA000007; PIDN: BAB34843.1;
A; Cross-references: Strain O157:H7, substrain F
                                                                                                                                                                                                                                                                                                       A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D90806
                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change C;Accession: D90806  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.;
                                                                                                                                                                      A; Gene:
                                                                                                                                                                                        A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species:
C;Date: 18-
                                                                                                                                                                                                                                                                                                                                                                       gasawara, N.; Yasunaga,
DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          curlin major subunit CsgA [imported] C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-133,'RORDSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424;
A;Experimental source: strain K-12, substrain
                                                                                     Query Match
Best Local S
Matches 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Deecription: major component of wild-type curli; interaction between CsgA and Cs; A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 21-42;44-50 <OLS2>
R;Olsen, A.N.; Arnqrist, A.M.
submitted to the BMBL Data Libb
A;Reference number: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 23.15
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A; Residues: 21-4;
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                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                             MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADYGQGADNSTIELTQNGFRNNATIDQWNAKNSDITYGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                      Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                                     Conservative
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                                                                               Score 501.5; DB 2
Pred. No. 1.6e-34;
1; Mismatches 30
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No. 4.7e-36;
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ж.,
                                                                                                                     152;
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Shinagawa,
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QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG

119

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R;Taylor, F.M.; Martindale, D.W.

Nucleic Acids Res. 21, 4610-4614, 1993

A;Title: Retroviral-type zinc fingers and glycine-rich repeats in a protein encoded by A;Reference number: $42135; MUID:94051569; PMID:8233798

A;Recession: $42135

A;Accession: $42135

A;Accession: $42135

A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-4;Accession: $164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-4;Accession: $164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-4;Accids Res. 1164-1174;1179-1198

A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.

A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.

A;Reference number: $03650; MUID:88189811; PMID:3357771

A;Recession: $03650

A;Molecule type: DNA

A;Residues: 236-250,'I',252-255,'N',257-773 <MAR>
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C;Date: 19
C;Accessic
R;Taylor,
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S42136
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1748 <TAY>
A;Cross-references: EMBL;L03710; NID:g161751; PID:g161752
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A;Residues: 1-152 <STO>
A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1;
A;Experimental source: strain O157:H7, substrain EDL933
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hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain
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;Species: Tetrahymena thermophila 
;Date: 19-Mar-1997 #sequence_revision 
;Accession: S42136; S42135; S03650 
;Taylor, F.M.; Martindale, D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
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65.8%; Pred. No. 1.6e-34;
cive 21; Mismatches 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       October 1992
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K.; Apodaca
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A; Residues: 1-2174 < KUR>
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F;1451-1464/Region: zinc finger CC
F;1478-1491/Region: zinc finger CC
F;1591-1514/Region: zinc finger CC
F;1530-1543/Region: zinc finger CC
F;1555-1568/Region: zinc finger CC
F;1579-1592/Region: zinc finger CC
F;1579-1615/Region: zinc finger CC
F;1602-1615/Region: zinc finger CC
F;1602-1615/Region: glycine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: strain 1021, megaplasmid pSymB R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N. L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; A;Title: The composite genome of the legume symbiont Sinorhizobium mel A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. UC.S.A. 98, 989-994, 2001
A;Title: The complete sequence of the 1,683-kb psymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
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                                                                                                                                                                                                                                  11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET
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                                                                                                                                                                    AIATAGAGAVGILAQSIGGGGGN----GGNATGGDAGFGSFQIGGGGGG---
                                                                               TITQSGYGNGADVG-----
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13; Mismatches
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2174;
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                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.; Vorholter, F.J.; Herna
                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.; Komp, C.; Lelaure .H.; Wong, K.; Yeh, K meliloti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.; Fisher, R.F.
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793
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Graphin protein agfB precursor - Salmonella enteritidis
Graphin protein agfB precursor - Salmonella enteritidis
Graphin protein agfB precursor - Salmonella enteritidis
Graphin Salmonella enteritidis
Graphin J.Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
Gracession: JC6040
Gracession: JC60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Function:
A;Description: minor component of thin aggregative fimbriae
A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: agfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; A;Experimental source: strain 276755-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-151 <C'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Salmonella enteritidis agfBAC operon encoding thin, A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6040
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A; Residues: 1-151 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: STY1180
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A;Accession: AH0635
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                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-151/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keywords: fimbria
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                                                                                                                                                                                                                                                                                                                                       Local
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                                                              107 NAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAH 142
108 AYGNSAAIIQKGSGNKANITQYGTQKTAVVVQKQSH 143
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                                                                                                                                                                                                          IYQYGSANAALALQSDARKSETTITQSGYGNGADYGQGADNSTIELTQNGFRNNATIDQW 106
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                                                                                                                                        IGQVGTDNSA-RVRQEGSKLLSVISQEGGNNRAKVDQAGNYNFAYIEQTGNANDASISQS
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                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                            12.9%; Score 100.5; D; 30.2%; Pred. No. 0.18; Eive 17; Mismatches
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; Pred. No. 0.15;
17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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EMBO J. 10, 2259-2266, 1991
A;Title: The ovo gene of Drosophila encodes a zinc finger protein required for female
A;Reference number: S16356; MUID:91293102; PMID:1712294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
S16356
                                                                                                                                                                                                                           A; Cross-re:
A; Introns:
                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1213 <MEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ovo protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S16356
                                                                                                                                                                                                                                                              A;Gene: FlyBase:ovo
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C;Species: Drosophila melanogaster
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
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A56038
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A; Residues: 1-1028 < GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Multiple products from the shavenbaby-ovo gene A;Reference number. A56038; MUID:95021209; PMID:7935398 A;Accession: A56038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: A56038
                                                                                                                                                   Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                           Cross-references: FlyBase:FBgn0003028 Introns: 931/3; 1152/3
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Cell. Biol. 14, 6809-6818, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                             422
                               63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 GQFNASAY 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 NNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 NNNNNNGGQTSMMGHPFYGGNPSAYGIILKDEPDIEYDEAKIDIGTFAQNIIQATMGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI-----
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                                                                             LQNAAAAAYIMSAGSG
                                                                                                        LLKVAAFAAIVVSGSALAGVVFQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQSD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TVGQ------YGGNNAAL------VNYDQ-----LVTRVVTHEMAHA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GENGYINCGGVG-GPNNS---LDGNNLLNFASVSNYNESNSKFHNHHHHHOH 152
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                                                                                                                                                   Conservative
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---GGNGYINCGGVG-GPNNS---LDGNNLLNFASVSNYNESNSKFHNHHHHHQH
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24.5%;
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                                                                                                                                             Score 98.5; DB
Pred. No. 2.8;
15; Mismatches
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Pred. No. 2
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                                                                       GGGCTGNGGGGASGPGGGPSANSGGGGGGG-----
                                                                                                                                                                                  DB 2;
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                                                                                                                                                 62;
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A; Molecule type: DNA
A; Residues: 1-145 < KI
A; Cross-references: (
C; Genetics:
A; Gene: AGR L 228
A; Map position: line:
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                               hypothetical protein AGR_L_228 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C;Accession: H98144
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H98144
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A;Status: prelimina
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A; Residues: 1-145 < KUR>
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A;Authors: Yoo, H.; Tao, Y.; Biddle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: AD3143
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefacien C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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Best Local S
Matches 38
                                                                                                                                               Residues: 1-145 < KUR>
                                                                                                                                                                                   Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                      Query Match
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38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIRKSFIASALVALVGLSAAAPAMANDVRIEQYGWSNSAGGAQEGYGNRIRTYQNGGYNR
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                                                                                                                             GB:AE007870;
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               12.3%;
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   23;
Score 96; DB
Pred. No. 0.41
23; Mismatches
                                                                                                                             PIDN: AAK88682.1;
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Pred. No. 0.
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                 DB 2;
0.41;
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Kutyavin, T
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   59;
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                                                                                                                             GSPDB:GN00170
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ckelz, B.;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1238 <KUR>
A;Cross-references: GB:AL590842;
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R;Parkhill, J.;
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Title: Genome sequence, MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                             R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barr
                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable exported protein YPO0309 [imported] - Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
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#sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
               PIDN:CAC89171.1;
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Query Match 12.0%; Score 93.5; DB 2; Length 1238; Best Local Similarity 25.1%; Pred. No. 7.3;	gth 1238;
Matches 45; Conservative 19; Mismatches 48; Indels (	dels 67; Gaps 9;
Qy 7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSG	SSG
	ITAMSSGISLINEANQG 464
QY 42 DSTLSIYQYGSANAALALQSDARKSET	LALQSDARKSETTITQSGYGN 77
Db 465 TSTADITVTGQINVSHGEGITLNALTTDGRTLVNVDVNNIASEYDAIRLYNYNYNDNYAT 524	:
QY 78 GADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAAL 125	DITVGQYGGNNAAL 125
Db 525 GVDDGTGADNGTSTIDLITRGALVSQQGYGINIETNTADTYVTVGGLVHGGNGTAI 580	:    :     : !VTVGGLVHGGNGTAI 580
Search completed: March 11, 2004, 18:42:06 Job time : 11.3 secs	

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Result

Database

Searched:

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# ALIGNMENTS

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N.A. ni; STRAIN=Ty2 367; PubMed=12 SR., Plunke odoyianni V.,	; STRAIN=CTI1 ; STRAIN=CTI1 7; PubMed=111 vugan G., Jamu ngall K.L., J m D., Brooks s P., Davies mlin N., Haq mlin N., Leatl herford K., 1 arrell B.G.; arrell B.G.; e sequence o: r Typhi CT18	STRAI ed=945 ammar rly cor 731(19 731(19 .X.; .K.; nce of	OR OR
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)931; Mayhew G.F., Rose D.J., C., Blattner F.R.;	9; 577608; 577608; 577608; BK.D., Thomson N.R., Pickard D., Wain J., Bentley S.D., Holden M.T.G., Sebaihia M., K., Chillingworth T., Connerton P., R.M., Dowd L., White N., Farrar J., Le A., Hien T.T., Holroyd S., Jagels K., Ler S., Moule S., O'Gaora P., Parry C., Simmonds M., Skelton J., Stevens K.,  E a multiple drug resistant Salmonella .";	ralta W.D., Normark S.; etween Salmonella typhimurium and etween Salmonella typhimurium and ron structure and regulation.";  SGSC1412 / ATCC 700720; h J., Clifton S.W., Latreille P., ante M., Du F., Hou S., Layman D., mes A., Grewal N., Mulvaney E., "., Stoneking T., Nhan M., !lla enterica serovar Typhimurium	51 AA. ddate) update) n SEF17). T1776.

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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emoedy L., Mueller K.-M., T:
"Purification and characterization of thin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., "DNA-based diagnostic tests for Salmonella species the structural gene for thin, aggregative fimbriae J., Clin. Microbiol. 31:2263-2273(1993).
                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
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3L; AE008749; AAL20074.1; -.
3L; AL627269; CAD08268.1; -.
3L; AE016840; AA069399.1; -.
3L; U43280; AAC43599.1; -.
3L; JC6039; JC6039.
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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Signal; Complete
NNAAL VNQTASDSSVMVRQVGFGNNATANQY
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SVMVRQVGFGNNATANQY ->
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Salmonella enteritidis.";

J. Bacteriol. 173:4773-4781(1991).

-:- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.

-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A

TEMPERATURES BELOW 37 DECREES CELSIUS. CURLI CAN BIND TO

FIBRONECTIN.
                                                                                                                                   MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emoedy L., Trust T.J.,
"Purification and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                       Arnqvist A., Olsen A., Pfeifer J., "The Cr1 protein activates cryptic fibronectin binding in Escherichia Mol. Microbiol. 6:2443-2452(1992).
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STRAIN=KIZ / MC4100;
MEDLINE=96414468; PubMed=8817489;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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STRAIN=K12 / MG1655;
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STRAIN=K12 / MC4100;
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Olsen A., Arnqvist
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RpoS sigma factor relieves H-NS-mediated transcriptional
ession of csgA, the subunit gene of fibronectin-binding c
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Q93U24;
28-FEB-2003
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            MEDLINE-21074935; PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans R.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.
                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-0157:H7 / ATCC 43895;
MEDLINE-21218556; PubMed=11319125;
MILCH G.A., Keen J.E., Elder R.O.;
"Mutations in the cegD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7."
Appl. Environ. Microbiol. 67:2367-2370(2001).
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SEQUENCE
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28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
Escherichia coli 0157:H7.
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EMBL;
EMBL;
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X90754; CAA62282.1; -.
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(C. STRAIN;-0157:H7 / RUMD 0509952;

(C. STRAIN;-0157:H7 / Rubdo E., Nakayama K., Kurokawa K., Ishii K., Yokoyama K., Hangashi T., Makaino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Iida T., Takami H., Hattori M., Shinagawa H.;

(T. Complete genome sequence of enterohemorrhagic Escherichia coli

(T. Complete genome sequence of enterohemorrhagic Escherichia coli

(T. O157:H7 and genomic comparison with a laboratory strain K-12.";

(DNA Res. 8:11-22(2001).

(C. PINCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI

(C. COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWT

(C. TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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SEQUENCE FROM N
STRAIN=0157:H7
STRAIN=CT18;
MEDLINB=21534947; PubMed=11677608;
MEDLINB=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wai
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
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Best Local S
Matches 29
SPECIES-S.typhimurium; STRAIN-SR-11;
MEDLINB-98117058; PubMed-9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium as Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                       Salmonella typhimurium, Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSGB
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-i- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.

-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A

TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO

FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
                                                                                                                                                                                                                                                    Enterobacteriaceae; Salmonella
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Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL627269; CAD08267.1; -. EMBL; AE016840; AAO69400.1; -.
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STRAIN=Ty2 / ATCC 700931;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyo
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora
Quail M.A., Rutherford K., Simmonds M., Skelton J.,
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                imbria; Signal; Complete proteome
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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OC Eukar
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OX NCBI
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JORONE
JORONE
SIGNATURA
STREET
STREET
TO1-CCT-1996 (Rel. 34, Created)
TO1-CCT-1996 (Rel. 34, Last sequence update)
TO1-CCT-2003 (Rel. 42, Last annotation update)
(Shaven baby protein).

Neoptera; Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila. NCBI\_TaxID=7227;

Arthropoda; Hexapoda;

Muscomorpha;

Drosophila melanogaster Eukaryota, Metazoa, Arth

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Best Local S
Matches 29
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                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                           EMBL;
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SEQUENCE FROM N.A.
SPECIES-S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
SPECIES-S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., La
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S.
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=96146512; PubMed=8550497; Collinson S.K., Clouthier S.C., Doran J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eimbriae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 178:662-667(1996). FUNCTION: CURLIN IS THE STRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
                                                                                                                                                                                                                                                            JC6040; JC6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURLIN MONOMERS
                                                                                                                                                                                                                                                                      AJ002301; CAA05316.1; -.
AE008749; AAL20073.1; -.
U43280; AAC43598.1; -.
                                                              49
                                                                                           47
                                                                                                                                      Similarity
AYGNSAAI I QKGSGNKANI TQYGTQKTAVVVQKQSH
                              NAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAH
                                                                                      IYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQW
                                                           IGQVGTDNSA-RVRQEGSKLLSVISQEGGNNRAKVDQAGNYNFAYIEQTGNANDASISQS
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151 AA;
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agfBAC operon encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Salmonella enterica serovar Typhimurium
                                                                                                                                    Score 100.5;
Pred. No. 0.
                                                                                                                                                                                               POTENTIAL.
MINOR CURLIN SUBUNIT.
                                                                                                                                                                                 COFC5430E6DD361D CRC64;
                                                                                                                       Mismatches
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                                                                                                                                                 DB 1;
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                                                                                                                       49;
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COMPONENT OF
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STRAIN=Oregon-R;
MEDLINE=9193102; PubMed=1712294;
MEVEl-Ninio M.T.M., Terracol R., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; Multiple products from the shavenbaby-ovo gene regulationship to genetic complexity."; Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00355; ZDF C2H2; 4.

PROSITE; PS00028; ZNC FINGER C2H2 1; 3.

PROSITE; PS50157; ZNC FINGER C2H2 2; 3.

Zinc-finger; Metal-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007087; Znf_C
Pfam; PF00096; zf-C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T00669; -. FlyBase; FBgn0003028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U11383; AAB60216.1;
EMBL; X59772; CAB36921.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for female germ line development."; EMBO J. 10:2259-2266(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95021209; PubMed=7935398; Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A56038; A56038.
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TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.
SUBCELLULAR LOCATION: Nuclear (Potential).
DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING COGENESIS. STORED IN THE BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 4 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l-Ninio M.T.M., Terracol R., Kaf
ovo gene of Drosophila encodes
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     C2H2
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C2H2-TYPE 1.
C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
A -> R (TW
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RESULT 7
OMPB_RICJA
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            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen S) (Sca5) (rOmpB) (Contains: 120 kDa surface-exposed protein (Surface protein compB) (120 kDa outer membrane protein ompB); 32 kDa beta peptid
                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                           (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is layer with hexagonal symmetry.
                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OMPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     006653;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                      Antigen;
                                       TIGRFAMs; TIGRO1414; autotrans_barl;
Antigen; S-layer; Cell wall.
                                                                                                          EMBL; AB003681; BAA20138.1;
                                                                                                                                    entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                            the European Bioinformatics Institute. These by non-profit institutions as long
                                                                                                                                                                                                                                                                                                   similarity).
-!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-YH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMPB RICJA
                                                                                            InterPro;
                                                                                                                                                              modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                              "Sequencing of the gene encoding the protein rOmp
                                                                                                                                                                                                                                                                                                                                                                                                              Uchiyama T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia
                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                   japonica."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                         FUNCTION: THE 120 kDa SURFACE-EXPOSED PRO
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING
                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 NNATANOY
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                                                                 Pro; IPR006315; Autotransport.
Pro; IPR005546; Autotransporter.
Pr03797; Autotransporter; 1.
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32 kDa BETA PEPTIDE.
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DLE AS A RICKETTSIAL
ING INFECTION (BY
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kDa beta peptide].
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Best Local
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                              Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S. Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical a laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harr. Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroy. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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Q10778;
Q10778;
                           EMBL; AE007026; AAK45866.1; PIR; A70762; A70762.
                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CDC 1551 /
MEDLINE=22206494;
                                                                                    EMBL; Z74020; CAA98335.1;
                                                                                                                                             or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1548c/MT1599,
RV1548C OR MT1599 OR MTCY48.17.
Mycobacterium tuberculosis.
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                                                                                                                                       equires a license agreement (S email to license@isb-sib.ch).
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InterPro; IPR000030; Microbac_PPE.
InterPro; IPR002989; Mycobac_Dentapep.
Pfam; PF01469; Pentapeptide_2; 11.
Pfam; PF00823; PPE; 1.
Pfam; PF00823; PPE; 1.
Pfam; PF01823; PPE; 1.
Pfam; PF01821; PF018271AL.
TRANSMEM 14 34 POTENTIAL.
                                              at human
Mol. Cell
-!- FUNCT
                                                                                                                                                                                    MEDIJINE-20556282; PubMed=10900227,
Chi N.-W., Lodish H.F.;
"Tankyrase is a Golgi-associated mitogen-activated substrate that interacts with IRAP in GLUT4 vesicle substrate that interacts with IRAP in GLUT4 vesicle T Riol. Chem. 275:38437-38444(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _HUMAN
_TNK1_HUMAN
_O95271; O95272;
                                                                                                     MEDLINE=21602874; PubMed=11739745; Cook B.D., Dynek J.N., Chang W., Shostak G., Smith "Role for the related poly(ADP-Ribose) polymerases
                                                                                                                                                                                                                                                                                                                                                                                          Smith S., de Lange T.;
"Cell cycle dependent localization
to nuclear pere complexes and cent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tankyrase 1 (EC 2.4.2.30) (TANKI) (Tankyrase I) (TI Tankyrase I) (TO TINES OR TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith S., Giriat I., Schmitt A., de Lange "Tankyrase, a poly(ADP-ribose) polymerase science 282:1484-1487(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                     FUNCTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99454782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99040105; PubMed=9822378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSUE=Testis;
                  FUNCTION: May regulate vesicle trafficking and modulate subcellular distribution of SLC2A4/GLUT4-vesicles. Has I
                                                                man telomeres.";
Cell. Biol. 22:332-342(2002).
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                                                                                                                                                                          AND MUTAGENESIS OF HIS-1184 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                     AND PHOSPHORYLATION
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258
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258
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25.7%;
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Pred. No. 1.5;
24; Mismatches
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                                                                                                       S.;
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| Nuclear protein; Repeat; ANK repeat; ADP | Phosphorylation; Alternative splicing. REPEAT 215 247 ANK 1. | ANK 1. | REPEAT 248 280 ANK 2. | REPEAT 248 280 ANK 3. | REPEAT 368 400 ANK 3. | REPEAT 401 433 ANK 5. | REPEAT 434 466 ANK 7. | REPEAT 521 556 ANK 7. | REPEAT 521 556 ANK 9. | REPEAT 590 622 ANK 9. | REPEAT 683 715 ANK 10. | REPEAT 716 748 ANK 11. | REPEAT 726 868 ANK 11. | REPEAT 736 868 ANK 11. | REPEAT 836 868 ANK 11. | REPEAT 836 868 ANK 13. | REPEAT 846 868 ANK 14. | REPEAT 859 901 ANK 15. | REPEAT 869 9
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EMBL; AF082557; AAC79842.1; -.
EMBL; AF082558; AAC79843.1; -.
EMBL; AF082559; AAC79844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50088; ANK_REPEAT; 15.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50105; SAM_DOWAIN; 1.
Transferase; GlycosylTransferase; NAD; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1415; ANKYRIN SMART; SM00248; ANK; 17. SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00023; ank; 19.
Pfam; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (s or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:000781; C:chromosome, telomeric region; IDA. GO:0003950; F:NAD ADP-ribosyltransferase activity; GO:0005515; F:protein binding; IPI. GO:0007004; P:telomerase-dependent telomere mainten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by MAPK kinases
PTM: ADP-ribosylated (-auto).
SIMILARITY: Belongs to the PARP family.
SIMILARITY: Contains 15 ANK repeats.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nicotinamide + {ADP-D-ribosyl}{(N+1)-acceptor.
SUBNNIT: Oligomerizes and associates with YMKS2. Interacts with the cytoplasmic domain of LNPEP/Otase in SLC2A4/GLUT4-vesicles.
Binds to the N-terminus of telomeric TRF1 via the ANK repeats.
SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative
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CATALYTIC A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:11941; TNKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (soId=O95271-2; Sequence=VSP_004538, VSP_004539)
tote=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIFICITY: Ubiquitous; highest levels in testis.
pon insulin-stimulation, phosphorylated on serine r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n of telomere length.
ACTIVITY: NAD(+) + {
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RESULT 10
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SEQUENCE FROM N.A.,
STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Arngvist A., Bian Z., Olsen A., Normark S.;
Hammar M., Arngvist A., Bearns is required for production of two csg operons is required for production are congored-binding curli polymers in Esche
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01-FEB-1995
01-OCT-1996
                                                                                                                                                        Gregor J.,
Mau B., Sha
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T., Yano M., Horiuchi T., Rajihaka M., September Scherichia coli K-12 genome
                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Escherichia coli, and
Escherichia coli 0157:H7.
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Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., R
                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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H->A: LOSS OF ACTIVITY;
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Matches
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"Sigma S-dependent growth-phase induction
"Scherichia coli can be achieved in vivo )
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[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arnqvist A., Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=0157:H7 / KIMD UJUJUT.
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
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MEDLINE=21074935; PubMed=11206551;
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L; D90741; BAA35831.1; -
L; AE005315; AAG55787.1; -
L; AE005315; AAG55787.1; -
L; AP002554; BAB34842.1; -
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G85665; G85665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        herichia coli can be achieved in vivo by sigma 70 in the the nucleoid-associated protein H-NS.";
Microbiol. 13:1021-1032(1994).
FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
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                                       FAVNELSKSSFNQAAII---GQAGTNNSAQLRQGGSKLLAVVAQEGSSNRA-KIDQTGDY
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17; Mismatches
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Q03646;
Q1-OCT-1996 (Rel. 3
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01-OCT-1996 (Rel. 3
Merozoite surface a
MEDLINE=91156685; PubMed=2000383; Smythe J.A., Coppel R.L., Day K.P., Kemp D.J., Anders R.F.;
                                                                                                              Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=70150;
                                                                       SEQUENCE FROM N.A.
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SEQUENCE 262
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SEQUENCE FROM N.A.

MEDIJINE-87283911; PubMed=3302276;

Riede I., Drexler K., Eschbach M.L., Henning U.;

Rink sequence of genes 38 encoding a receptor-recognizing probacteriophages T2, K3 and of K3 host range mutants.";

J. Mol. Biol. 194:31-39(1987).

J. Mol. Biol
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Pfam; PF05268; GP38; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, T4-like viruses.
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or send a
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SPECIES=M.tuberculosis; STRAIN=H37Rv; MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Ga
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FUNCTION: May play a role in the merozoite a
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Matches 30
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Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey B.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J., Rutter. S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.S., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                         EMBL; Z73966; CAA98228.1; ALT_FRAME. EMBL; AE007065; AAK46440.1; -- EMBL; EX248341; CAD96978.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as a modified and this statement is not removed. Us entities requires a license agreement (See http
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=M.bovis; STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Gryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY.
                                                                                                                                                                                                           Hypothetical protein; CONFLICT 312 31:
                                                                                                                                                                                                                                        Pfam; PF00934; PE; 1.
ProDom; PD001223; PE_region; 1.
                                                                                                                                                                                                                                                                                                            TIGR; MT2159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                            TubercuList; Rv2098c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                           send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFAMILY.

SUBFAMILY.

CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 59. Ref.1 sequence has been checked authors in Ref.1 and they report that no errors have been f
265
                                                                                                                                                                                                                                                                                                                        AE007065; AAK46440.1; -. BX248341; CAD96978.1; -.
                              75
                                                                                                                                                                                                                                                                                                                                                                                           an
                                                                                                                                            Similarity
                                                                                                                                                                                                                                                         St; N. ...; IPR000084; Pr
YGNGGAAGSGGNGGDAGTGVSSDGF---AGLGGSGGRGGDAGLIGVGGGGGN
                              YGNGADVGQGAD--NSTIELTQNGFRNNATIDQWNAKNSD---ITVGQYGGN
                                                              AGLIGHGGAGGNGGDGGHGGSGKAGGSGGSGGFGQFGGAGGLL.
                                                                                           AGVVPQWGGGGN----
                                                                                                                                                                                                                                                                                                                                                                                          email to license@isb-sib.
                                                                                                                                                                                             491
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184:5479-5490(2002).
                                                                                                                                                                                            AA,
                                                                                                                                                                                            41979 MW;
                                                                                                                                            11.3%;
                                                                                                                                                                                                                                                                          PE_region
                                                                                                                                                                                          HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG
                                                                                                                             13;
                                                                                                                                           Score
Pred.
                                                                                                                               Mismatches
                                                                                                                                            No ,
                                                                                                                                                                                                                                                                                                                                                                                             ch)
                                                                                                                                                                                                                                                                                                                                                                                                         moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                              w
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                                                                                                                                                            DB 1;
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6.
                                                                                                                             . 39;
                                                                                                                                                            Length 491,
                                                                                                                                                                                            CRC64;
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empe C., Simon
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Matches
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Best Local (
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SEQUENCE
                                                                                                                                                                                                                                                                         SIGNAL
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PRINTS; PR00182; ECOLNEIPORIN.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
Outer membrane; Porin; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CU385 / Serogroup B / Serotype 4 / Subty
MEDLINE=93116587; PubMed=1335540;
Zapata G.A., Vann W.F., Rubinstein Y., Frasch C
"Identification of variable region differences
meningitidis class 3 protein sequences among fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ward M.J., Lambden P.R., Heckels J.E.; "Sequence analysis and relationships between meningococcal class 3 serotype proteins and other porins from pathogenic and non-pathogenic Neisseria species."; FEMS Microbiol. Lett. 73:283-289(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMB2_NEIMB STANDARD; PRT; 331 AA. P30688; O1-APR-1993 (Rel. 25, Created) O1-APR-1993 (Rel. 25, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Major outer membrane protein P.IB precursor (Protein IB) (PIB) (PDFin) (Class 3 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a

    -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer
    -!- SIMILARITY: Belongs to the Gram-negative porin family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Serves as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serotypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CCUG 37604 / M981 / Serogroup B / MEDLINE=93051225; PubMed=1330818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
Neisseriaceae; Neisseria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                          IR; S28441; S28441.
InterPro; IPR001702; Porin_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homotrimer
    128
                                                                                                                                                                                                                                                                                                                                                                      ; X65531; CAA46501.1;
S21409; S21409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Microbiol. 6:3493-3499(1992).
UNCTION: Serves as a slightly
                                                                                     54
                                                           70
                                                                                                                  13
                                                                                                                                           4
                                                                                                                                                                       42;
                                                                                                                                                                                      Similarity
KSDYLGVNKIAEPEARLISVRYDSPEFAGLSGSVQYALNDNAGKY
                                                                                                          LKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGS-
                            KNSDITVGQYGGNNAAL--VNYDQLVTRVVTHEMAHANNATANQY
                                                      NGLKAIWQVEQKASIAGTDSGWGNRQSFIGLKGGFG--KLRVGRLNSVLKDTGDINPWDS
                                                                                   NAALALOSDARKSETTITOSGYGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
J385 / Sei
                                                                                                                                                                                                                              331 AA;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                             70
                                                                                                                                                                                                                            35741 MW;
                                                                                                                                                                                    11.2%;
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                                                                                                                                                                                                                                                                                                                                         Gram-ve
                                                                                                                                                                    Score 87; DB
Pred. No. 2.8;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          is not removed.
                                                                                                                                                                                                                                          MAJOR
NG ->
                                                                                                                                                                                                                           35EA35B7EBD28301 CRC64;
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                                                                                 -GADVGQGADNSTIELTQNGFRNNATIDQWNA
                                                                                                                                                                                                                                                                                  Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                            (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         among five group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration
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S В Ś B Ś

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EMBL; U51055; J
EMBL; U51056; J
EMBL; U51057; J
EMBL; U51058; J
EMBL; U51059; J
EMBL; U51061; J
EMBL; U51061; J
EMBL; U51062; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERCEPTION: Essential for biological clock functions. Determines the period length of circadian and ultradian rhythms; an increase in PER dosage leads to shortened circadian rhythms and a decrease leads to lengthened circadian rhythms. Essential for the circadian rhythmic component of the male courtship song that originates in the thoracic nervous system. The biological cycle depends on the rhythmic component of the male courtship song that originates in the thoracic nervous system. The biological cycle depends on the rhythmic formation and nuclear localization of the TIM-PER complex. Light induces the degradation of TIM, which promotes elimination of PER. Nuclear activity of the heterodimer coordinatively regulates PER and TIM transcription through a negative feedback loop. Behaves as a negative element in circadian transcriptional loop. Does not appear to bind DNA, suggesting indirect transcriptional inhibition (By similarity).

-i. SUBUNIT: Forms heterodimer with timeless (TIM); the complex then translocates into the nucleus (By similarity).

-i. SUBCILIUAR LOCATION: Nuclear at specific periods of the day.

-i. SUBCILIUAR LOCATION: Nuclear at specific periods of the day.

-i. SUBCILIUAR LOCATION: Nuclear at specific periods of the day.

-i. SUBCILIUAR LOCATION (By similarity).

-i. SUBCILIUAR LOCATION (By similarity).

-i. SUBCILIUAR LOCATION (By Similarity).

-i. PIM: PEROSPHORYLATED WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLATION COULD BE IMPLICATED IN PER-TIM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular evolution Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93196482;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN ATLIXCO.

MISCELLARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evol. 14:741-753 (1997).
AAB41360.1; -... AAB41361.1; -... AAB41363.1; -... AAB41363.1; -... AAB41365.1; -... AAB41365.1; -... AAB41367.1; -... AAB413
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PubMed=8450754;
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1; P91722;
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G -> V (IN STRAIN PORTO ALEGRE 4).

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S -> A (IN STRAINS GUADELOUPE AND GUANA).

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12	11	10	9	80	7	σ	υī	4	u	N	_	Result
104	104.5	105	105	106	107	108.5	113.5	113.5	122	385	427.5	495.5	537	591.5	686	Score
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Q92uu8 rhizobium m	Q841y5 campylobact	Q8zn57 salmonella	Q9xcj4 salmonella	Q94821 tetrahymena	Q8eih4 shewanella	Q7xdr3 oryza sativ	Q8xsd6 ralstonia s	Q8y106 ralstonia s	Q9s3j5 escherichia	Q54069 salmonella	Q7x237 enterobacte	Q8cw63 escherichia	Q7x240 citrobacter	Q7x243 citrobacter	O33802 salmonella	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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12.1	12.1	12.1	12.2	12.2	12.2	12.3	12.3	12.3	12.3	12.3	12.4	12.5	12.5	12.5	12.5	12.5	12.6	12.6	12.6	12.6	12.6	12.7	12.8	12.8	12.9	13.1		13.2
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Q9ngf7 drosophila	Q9ngf6 drosophila	Q8cw64 escherichia	Q9kkb4 rickettsia	Q840u5 rickettsia	Q8ev84 mycoplasma	Q9kka8 rickettsia		Q89ji4 bradyrhizob		Q8u6n9 agrobacteri	Q7x238 enterobacte	Q9kkb1 rickettsia	Q98ln6 rhizobium l	Q9x687 salmonella			Q7uwz8 rhodopirell	Q8mpn4 drosophila		Q8t819 drosophila	Q9w4f0 drosophila	Q7v8s5 prochloroco	Q7x244 citrobacter	O33801 salmonella	Q7x241 citrobacter	Q8efu3 shewanella	Ħ	Q8eih3 shewanella

### ALIGNMENTS

3802 033802 033802 01-JAN-19 01-JAN-19 01-DEC-20 AgfA prota AgfA, Enterobac NCBI_TAXI Enterobac NCBI_TAXI II II II SEQUENCE MEDLINE-9 Sukupolvi Normark Sells."; Infect. I EMBL; Infect. I EMBL; Salmonell Sells."; Infect. I EMBL; Salmonell Cells."; Infect. I EMBL; Salmonell Sells."; Infect. I EMBL; Infect. I I EMBL; Infect. I I EMBL; Infect. I I I I I I I I I I I I I I I I I I I	0	-	_	_	_			re		н	<b>~</b>	-	<b>.</b>	-	-	<b>+</b>	,,,		+	_	_	_	_	_	_	_	<b>-</b> .	٠,		<u>.</u>	~ <del>~</del>
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EMBL, AJ515701; CAD56675.1:
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EMBL; AJ515700; CAD56672.1; -
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Bacteria; Proteobacteria;
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77.5%;
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ose and Curli Fimbriae by Members of the Family
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                                                                        Score 537; DB
Pred. No. 9.7e
17; Mismatches
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. No. 9.7e-34;
ismatches 24;
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AC Q7X2
DT 01-0
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DT 01-0
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GN CSGA
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RP SEQU
RC STRA
RA Zoga
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Best Local
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01-OCT-2003
01-OCT-2003
01-OCT-2003
  STRAIN=Fec39;
Zogaj X., Bok
                                                                                    NCBI_TaxID=28141;
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Q8CW63;
01-MAR-2003
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    Bokranz
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RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesc RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., RAM Mayhew G.F., Rose D.J. Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome of uropathogenic Escherichia coli.";
RI Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CM Complete proteome.
COMPLEX PROC. MAN 19:17020-17024(2002).
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                                SEQUENCE FROM N.A.
                                                                                                Bacteria; Proteobacteria;
                                                                               Enterobacteriaceae;
                                                                                                                Enterobacter sakazakii.
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Enterobacteriaceae; Escher
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                                                                                                                                                                                                                                                                                                            GGNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                                                                                                                                                                                                                                                                             GNNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAIAATVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAQ 60
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3 (TrEMBLrel. 23, 1
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                                                                                 Enterobacter.
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21; Mismatches
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annotation updat
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RESULT 7
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AC Q9S3
OT 01-M
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Best Local S
Matches 88
                                                                              Q9S3J5 PRELIMINARY;
Q9S3J5;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
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Curlin subunit monomer (F
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Q54069;
01-NOV-1996
01-NOV-1996
01-DEC-2001
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NON_TER
SEQUENCE
                     Escherichia coli
Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Production of Cellulose and Curli Fimbriae Enterobacteriaceae Isolated from the Human G Infect Immun. 72:4151-4158(2003).
EMBL; AJ515702; CAD56678.1; -.
  Enterobacteriaceae;
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Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                         GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQQADNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNAALVNYDOLVTRVVTHEMAHANNATANOY
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                                                                                                                                                                                                                                                                                                                    IELTQNGFRNNATIDQ
                                                                                                                                                                                                                                                                                                                                                                                 GNHXGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST
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76 AA;
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6 (TrEMBLrel.
1 (TrEMBLrel.
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  Escherichia
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Last annotation updat
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                                                                                                                                                Created)
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Pred. No. 1.9e
0; Mismatches
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                        Enterobacteriales;
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RESULT 8
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Best Local S
Matches 26
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                               EMBL; AL646061; CAD14589.1; -.

GO; GO:0004519; F:endonuclease activity; IE
GO; GO:0003676; F:nucleic acid binding; IE
InterPro; IPR001604; Endonuclease.
InterPro; IPR008619; Fil_haemagg.
InterPro; IPR008619; Fil_haemagg act.
Pfam; PF05594; Fil_haemagg act.
Pfam; PF05594; Fil_haemagg; IO.
PF0SITE; PS01070; NUCLEASE NON SPEC; 1.
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Q8Y106;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                               Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21681879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mar
Salanoubat M., Brottier P., Camus J.C., Cattol
Arlat M., Billault A., Brottier P., Camus J.C., Cattol
Chandler M., Choisne N., Claudel-Renard C., Cunnac S.
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy
Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation updat Probable hemagglutinin-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli 078:K80 isolates associated
"Inserti on in csg8 and reduced persistence in poultry infect
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1; -.
NON_TER 29 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the plant pathogen Ralstonia Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderiaceae; Ralstonia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
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3501 AA
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                                                                                                                                                                             SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA----
OYGGN
                                                                                      LALOSDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDOWNAKNSDITVG
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                                            KSVQVQARTGDITVSGSGISALSDVDLLAKQGKVDIVAGNDTSSRHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 AA; 2789 MW;
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121
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                                                                                                                                                                                                                                 19;
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                                                                                                                                                                                                                                                    Score 113.5;
Pred. No. 8.
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Cattolico L.,
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Schiex T.,
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RESULT 10
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AC Q7XDR
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Matches
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative glycine-rich protein.
0SUMBB0039p10,07G10.
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S. Arlat M., Billault A., Brottier P., Camus J.C., Catcolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demang. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebbult P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum. Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable hemagglutinin-related protein.
RSP0540 OR RS06117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7XDR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid megaplasmid.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8XSD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBXSD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pro; IPR008619; Fil haemagg.
Pro; IPR008638; Haemagg act.
PP05594; Fil haemagg; Z0.
PF05860; Haemagg act; 1.
PF05860; Haemagg act; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 113.5;
Pred. No. 8.
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                                                                                                                    Tracheophyta;
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RESULT ORBITH ACT OF THE PROPERTY OF THE PROPE
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Best Local S
Matches 33
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Best Local :
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Q8EIH4;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                         Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
                                                                                                                                                                                                                                                            Hypothetical protein; Complete SEQUENCE 502 AA; 52441 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heidelberg J.F., Paulse
Read T.D., Eisen J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
Alteromonadaceae; Shewane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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STRAIN-cv. Nipponbare;
Buell C.R., Wing R.A., McCombie W.R., Messing
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ
EMBL; AE017101; AAD54078.1; -
EMBL; AE017101; AAD54078.1; -
                                                                                                                                                                                                                                                                                                           TIGR; S00865;
                                                                                                                                                                                                                                                                                                                                                Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MR-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shewanella oneidensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conserved hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22297686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=70863;
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                                                                                                                                                                                                                                                                                                                                                                                         Genome sequence of the dissimilatory metal ion-reducing
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SEQUENCE FROM N.A.
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    291
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                                                                                                                                                                                                                                                                                                                           AE015532; AAN53941.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                              Similarity
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QGDDNDITIKQKGDSNGAEFQVWGDSNDVDLKQRGDANFATFGAYGTDN-DFDLSSKGDN
                                        DARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN
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                                                                                    GDNHTGFVYALAGSENDISMEQEGSNNTAYLSMTTGDDNTVDITQDGDSNTVGDSLIADI
                                                                                                                                 GGNHNG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYCHCSGSCTCSGSSEATNTWYCQYANANAGGNGGGNGQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nippombare;
Nippombare;
Phromosome 10 Sequencing Consumpture, activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paulsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shewanella.
                                                                                                                                                                                            13.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eshadri R., Ward N., Methe B., Clayton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gammaproteobacteria;
                                                                                                                                                                          15;
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                                                                                                                                                                        Score 107; DB
Pred. No. 2.8;
L5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last
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Pred. No. 0.72;
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D08CA23D6C46B62D CRC64;
                                                                                                                          -GGN-----ALALQS
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                                                                                                                                                                        45;
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databases.
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                                                                                                                                                                   Gaps
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RESULT 13
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Best Local S
Matches 35
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"Retroviral-type zinc fingers and glycine-rich repenceded by cnlb, a Tetrahymena gene active during Nucleic Acids Res. 21:4610-4614(1993).

EMBL; X06462; CAB37333.1; --
EMBL; X06462; CAB37333.1; --
EMBL; X03710; AAC37171.1; --
EMBL; X03710; AAC37171.1; --
EMBL; S42136; S42136.

HSSP; P05888; 1AAF.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR001878; Znf_CCHC.
Pfam; PP00098; zf-CCHC.
Bacteria; Proteobacteria; G
Enterobacteriaceae; Salmone.
NCBI_TaxID=602;
                                                                                                                                                 Q9XCJ4;
Q9XCJ4;
01-NOV-1999
01-NOV-1999
01-MAR-2003
                                                                                                                                  ShdA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; ZnF C2HC; 7.
PROSITE; PS50158; ZF CCHC; 7.
CONFLICT 251 251 M
CONFLICT 256 256 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetrahymena thermophila.
Eukaryota; Alveolata; Cili.
Tetrahymenina; Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q94821; P92146; P92145; P92144; P92143; P92142; P
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=94051569; PubMed=8233798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Multiple introns in a conjugation-specific thermophila.";
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                                                                                                                                                      (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                   Gammaproteobacteria;
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Last sequence tast annoted
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H 3
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Pred. No. 14;
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annotation
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> N (IN REF. 1).
0B03F210104008A3 CRC64;
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ing meiosis
                                                                     Enterobacteriales;
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RESULT
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Best Loc
Matches
                                                  STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J.,
Courtney L., Porwollik S., Ali J., Dante N
Leonard S., Nguyen C., Scott K., Holmes A.
Ryan E., Sun H., Florea L., Miller W., Sto
                                                                                                                                                                                                                                                                                                                     Q8ZN57
Q8ZN57;
Q8ZN57;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to the C-terminal region of AIDA, IcsA, sub
Peyer's patch colonization and shedding factor.
SHDA OR STM2513.
"Complete LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1999) to the EMBL/GenB
EMBL; AF140550; AAD25110.2; -
InterPro; IPR0063115; Autotransport.
InterPro; IPR005346; Autotransporter.
InterPro; IPR005499; Pertactin.
InterPro; IPR002173; PfkB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR01414; autotrans_barl; 3. PROSITE; PS00584; PFKB_KINASES_2; 2. SEQUENCE 2035 AA; 207032 MW; 295DB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genus Salmonella.'
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                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                   Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF03797; Autotransporter; Pfam; PF03212; Pertactin; 1.
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STRAIN=ATCC14028;
                                         Waterston
                                                                                                                                                                                                                               NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kingsley R.A.,
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                    genome sequence of Salmonella
                                         R., Wilson R.K.;
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, Dante M., Du F., Hou
Holmes A., Grewal N.,
r W., Stoneking T., Nh
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EMBL; AEOC InterPro;

Autotransport

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01-JUN-2003 (
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                                                      MEDLINE=92394895; PubMed=1522068; Tummuru M.K., Blaser M.J.; "Characterization of the Campylobacter fetus that the sapA promoter is deleted in spontane J. Bacteriol 174:5916-5922(1992).
  SEQUENCE FROM N.A. STRAIN=23D;
                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                       structure.
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Pfam; PF03
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erPro; IPR006315; Autotransporter
erPro; IPR005546; Autotransporter
erPro; IPR004899; Pertactin.
erPro; IPR002173; PfkB.
erPro; IPR002173; PfkB.
erPro; IPR02173; PfkB.
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                                                                                                                                                                                                                                                                                           5477; PubMed=2229082; Gotschlich E.C.;
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mutant strains.";
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                                                                                                                                                                                                                                                                                                                                                             Blaser M.
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99069317; PubMed=9851986; Thompson S.A., Shedd O.L., Ray K.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   "A lipopolysaccharide-binding domain of the Campylobacter layer protein resides within the conserved N terminus of a silent and divergent homologs.", J. Bacteriol. 177:1734-1741(1995).
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Dworkin J., Tummuru M.K., Blaser M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93348254; PubMed=8346244;
Tummuru M.K., Blaser M.J.;
"Rearrangement of sapA homologs with conserved and variable regions
Campylobacter fetus.";
                                                                                                                                                                                                           SMBL; AY211269; AAO64216.1; -.
InterPro; IPR005546; Autotransporter.
                                                                                                                                                                                                                                                                                PubMed=12694614;
                                                                                                                                                                                                                                                                                                                                                   "Campylobacter fetus
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                       secretion system.
                                                                                                                                                                                                                                                                      Z.C.,
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478
                      120
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                                                                                                                                                                                     PF03797; Autotransporter;
NCE 1286 AA; 134079 MW;
                                                                                                             5 KVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNS---SGPDSTLSIYQYGSANAALALQS
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GHSAKDANENSIQI SNGGNINNI VGGHAQDHINLNIIN
                    GNNAALVNYDQL-----VTRVV-THEMAHANNATAN
                                            SANENKVTITE-GTANVADIYGGKSISNNSI--
                                                                  DARKSETTITQSGYGNGADV--GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG
                                                                                       QVASENLVIISGGTIN--VPTIGGGSATNATNNQVTISGGKVTSSTIYGGNAN-----K
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                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                       genotypic
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                                                                                                                                                   Score 104.5;
Pred. No. 13;
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                                                                                                                                        Mismatches
                                                                                                                                                                                   A1FF9CBC34158789 CRC64;
                                                                                                                                                                                                                                                                                                                                                  proteins
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the Campyloba
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                    149
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Search completed: March Job time: 32.5 secs 2004, 18:40:11

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Database :
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Gapop 10.0 ,
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	0
92	92	92	92	92	92	92	93	93	93	95	98	98.5	104.5	109	109	109	113	115	
11.9	11.9	11.9	11.9	11.9	11.9	11.9	12.0	12.0	12.0	12.3	12.6	12.7	13.5	14.1	14.1	14.1	14.6	14.8	14.0
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AAB27212	AAY44402	AAU79539	AAY44404	AAU79538	AAY44403	AAB36331	AAB36328	AAB36336	AAB36323	ABU21488	ABR82645	AAB36342	AAB36344	AAB36319	AAB36324	AAB36340	ABR82644	AAB36320	THE COUNTY
Aab27212	Aay44402	Aau79539	Aay44404	Aau79538	Aay44403	Aab36331	Aab36328	Aab36336	Aab36323	Abu21488	Abr82645	Aab36342	Aab36344	Aab36319	Aab36324	Aab36340	Abr82644	Aab36320	***************************************
Human tan	Human tan	Truncated	Human tru	Truncated	Human tru	Escherich	Salmonell	Salmonell	Salmonell	Protein e	E. coli c	Salmonell	Escherich	Salmonell	Salmonell	Salmonell	E. coli c	Salmonell	, parmoner t

# ALIGNMENTS

RESULT 1 AAB36347 ID AAB3 WPI; 2000-672631/65. N-PSDB; AAC64623. Salmonella enteritidis. Escherichia coli. 05-APR-1999; 05-APR-2000; 2000WO-CA000356 12-OCT-2000 WO200060102-A2 Synthetic. vaccine; immune response; immunogen. Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; 26-FEB-2001 AAB36347; AAB36347 standard; AgfA::PT3#2 amino acid sequence SEQ ID NO:14. (UYVI-) UNIV VICTORIA. Doran JL, (first entry) 99US-0127888P protein; Collison SK, 151 ₿ Kay WW;

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species, the native

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RESULT 2
AAB36352
ID AAB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live component the inserted epitope, and hybrid fimbriae are usually strong CC against the inserted epitope, and hybrid fimbriae are easy and CC inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Best Local
Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                  White AP,
                                                                                           N-PSDB;
                                                                                                            WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36352 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
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                                                                                                                                                  Doran JL,
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                                                                                                                                                Collison
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Pred. No. 5.4e-67;
Mismatches 0;
                                                                                                                                                SK,
                                                                                                                                              Kay ww
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 151;
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Disclosure; Page 138; 139pp; English

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RESULT 3
AAB3G346
ID AAB3
XX AAB3CF
AC AAB3
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                                                                                          05-APR-1999;
                                                                                                                                                                                         05-APR-2000;
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Escherichia coli.
(UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                  WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#1 amino acid sequence SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
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                                                                                               99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                response;
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91.1%;
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Pred. No. 4.3e-61;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA cC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SERT1/TARF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC useful for the expression of recombinant AgfA protein which is useful for polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are easy and context of the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                 Salmonella
                                                  Salmonella; AgfA; vaccine
                                                                                                                           25-MAR-2003
26-JUN-1995
                                                                                                                                                                                    AAR74625;
                                                                                                                                                                                                                   AAR74625 standard; protein; 151
                                                                                      AgfA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                               118 ------YDQLYTRVYTHEMAHASVMYRQVGFGNNATANQY 151
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121 NNAALVNYDQLYTRVYTHEMAHA-----NNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                           (revised)
(first en
                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 696; DB 3;
Pred. No. 2.4e-59;
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RESULT 5
AAB36341
ID AAB3
XX AAB3
AC AAB3
AC AAB3
DT 26-F
XX Salm
XX WO20
XX Salm
XX WO20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
 WPI; 2000-672631/65
                          White AP,
                                                                                                                                                                                   Salmonella enteritidis.
                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                    Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                       05-APR-2000; 2000WO-CA000356
                                                                                                                                                          WO200060102-A2
                                                                                                                                                                                                                                                                              26-FEB-2001
                                                                                                                                                                                                                                                                                                          AAB36341;
                                                                                                                                                                                                                                                                                                                                  AAB36341 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151
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N-PSDB; AAQ87467.
                                                                                                                                 12-OCT-2000
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                                                    (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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A
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                           Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clouthier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 693; DB 2;
Pred. No. 4.7e-59;
3; Mismatches 11
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                           Kay
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Minimum DB
Maximum DB
                                                                                                                                                 Database
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Maximum Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                               Searched:
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                                                                                                                                                                                                                                                      seq length: 0
seq length: 2000000000
                                                                                           A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
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Gapop 10.0 ,
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775
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                                                                                                                                                                                                                                                                                                                                              1586107 seqs, 282547505 residues
                                                                                                                                                                               Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
geneseqp1980s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                 Gapext 0.5
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                                                                                                                                                                                     summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                       .....HASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                              1586107
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ,	σ	4	ω	N	1	Regult No.
115	123	123	123	132	237	391	463	514	514	523	528	578	602	603	609	611	612	659	692	693	693	696	714	775	Score
14.8	15.9	15.9	15.9	17.0	30.6	50.5	59.7	66.3	66.3	67.5	68.1	74.6	77.7	77.8	78.6	78.8	79.0	85.0	9	89.4	89.4	89.8	92.1	100.0	Query
22	23	23	23	22	45	122	142	120	120	151	151	151	151	151	151	151	151	151	151	151	151	151	151	151	Length
W	ω	w	w	w	ω	N	Ŋ	N	N	7	w	w	ω	w	w	w	ω	w	N	w	ผ	w	w	ω	몺
AAB36325	AAB36338	AAB36326	AAB36321	AAB36318	AAB36316	AAR52663	AAR52664	AAW23569	AAR62761	ABR82651	AAB36343	AAB36348	AAB36351	AAB36354	AAB36350	AAB36349	AAB36353	AAB36355	AAW23570	AAB36341	AAR74625	AAB36346	AAB36352	AAB36347	ID
Aab36325 Salmonell	Aab36338 Salmonell		Aab36321 Salmonell	Aab36318 Salmonell		Aar52663 FNB curli	Aar52664 Fibronect	Aaw23569 Salmonell	Aar62761 AgfA sequ	Abr82651 E. coli C	Aab36343 Escherich	Aab36348 AgfA::PT3	Aab36351 AgfA::PT3	4 AgfA	Aab36350 AgfA::PT3	Aab36349 AgfA::PT3	Aab36353 AgfA::PT3	Aab36355 AgfA::PT3	Aaw23570 Salmonell	Aab36341 Salmonell	Aar74625 AgfA sequ	Aab36346 AgfA::PT3	Aab36352 AgfA::PT3	7 AgfA::	Description

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CggA and AgfA-homologue fimbria bubnints, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

WPI; 2000-672631/65. N-PSDB; AAC64623.

40 92 41 92
12.0 11.9 11.9 11.9
19 19 23 673
ரையையைய
AABJ6336 AAB36328 AAB36331 AAY44403 AAU79538
Abu21488 Aab36323 Aab36336 Aab36328 Aab3631 Aay44403 Aau79538
Salmonell Salmonell Salmonell Salmonell Human tru Truncated

#### RESULT 1 AAB363 XX AAB33 XX AAB33 XX AAB33 XX AAB33 XX AAB3 XX AAG6 XX AG6 XX Salm OS Esch OS Syntt XX W020 XX W020 XX W12-0 XX U12-0 XX U17-0 XX U17-0 XX WP1 (UYV PA (UXV PA Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen. 05-APR-1999; Synthetic. Salmonella enteritidis. AAB36347 standard; protein; 151 AA White AP, 05-APR-2000; 2000WO-CA000356 12-OCT-2000. WO200060102-A2 Escherichia AgfA::PT3#2 amino acid sequence SEQ ID NO:14. 26-FEB-2001 (UYVI-) UNIV VICTORIA Doran JL, COLI. (first entry) 99US-0127888P Collison SK, Kay WW;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella. Escheriation depended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 system the heterologous antigens are presented in high numbers (up to $00,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to parify in large amount. The present sequence is given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
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                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                             AgfA::PT3#8 amino acid sequence SEQ ID NO:26
                                                                                                            26-FEB-2001
                                                                                                                                                                                           AAB36353 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the present invention
                                                                                                                                                                                                                                                                                                                         121 LVTRVVTHEMAHA-------SVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
  immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                 LVTRVVTHEMAHAGGNNAAL VNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 659; DB 3;
Pred. No. 9.1e-56;
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                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                            Sequence 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/65.
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Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 138; 139pp; English.
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121
                                  121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                       123;
                                                                       61
                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ
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NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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                                                                                                                                                                                                                                                                                              AA,
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                                                                                                                                                                                                                                    Score 612;
Pred. No. 3.
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AAB36349

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Query Match
Best Local
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                                                                                                                                                                                                                             back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid finbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                               Sequence
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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81.5%;
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                                                  Score 611; DB
Pred. No. 4e-5;
6; Mismatches
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ

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RESULT 10
AAB36350
CC directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologous species; replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA. CC comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA corottel containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence host cell, from the host cell and introducing the coliver into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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RESULT 11
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Best Local
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, (EgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinantion of a recombinant gene hack into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                               White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                           Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid sequence SEQ ID
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Pred. No. 6.3e-51
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Best Local (
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                                                                                                                   WPI; 2000-672631/65.
N-PSDB; AAC64627.
                                                                                                                                                                                                                               05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                  Escherichia
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                                                                                                                                                                                 (UYVI-) UNIV VICTORIA
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                                                                                                                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                  coli.
                                                                                                                                                                                                                                                                                                                                                                                          amino acid sequence SEQ ID NO:22
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                                                                                                                                                        Collison
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Pred. No. 2.4e-50;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described

Disclosure; Page 137; 139pp; English.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

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RESULT 13
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Best Local S
Matches 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     copy of that gene; and (4) eliciting an immune response in an animal, and comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
WPI; 2000-672631/65
                                 White AP,
                                                                                                        05-APR-1999;
                                                                                                                                         05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                  Salmonella; agfA; chromosomal gene replacement; fimbrin;
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                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                     Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                     vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#3 amino acid sequence SEQ ID NO:16
                                                                 (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
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                             Doran JL,
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                                                                                                      99US-0127888P.
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                                 Collison
                                                                                                                                                                                                                                                                                                                     immunogen
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Pred. No. 3e-50;
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                                                                                                                                                                                                                                                                                                                                      epitope;
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CC directing recombination of a recombinant gene into the chromosome of the Chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, comprising separating a raplacement segment or segments of foreign amino acid polymer comprising a recombinant AgfA C protein containing a replacement segment or segments of foreign amino acid golymer comprising a recombinant AgfA C protein containing a replacement segment or segments of foreign amino acid polymer containing a replacement segment or segments of foreign amino acid polymer into the animal in conjunction with a carrier or diluent. (I) is C polymer into the animal in conjunction with a carrier or diluent. (I) is C polymer into the expression of recombinant AgfA protein which is useful for C polymer into the expression of recombinant AgfA protein which is useful for C system the heterologous antigens are presented in high numbers (up to 50,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live cagainst the inserted epitope, and hybrid fimbriae are usually strong c immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and c inexpensive to purify, in large amount. The present sequence is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Bacherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
Sequence 151
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밁 Ś Ş Query Match Best Local S Matches 122 121 121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 122; 61 61  $\vdash$ 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ Similarity NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ Conservative 74.6%; 6 Score 578; DB 3; Pred. No. 6.3e-48; Mismatches 151 Length 151; Indels 0 Gaps 120 120 60 60

밁

RESULT 14 AAB36343 AAB36343 standard; protein; 151

Escherichia coli CsgA amino acid sequence SEQ ID NO:7

26-FEB-2001

(first entry)

Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope, vaccine; immune response; immunogen

Escherichia coli.

WO200060102-A2

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RESULT 15
ABR82651
ID ABR82
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DE E. CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC assembly system of strains of Salmonella, Escherichia coli and CE Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant on a recombinant gene CC back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the colymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC sould copies/cell), the hybrid fimbrian protein possesses both the carrier fimbrial subunit protein passesses both the communogenicity and adhesion properties relevant for an efficient live care inmunogens, which may be important for directing an immune response CC against the inserted epitone, and hybrid fimbriae are usually strong CC communogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                    E. coli CagA subunit 15 kDa protein.
                                                          04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                     ABR82651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present
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                                                                                                                                 standard; protein;
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                                                                                                                                                                                                                                  GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
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                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         describes a recombinant agfA gene (I) where a segment of a foreign DNA
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Pred. No. 4.3e-43;
0; Mismatches 27;
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Best Local S
Matches 103
                                                                                                                                                                                                                                                                   The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli 15 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmo or Shigella infections.
                                                                                                                                                                                                                                        Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 41-42; 42pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JAN-2002; 2002GB-00002275
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GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                            LVTRVVTHEMAHASVMVRQVGFGNNATANQY
                                                           TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                    SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
                                                                                                                      MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
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Pred. No. 1.3e-42;
0; Mismatches 28
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
   GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen
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US-08-233-788A-59
US-08-233-788A-57
US-09-186-387-8
US-09-181-835-8
US-09-841-835-8
US-09-841-835-2
US-09-841-835-2
US-09-841-835-2
US-09-9841-835-2
US-09-972-115A-8
US-08-864-038A-3
US-08-968-685A-10
US-09-056-556-204
US-09-072-596-199
US-09-072-596-199
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US-09-119-402A-2
US-09-841-786-4
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1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

Query Match 89.3%; Best Local Similarity 90.7%; Matches 137; Conservative

Score 692; DB 1; Length 15: Pred. No. 3.9e-62; 3; Mismatches 11; Indels

Length 151

0

Gaps

60 0

Query Match	DNELLA  Ser, 701 Fifth Avenue  1.e 48-DOS 41.0, Version #1.25 233,788A 70 220043.403C2.	IESULT 1  IS-08-233-788A-59  Sequence 59, Application US/08233788A  Patent No. 5635617  GENERAL INFORMATION:  APPLICANT: Doran, James L.  APPLICANT: Kay, William W.  APPLICANT: Collinson, Karen S.  APPLICANT: Clouthier, Sharon C.  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR	28 78.5 10.1 2353 3 US-09-377-155-33 29 78.5 10.1 2353 3 US-09-669-974-3 30 78.5 10.1 2353 4 US-09-669-974-3 31 78.5 10.1 2353 4 US-09-268-347-47 32 78.5 10.1 2353 4 US-09-268-347-47 33 78.5 10.1 2354 4 US-09-268-347-36 34 78.5 10.1 3241 4 US-09-268-347-36 35 77.5 10.0 31.8 4 US-09-107-532A-581.8 36 77.5 10.0 31.8 4 US-09-107-532A-581.8 37 79 9 415 4 US-09-453-7028-257 38 77 9.9 1650 4 US-09-25-7698-280 39 76.5 9.9 238 4 US-09-25-9680A-42 40 76.5 9.9 956 4 US-09-552-9818-3 41 76.5 9.7 98 3 US-09-19-172-41 42 75.5 9.7 789 3 US-09-919-172-41 43 75.5 9.7 789 4 US-09-850-351A-6 45 75.5 9.7 789 4 US-09-850-351A-6
151;		DETECTION	Sequence 33, Appli Sequence 4, Appli Sequence 33, Appl Sequence 37, Appl Sequence 36, Appl Sequence 17, Appli Sequence 5818, Ap Sequence 257, Appl Sequence 257, Appl Sequence 39, Appl Sequence 42, Appl Sequence 63, Appl Sequence 61, Appli Sequence 61, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli

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US-08-233-788A-57
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                        Sequence 8, Application US/09196387 Patent No. 6277613
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GENERAL INFORMATION:
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APPLICANT: Doran, James L.

APPLICANT: Kay, William W.

APPLICANT: Collinson, Karen S.

APPLICANT: Clouthier, Sharon C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION

TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 372836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS: LENGTH: 120 amino acids
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT JOSHUA
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REFERENCE/DOCKET NUMBER: 92.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                             82
                                                                                                                                                                                                                                                                                                                                                                                        22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                       GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQY 118
                                                                                                                                                                                                                                                                                                                                                 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08233788A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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US-09-841-835-8
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                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09841835
                                                                                                                                                                                                                                                                       Patent No.
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                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: de Lan
APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/0 FILING DATE: June 10, 19 ATTORNEY/AGENT INFORMATION:
                                    STATE: New COUNTRY: US ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
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                                                                                           CITY:
                                                                                                        STREET:
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TOPOLOGY: linear
                                                                                                                         ADDRESSEE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                          158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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35; Conservative
                                                                                         Hackensack
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                                                     New Jersey
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                                                                                                  411 Hackensack Avenue,
                                                                                                                                                                                                                de Lange, Titia
Smith, Susan
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                                                                                                                         Klauber & Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%; Score 92; DB
30.4%; Pred. No. 0.54
7ative 15; Mismatches
                                                                                                                                                             OF USE
12
                                                                                                                                                                                               A PROTEIN THAT
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                                                                                                        4th Floor
                                                                                                                                                                                               BINDS TO TRF1 AND METHODS
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IBM PC compatible

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Best Local :
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                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: June 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS LENGTH: 673 amino acids
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APPLICATION NUMBER:
                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
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NAME: Jackson Esq., David A.
REGISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
FELECOMMUNICATION INFORMATION:
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                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                      APPLICATION NUMBER:
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Similarity 30.4%;
35; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A PROTEIN THAT BINDS TO TRF1 AND METHODS
                                                                                                             09/095,225
                                                                                                                                                                                      US/09/196,387
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ER: 600-1-230 CIP1
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                                                        ; MOLECULE TYPE: protein US-09-841-835-10
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Tocal Similarity
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GENERAL INFORMATION:
Matches
              Query Match
Best Local Similarity
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                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                        NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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                                                                                       TOPOLOGY:
                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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New Jersey
                                                                                                    amino acid
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 Conservative
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Smith, Susan
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              11.9%;
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5; Mismatches
              Score 92;
Pred. No.
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Pred. No.
 Mismatches
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                            DB 4;
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 57;
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 Indels
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Gaps
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6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR

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US-09-841-835-2
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                                                                                     RESULT 8
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US-09-196-387-2
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                              Sequence 2, Application US/09841835 Patent No. 6506587
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 09/0:
FILING DATE: June 10, 19:
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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HITLE OF INVENTION: A PROTEIN THAT
HITLE OF INVENTION: OF USE THEREOF
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                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                   158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                    65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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35; Conservative
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Smith, Susan
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APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Maczyslaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
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US-09-972-115A-8
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GENERAL INFORMATION:
              Sequence 8, Application US/09972115A Patent No. 6599728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
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HYPOTHETICAL:
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TELEPHONE: 201-487-5800
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 0760:
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                                                                                                             158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                                                                                                                              65 KSETTIT----OSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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Pred. No. 1.3;
15; Mismatches
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Best Local Similarity
Watches 35; Conserve
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 Query Match
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
PILING DATE: May 28, 19;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP
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                                                                                                                                                                                                                                          TELEFAX: (212) 953-7733
NFORMATION FOR SEQ ID NO:
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                                                                                                                                             TOPOLOGY: lin
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 738
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MEDIUM TYPE: Diskett
                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                          TELEPHONE: (212) 986-2340
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                                          NAME/KEY: peptide LOCATION: from 1 to 738 IDENTIFICATION METHOD:
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                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                         TELEPHONE:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                               CELL TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                                                                                                                                                                           amino acid
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VENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

VENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY

VENTION: TO SAID POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                         Bruce Hamburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JAPAN
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                                                                                                             Pinctada fucata
mantle epithelial
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 11.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.50 inch, 1.44 MB storage
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                                               (by experiment)
                                                                                                                                                                                                                                                                                                            F-5610
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 Score 89.5;
                                                                                                               cell
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 B
 <u>د</u>
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Length 738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, App. ... No. 621498
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6214981
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TUCKER, K
APPLICANT: PLOSILA,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                 TOPOLOGY: ur
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212)
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212, TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31,232 REFERENCE/DOCKET NUMBER: 79
                                                                                                                                                                                                                                                                                                                               STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: N
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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141 -GFGNNATA 148
                                             156 E---TVQQISELLPIIRGQKALNDIYQLADTNLQKYRRTHAQGHASTAVGAMSYAKGHFS
                                                                       110 NSDITYGQYDQLVTRV-----
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                                                                                                       86
                                                                                                                                                                                                                           48;
                                                                                                                                   57 LALQSDARKSETTITQSGYGNGADVG-QGADNSTI----ELTQNGFRNNA--TIDQWNAK 109
                                                                                                                                                               44 LSFARIAALAVLVIGATLNGSAYAGIGISEADGG--KGGANARG-DKSIAI---GDIAQA
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                                                                                                                                                                                             1 MKLLKVAAFAAIVV----SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAA 56
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                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                             2123 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (212)
                                                                                                                                                                                                                                                                                               peptide
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                           62;
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213 NAFGTRATA 221

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RESULT 13
US-09-056-556-204
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US-09-252-991A-32096
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Best Local Similarity 21.5
Conservative
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SEQ ID NO 32096
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 204, Applica Patent No. 6350456 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
              ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A
APPLICANT: Dillon, Davin C
                                                                                                                   APPLICATION NUMBER: US/09/056,556 FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                            ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                        TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 KVSNFGTL--NNASVSGSIKDASGNVGVNVAAGDNNQQANAAALASADASFVFGTATAS- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 KVAAFAAIVVSGSALAGVVPQWGG------GGNHNGGGNSSGPDSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MARC J. Rubenfield et al.
WENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09056556
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                                                                                                                                                                                                                                                                                                  USA
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UMBER: US 60/074,788
1998-02-18
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21.5%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                      701 Fifth Avenue
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US-09-072-596-199
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Query Match
Best Local Similarity
Matches 29; Conserv
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Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4
TELEFAX: (206) 682-603
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                            STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 05-M2
                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYN 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 IGLTGSGLLGF-----GGLNSGTGN-----IGLFNSGTGNVGIGNSGTGNWGIGNSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              98104-7092
                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQYD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVENTION:
                                                                                                                                 943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09072596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lodes, Michael J.
Hendrickson, Ronald C.
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Vedvick, Thomas S.
Twardzik, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campos-Neto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reed, Steven G.
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                                                                                                                                                                                                 (206)
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                                                                                                                                                                                               622-4900
               10.8%; Score 83.5; 25.4%; Pred. No. 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.8%; Score 83.5;
25.4%; Pred. No. 6;
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                                                                                                                                                                                                                               210121.417C9
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                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                              DB 4;
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                              Length 943;
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Conservative

16;

Mismatches

50;

19;

Gaps

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WESULT 15
US-09-477-135A-131
Sequence 131, Application US/09477135A
Patent No. 6572865
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis
CURRENT FILING DATE: 52888;
CURRENT FILING DATE: 900-01-03
PRIOR APPLICATION NUMBER: US/09/477,135A
CURRENT FILING DATE: 1997-12-15
PRIOR FILING DATE: 1997-12-15
PRIOR PILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 131
LENGTH: 943
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-477-135A-131
Search completed: March 11, 2004, 18:44:45
Job time: 34.4 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.8%; Score 83.5; DB 4; Length 943; Best Local Similarity 25.4%; Pred. No. 6; Matches 29; Conservative 16; Mismatches 50; Indels 19
                                                                                                                                                                                                                                                                      313 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYN 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 IGLTGSGLLGF-----GGLNSGTGN------IGLFNSGTGNVGIGNSGTGNWGIGNSG 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQYD 119 ; | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | 
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Result
No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein -
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                                                                                                                                                                                                                                                                                                                                                              Score
                                                                     86.5
86.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*

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15: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10 PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                     9 9 14
  10 US-09-972-115A-8

10 US-09-93-306-1146

10 US-09-913-214A-9

10 US-09-913-214A-9

10 US-09-913-363-156

14 US-10-080-170-348

14 US-10-156-761-8763

15 US-10-369-493-20619

15 US-10-374-780A-2086

16 US-10-374-780A-2086
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US-09-841-835-8
US-09-841-835-10
US-09-841-835-2
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Sequence 20638, A
Sequence 8, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 4, Appli
Sequence 146, Appli
Sequence 9, Appli
Sequence 156, Appli
Sequence 348, App
Sequence 348, App
Sequence 20619, A
Sequence 2061, Appl
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
78	78.5	78.5	78.5	78.5	78.5	79	79	79.5	79.5	79.5	80	80	80.5	80.5	81	82	82	82	82.5	82.5	83	83	83	83.5	83.5	83.5	83.5	83.5	84.5
10.1	10.1	10.1	10.1	10.1	10.1	10.2	10.2	10.3	10.3	10.3	10.3	10.3	10.4	10.4	10.5	10.6	10.6	10.6	10.6	10.6	10.7	10.7	10.7	10.8	10.8	10.8	10.8	10.8	10.9
251	3241	2834	2732	2353	714	594	251	518	253	65	892	255	873	251	812	2893	254	253	2468	407	257	254	254	943	943	943	943	943	271
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US-09-880-748-1130	US-09-841-786-1	US-10-085-959-252	US-10-238-075-1119	US-09-797-862-33	US-09-841-786-4	US-10-156-761-13173	US-09-880-748-1122	US-09-976-297-2	US-09-880-748-1850	US-09-996-194-16	US-09-952-267-5	US-09-880-748-1153		US-09-880-748-1554	-10	US-09-882-227-522	US-09-880-748-1226			US-10-156-761-12940	٠	-09-880-748	-09-880-748	-10-084-843	US-10-193-002-199	US-09-997-181-131	US-09-997-182-131	US-09-996-634-131	US-10-156-761-11721
Sequence 1130, Ap	Sequence 1, Appli		Sequence 1119, Ap	Sequence 33, Appl	Seguence 4, Appli	13173,	Sequence 1122, Ap	Sequence 2, Appli	Sequence 1850, Ap	Sequence 16, Appl	Sequence 5, Appli	Sequence 1153, Ap	Sequence 13, Appl	Sequence 1554, Ap	Sequence 9134, Ap	522,				Sequence 12940, A		1165,	1136,	204,	Sequence 199, App	131	Sequence 131, App	131,	Sequence 11721, A

#### ALIGNMENTS

US-10-369-493-20638

Sequence 20638, Application US/10369493 Publication No. US20030233675A1

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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/03-02-28
PRIOR APPLICATION NUMBER: US/03-039
PRIOR APPLICATION NUMBER: US/03-039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
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                                                                                                                                                              Matches
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Best Local (
                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Rhodopseudomonas palustris FEATURE:
19 AAFAADSNTVYLNOTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
                                                                                                               7 AAFAA-----GNSSGPDSTLSIYQY
                                                                                                                                                                                   Similarity
                                                                                                                                                              Conservative
                                                                                                                                                         13.4%; Score 104; DB 15; Length 445; 26.6%; Pred. No. 0.03; tive 25; Mismatches 61; Indels 3
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US-09-841-835-8
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                                    Sequent No. Uszur Patent No. Uszur Patent No. Uszur Patent INFORMATION:
                                                                  Sequence 10, Application US/09841835
Patent No. US20020076795A1
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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Patent No. US20020076795A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                     APPLICANT:
     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 673 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: A PROTEIN THAT BINDS TO TREI AND METHODS TITLE OF INVENTION: OF USE THEREOF
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APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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ZIP: 0760
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                                                                                                                                                                  158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                              65
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                                                                                                                                                                                                                                  VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSPTSS-SSSSPSSPGSSLAESPEAA
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Y: linear
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                     Smith
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                                  de Lange, Titia
                                                                                                                                                                                                                                                                                                              Conservative
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A PROTEIN THAT BINDS
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30.4%; Pred. No. 0.
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TO TRF1 AND METHODS
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                                                                                                                                                                                                                                                                                                                                          sequence 2, Application US/09841835
Patent No. US20020076795A1
                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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TELEPHONE: 201-487-5800
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CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/841,835
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NUMBER OF SEQUENCES:
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                                                                                                          ZIP: 07601
                                                                                                                                                           CITY: Hackensack
                                                                                                                          COUNTRY:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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35; Conserv
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New Jersey
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30.4%; Pred. No. 1
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                                                                                                                                                                              4th Floor
           Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
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PRIOR APPLICATION DATA:

US/09/841,835

APPLICATION NUMBER: CLASSIFICATION: APPLICATION NUMBER:

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                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09972115A Publication No. US20030032769A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
                                                                                                                                                       Matches
                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local S
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CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A Second Mammalian Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Geron Corporation APPLICANT: Gregg, Morin B.
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 080/0030
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MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                             ENGTH: 1327
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LENGTH: 1327 amino acids
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TELEPHONE: 201-487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                  65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                           99 VAAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEÄA 157
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                                                                                                                6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
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Walter, Funk D.
Mieczyslaw, Piatyszek A.
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                                                                                                                                                       Conservative
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                                                                                                                                                  11.9%; Score 92; DB 30.4%; Pred. No. 2; ative 15; Mismatches
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ER: 600-1-230 CIP1
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                                                                                                                                                                                         DB 10; Length 1327;
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Query Match
Best Local Similarity
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US-09-793-306-146
                                                                                                     US-09-793-306-146
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                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 146
LENGTH: 597
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. US200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 146,
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                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
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SOFTWARE: Patentin Ver. 2
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PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
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APPLICANT: DeMaggio, Anthony
APPLICANT: Goldman, Phyllis
APPLICANT: MCBlligott, David
                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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ORGANISM: Homo sapiens
                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: mTTC#3-His
                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy ITLE OF INVENTION: of Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lodes, Michael
Corixa Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovendale, Pamela
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                                        11.2%; Score 87; I
26.6%; Pred. No. 2
                     15;
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                     Mismatches
                                                             DB 9; Length 597;
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                     26;
                     Gaps
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RESULT 9
US-09-712-363-156
; Sequence 156, Application US/09712363
; Patent No. US20020164588A1
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                                               APPLICANT: Elsenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
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CURRENT FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 08/968,685
PRIOR FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tucker, Kenneth
APPLICANT: Plosila, Laura
TITLE OF INVENTION: MEGAVELLA CATARRHALIS OUTER MEMBRANE PROTEIN-106 POLYPEPTIDE,
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REFERENCE: 7969-089-999
FILE REFERENCE: 7969-089-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2122
TYPE: PRT
ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LALQSDARKSETTITQSGYGNGADVG-QGADNSTI----ELTQNGFRNNA--TIDQWNAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSFARIAALAVLVIGATLNGSAYAGIGISEADGG--KGGANARG-DKSIAI---GDIAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKILKVAAFAAIVV----SGSALAGVVPQWGGGGNHNGGGNSGFDSTLSIYQYGSANAA 56
                                                                                                                                                                                                                                                                                                                                                              -GFGNNATA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGSQSIAIGDNKIVHNS--NNNANIGAKASGNESIAIGGDVLASGHASIAIGSDDLYLKK 155
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25.4%; Pred. No.
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                                                                                                      COMPARATIVE ANALYSIS
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US-10-080-170-348
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SEQ ID NO 348
LENGTH: 527
                                                                                                                                                                  Matches
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                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 156
LENGTH: 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COLE, S.T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

FILE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 03495.0218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
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Best Local (
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CURRENT FILING DATE: 2002-06-10
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PRIOR PELICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR PELICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR PELICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
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DR APPLICATION NUMBER: 60/117,844

DR FILLING DATE: 1999-01-29

DR APPLICATION NUMBER: 60/118,206,

DR FILLING DATE: 1999-02-01

DR APPLICATION NUMBER: 60/126,593

DR APPLICATION NUMBER: 60/126,593

DR FILLING DATE: 1999-03-26
                                                                                      387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 TYQLREGSNIIGRGQDAQFRLPDTGVSRRHLEIRWDGQVALLADLNSTNGTTVNNAPVQE 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 GYAPQGGGYAEPAGRDYDYGQSGAPDYGQPAPGGYSGYGQGGYGSAGTSVTLQLDDGSGR 446
                                                                                                                        21 GVVPQWGG----GGNHNGGGNSSGPD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 WNAKNSDITVGQYDQLVTRVVTHEMAHASVMVR 138
                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GVVPQWGG-----GGNHNGGGNSSGPD-----STLSIYQYGSANAALALQSDARKSE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35,
                                                                           GYAPQGGGYAEPAGRDYDYGQSGAPDYGQPAPGGYSGYGQGGYGSAGTSVTLQLDDGSGR 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 22.9
35; Conservative
TYQLREGSNIIGRGQDAQFRLPDTGVSRRHLEIRWDGQVALLADLNSTNGTTVNNAPVQE 506
                                            TTITQSG---YGNGADV-----
                                                                                                                                                                Conservative
                                                                                                                                                                          11.2%;
22.9%;
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                                                                                                                                                              13;
                                                                                                                                                                               Score 86.5;
Pred. No. 2
                                                                                                                                                              Mismatches
                                                                                                                 ----STLSIYQYGSANAALALQSDARKSE
                                                                                                                                                                                                DB 14;
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                                                                                                                                                          56;
                                     -GOGADNSTIELTONGFRNNATIDO 105
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106 WNAKUSDITVGQYDQLVTRVVTHEMAHASVMVR 138

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                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 8763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20619, Application US/10369493 Publication No. US20030233675A1
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                               TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052) B CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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APPLICANT: Hinl
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APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL FOLYNUCLEOTIDES
FILE REFERENCE: 249-262
NAME/KEY: unsure
LOCATION: (1)..(486)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                               ORGANISM: Rhodopseudomonas
                                                                                                                                                            LENGTH: 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507 WQLADGDVI------RLGHSEIIVR 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TTITQSGYGNGADVGQGADNSTIE--LTQNGFRNNATIDQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
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Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
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HORIKAWA, HIROSHI
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Pred. No. 2.
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GENERAL INFORMATION:

APPLICANT: Sherman, Bradley K

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Riechmann, Jose Luis Jiang, Cai-Zhong Heard, Jacqueline E Haake, Volker

APPLICANT:

Creelman, Adam, Luc J Ratcliffe, Oliver

Robert A

Reuber, T. Lynne Keddie, James Broun, Pierre E Pilgrim, Marsha L

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                                       US-10-374-780A-2086
                                                        RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Office 97
SEQ ID NO 56
Sequence 2086, Application US/10374780A Publication No. US20040019927A1
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: BB1454 US NA
CURRENT APPLICATION NUMBER: US/10/174,363
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/298,973
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEC.
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Publication No. US20030077623A1
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Best Local Similarity
Matches 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Butler, Karlene H. APPLICANT: Cahoon, Rebecca E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Polynucleotides And Polypeptides Involved In Post-Transcriptiona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1048
TYPE: PRT
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                                                                                                             214 TITPEVTSRGVNRAVMKQLV 233
                                                                                                                                                   121 LVTRVVTHEMAHASVMVRQV 140
                                                                                                                                                                                      154 EQLSVEQGAPSQAIQPIPSSSKAFKFPMRPGKGQSGKRCIVKANHFFAELPDKDLHHYDV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 IIH----
                                                                                                                                                                                                                           77 NGADVGQGADNSTIE-----
                                                                                                                                                                                                                                                                 95 GGYGGGRGGGPSSGPPQRQSVPELHQATSPTYQAVSSQPTLSEVSPTQVPEPTVLAQQF- 153
                                                                                                                                                                                                                                                                                                      27 GGGGNHNGGGNSSGPDSTLSI-------YQYGSANAALALQSDARKSETTITQSGYG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 SVVVAGTDYRDIVAGVLPSLGGVKKAYAIGDGSGPFAPFKDLASDTPFSAPEFGAADGFV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AIVVSGS----ALAGVVPQWGGGGNHNGGGNSSGP-----DSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG 116
                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                         h 11.0%; Score 85.5; D
Similarity 25.7%; Pred. No. 6.8;
36; Conservative 17; Mismatches
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Harvell, Leslie T
Rafalski, Antoni J
Sakai, Hajime
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2.3;
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APPLICANT: SHOPNON SHIP SHOPLICANT: SAKAKI, YOSHIYUKI APPLICANT: SAKAKI, YOSHIYUKI APPLICANT: HATTORI, WASAHIRA TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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US-10-156-761-9343
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9343, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.2
SEQ ID NO 2086
LENCTH: 1048
TYPE: PRT
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Best Local (
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                                                                                                                                                                                                                                                                                                                  APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 10/225,068 PRIOR FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Arabidopsis thaliana FEATURE:
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THE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/338,692
FILING DATE: 2001-12-11
APPLICATION NUMBER: 10/171,468
FILING DATE: 2002-06-14
APPLICATION NUMBER: 10/225,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 10/225,067
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FILING DATE: 2001-08-22
APPLICATION NUMBER: 60/336,049
FILING DATE: 2001-11-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGADVGQGADNSTIE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGYGGGRGGGPSSGPPQRQSVPELHQATSPTYQAVSSQPTLSEVSPTQVPEPTVLAQQF- 153
                                                                                                                                                                                                                                                            IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.0%; Score 85.5; D
25.7%; Pred. No. 6.8;
cive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----LTONGFRNNATIDOWNAKNSDITVGOYDO 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
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                                                                                                                                                                                                                                                       ; ORGANISM: Streptomyces avermitilis US-10-156-761-9343
                                                                                                                                                                                                                                                                                     ; SEQ ID NO 9343
; LENGTH: 438
; TYPE: PRT
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 37; Conserv
 115
                                                                                              59
                            97 FRNNATIDOWNAKNSDITVGQYDQLV 122
                                                              55
                                                                                                                         1 MRSIRAAAVGAVTMSLALAASAC----GGGSSTGGGSNDSP-KTLT-YWASNQGASIAVD 54
                                                                                                                                                     1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALA--
                                                          KKVLQPELDKFEEQTGIKVKLEVVPWSDLLNRILTATTSGQGPDVLNIGNTWSASLQATG 114
                                                                                              ---LQSDARKSE---
                                                                                                                                                                                          Conservative
ALLPWDAKNFD-KIGGKDRFV 134
                                                                                                                                                                                                      11.0%; Score 85; 25.3%; Pred. No. 2
                                                                                          ------TTITQSGYGNGADVGQGADNSTIELTQNG
                                                                                                                                                                                         22;
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                   DB 14; Length 438;
                                                                                                                                                                                         51;
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                                                                                                                                                                                       36;
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Search completed: March 11, 2004, 19:18:35 Job time: 25.6 secs

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
                                                                           Database :
                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                             Searched:
PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                        March 11, 2004, 18:24:14; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec
                                                                                                                                                                                                                                                                            283366 seqs, 96191526 residues
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALA......HASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                       US-09-543-407-14
775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                           283366
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

,	20	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	0	Ŋ	4.	ω	N		Result
	200	86.5	87	87	87	88.5	89	89.5	89.5	90	90.5	90.5	90.5	91	91	91	93	95	96	96.5	98.5	104.5	104.5	104.5	506.5	506.5	528	693	693	Score
				11.2	11.2		•		11.5	•	11.7	11.7	11.7	11.7	11.7	11.7	12.0	12.3	12.4	12.5		13.5		13.5	65.4	65.4	68.1	89.4	89.4	Query Match 1
	527	478	678	646	590	479	573	262	256	479	151	145	145	1213	1028	301	2174	1748	770	552	151	151	151	151	152	152	151	151	151	Length I
	v	N	N	٢	N	N	Ŋ	N	N	N	N	2	N	N	N	N	N	N	N	N	N	ผ	N	N	N	N	N	N	N	B
	B70700	JN0892	A70762	S19916	E70946	A38307	C86266	S00275	T03371	JN0891	AH0635	H98144	AD3143	S16356	A56038	B84533	E95965	S42136	T51024	D70604	JC6040	G85665	C90806	S70787	H85665	D90806	S70788	AI0635	080	ID
	hypothetical prote	rotei	probable PPE prote	leishmanolysin (EC	probable PPE prote	metalloproteinase	F3F19.21 protein -	tail fiber protein	glycine-rich prote	metalloproteinase		hypothetical prote	conserved hypothet		מי		ø		related to C2H2 zi	probable PPE prote	fimbrin protein ag	curlin minor chain	minor curlin subun	m	hypothetical prote	curlin major subun	curlin protein csg	major curlin chain	otein a	Description

444	41 42	38 39	36 37	ω ω 5	33	μ	30
83.5 83.5	83.5 83.5	8 8 4 4	84.5	85.5 85	.86	86	86.5
10.8	10.8	10.8	11.0 10.9	11.0	11.1	11.1	11.2
440 1067 3300	285 340	407 590	967 440	575 3 <b>4</b> 7	599	447	645
NNN	222	<b>–</b> 2	NN	NN	N	N	N
T15352 S35423 D70575	PL0221 H84219 A83401	T21956 A45621	S66852 AD1539	S35327 B39112	A44951	G84687	F70825
nypothetical prote protein kinase sgg probable PPE prote	leishmanolysin (EC hypothetical prote hypothetical prote	hypothetical prote leishmanolysin (EC	hypothetical prote probable sugar ABC	protein kinase sgg merozoite 45K surf	leishmanolysin (EC	6	probable PPE prote

## ALIGNMENTS

Qy 121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151 :  :	Oy 61 SDARKSETTITQSGYGNGADYGQGADNSTIELTQNGFRNNATIDOWNAKNSDITVGQYDG	Qy 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ	Query Match 89.4%; Score 693; DB 2; Length 151; Best Local Similarity 90.7%; Pred. No. 5e-52; Matches 137; Conservative 3; Mismatches 11; Indels	C;keywords: rimbria F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <m< th=""><th>c component of thin aggregative</th><th>A;Note: sequence extracted from NCBI backbone (NCBIP:45936) C:Genetics: A:Gene: acfA</th><th>A; Residues: 21-33 <co3></co3></th><th>A; Contents: 2/000 A; Accession: A44898 A. Status: nyaliminary</th><th>A;Title: Purification and characterization of thin, aggregative fimbriae A;Reference number: A44898; MUID:91310586; PMID:1677357</th><th>A;Note: the authors translated the codon ACG for residue 44 as R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, J. Bacteriol. 173, 4773-4781, 1991</th><th></th><th>A;Accession: PC6015 A;Molecule type: protein</th><th>111111111111111111111111111111111111111</th><th>A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative A;Reference number: JC6039; MUID:96146512; PMID:8550497 A:Accession: JC6039</th><th>C;ACCEBBLOR: JCb0J9; FCb0J5; A44838 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; J. Racteriol. 178. 662-667. 1996</th><th>fimbrin protein agfA precursor - Salmonella enteritidis C;Species: Salmonella enteritidis C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999</th><th>RESULT 1 JC6039</th></m<></sig>	c component of thin aggregative	A;Note: sequence extracted from NCBI backbone (NCBIP:45936) C:Genetics: A:Gene: acfA	A; Residues: 21-33 <co3></co3>	A; Contents: 2/000 A; Accession: A44898 A. Status: nyaliminary	A;Title: Purification and characterization of thin, aggregative fimbriae A;Reference number: A44898; MUID:91310586; PMID:1677357	A;Note: the authors translated the codon ACG for residue 44 as R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, J. Bacteriol. 173, 4773-4781, 1991		A;Accession: PC6015 A;Molecule type: protein	111111111111111111111111111111111111111	A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative A;Reference number: JC6039; MUID:96146512; PMID:8550497 A:Accession: JC6039	C;ACCEBBLOR: JCb0J9; FCb0J5; A44838 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; J. Racteriol. 178. 662-667. 1996	fimbrin protein agfA precursor - Salmonella enteritidis C;Species: Salmonella enteritidis C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999	RESULT 1 JC6039
	OWNAKUSDITVGQYDQ 120                QWNAKUSDITVGQYGG 120		.h 151; lels   0;   Gaps   0;	ll <mat></mat>	fimbriae tissue plasminogen activator	9			gative fimbriae from Salmonell.	44 as ile Kay, W.W.	•	The Carte		.n, aggregative fimbriae.	P.A.; Kay, W.W.	:hange 08-Oct-1999	

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N;Alternate names: csgA protein; major curlin protein C;Species: Escherichia coli C;Species: Escherichia coli C;Jate: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01 C;Accession: S70788; G64846; S31202; S34560; S34559 R;Hammar, M; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995 Mol. Microbiol. 19, 661
           A; Experimental source: strain K-12, R;Olsen, A.; Arnqvist, A.; Hammar, Mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                                                                                                                               Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X90754; NID:gl147558; PIDN:CAA62282.1; PID:gl147564
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 19:
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley,
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid;
A;Molecule type: DNA
A;Residues: 1-151 <HAM>
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Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A:Title: Complete genome sequence of a multiple drug resistant A; Reference number: ABO502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S70788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: STY1181
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A; Residues: 1-151 < PAR>
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                                                                                                       Cross-references: GB:AE000205; GB:U00096; NID:g1787265;
                                                                                                                                                                                     Molecule type: DNA
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Best Local S
Matches 137
                                                                                                                                                                                                                      Status: nucleic acid sequence not shown; translation
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                                                                                                                                                           -151 <BLAT>
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              Hammar, M.;
, 1993
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Pred. No. 5e-52;
                                                                             substrain
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                                                                             MG1655
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                                            S.; Normark,
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e, N.; Farrar
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ey, M.;
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R;Hayashi, T.; Makino, gasawara, N.; Yasunaga, DNA Res. 8, 11-22, 2001
                                                                                              curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, su C;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: D90806
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                                                                                                                                                                             D90806
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A;ANOlecule type: DNA
A;Residues: 1-133,'RQRDSGWLW' <0LS3>
A;Cross-references: EMBL:L04979; NID:g290424;
A;Cross-references: strain K-12, substrain
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A; Accession: S34559
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R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-6,'V',8-151 <OLS1>A;Cross-references: EMBL:L04979
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Best Local S
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                                                     T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii
N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
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                                                                                                                                                                                                                                                                               121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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quence of enterohemorrhagic Escherichia MUID:21156231; PMID:11258796
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                  coli
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A;Title: Complete genome sequence of enterohemorrhagic Escherichi A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Recession: D90806
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-152 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                              A; Gene:
                                                                                 Matches
                                                                                                                        Query Match
                                                                                 Local Sim
                                                                                                                                                              ECs1420
                                                                                                   Similarity
                        MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGHHGGGGNNSGPNSELNIYQYGGGNSALAL
                                                                                 Conservative
                                                                                               65.4%;
                                                                               21;
                                                                           Score 506.5; DB 2;
Pred. No. 3.6e-36;
1; Mismatches 28;
                                                                             Indels
                                                                                                                 Length
                                                                                                                 152;
                                                                           1.
                                                                                                                                                                                                               GSPDB:GN00154
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QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYD

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A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62281.1; PID:g1147563
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augus
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64846
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A;Residues: 1-152 <STO>
A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1;
A;Experimental source: strain O157:H7, substrain EDL933
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C;Accession: H85665
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                                              A; Molecule type: DNA
                                                                       A;Status: nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Species: Escherichia coli
;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
;Accession: S70787; P64846
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                        1-151 <BLAT>
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    GB: AE000205;
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                                                                       not shown; translation
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    GB:U00096;
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NID:g1787265; PIDN:AAC74125.1;
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K.; Aj
  PID:g1787278
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ey, M.;
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A; Molecule type: DNA A; Residues: 1-151 <S' A; Cross-references: (

1-151 <STO>

GB: AE005174;

NID:g12514573;

PIDN: AAG55787.1;

GSPDB:GN00145;

UWGP: 21

A; Reference number: A; Accession: G85665

A85480;

of enterohemorrhagic Escherichia 80; MUID:21074935; PMID:11206551

K.; A

**Apodaca** 

Mayhe

A;Status:

preliminary

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A;Gene: csgB
A;Map position:
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
G85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Description: minor component of wild-type curli; interaction between CsgA and CsgB A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli th and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted.cSIGs F;22-151/Product: minor curlin chain #status predicted <MAT>
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A; Residues: 1-151 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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Best Local :
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Best Local &
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                                                                                                                                                                                        NLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVVQRQSQMAIRV
                                                                                                                                                                                                                     SETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYDOLVTRV 125
                                                                                                                                                                                                                                                                                    FAAIVVSGSAL--AGVVPQWGGGGNHNGGGNSSGPDSTLSIY-QYGSANAALALQSDARK 65
                                                                                                                                                                                                                                                       FAVNELSKSSFNQAAII---GQAGTNNSAQLRQGGSKLLAVVAQEGSSNRA-KIDQTGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAVNELSKSSFNQAAII----GQAGTNNSAQLRQGGSKLLAVVAQEGSSNRA-KIDQTGDY
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                                                                                                                                                                                                                                                                                                                              Score 104.5; DB Pred. No. 0.054;
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source:

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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C.Accession: D70604
R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
Nature 393, 537-544, 1998
Naturors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.;Authors: Deciphering the biology of Mycobacterium tuberculosis from the comple
A.;Beference number: A70500; MUID:98295987; PMID:9634230
A.;Accession: D70604
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C;Genetics:
A;Gene: csgB
A;Status: preliminary; nucleic acid sequence not shown; translation not
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                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: fimbria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:U43280; NID:gl184712; PIDN:AAC43598.1; A;Experimental source: strain 276755-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Salmonella enteritidis agfBAC operon encoding A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6040
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C;Species: Salmonella enteritidis
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Best Local S
Matches 34
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;1-21/Domain: signal sequence #status
;22-151/Product: fimbrin protein agfB
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                                                                                                                                                                                                                                                                                                                                                                                   QSHMAIRVTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARVRQEGSKLLSVISO--EGGNNRAKVDQAGNYNFAYIEQTGNAN-----DAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQYGTQKTAİVVQRQSQMAIRV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAAIVVSGSAL--AGVVPQWGGGGNHNGGGNSSGPDSTLSIY-QYGSANAALALQSDARK
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ilarity 29.2%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                            139
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26.2%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -AIIQKĠSGNKANITQYGTQK--
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#status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; DB 2;
0.17;
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                                                                                                                                                  Holroyd, (
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                                                              genome
                                                                                                                                                      Ø
                                                   cnjB protein - Tetrahymena Luckunymena Crispecies: Tetrahymena thermophila Crispecies: 19-Mar-1997 #sequence revision Criscossion: $42136; $42135; $03550 Criscossion: $42136; $42135; $03550
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RESULT 12 S42136

R; Taylor, F.M.; Martindale, submitted to the EMBL Data A; Reference number: A; Accession: S42136

842136

Library, October 1992

18-Jul-1997

#text\_change

07-Dec-1999

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A;Residues: 1-770 <SCH>
A;Residues: 1-770 <SCH>
A;Cross-references: EMBL:AL389901; GSPDB:GN00116; NCSP:B7F21.50
A;Experimental source: BAC clone B7F21; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                    R;Schulte, U.; Aign, V.; Hoheisel, submitted to the Protein Sequence
                                                                                                                                                                                                                                               A; Map position: (A; Introns: 117/1
                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T51024
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Date: 21-Jul-2000
C; Accession: T51024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related to C2H2 zinc finger transcription factor D-Sp1 [imported]
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C; Superfamily: Phaseolus
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A;Cross-references: GB:Z92774; GB:AL123456; NID:g3261729; PIDN:CAB07133.1; PID:g187728.
A;Experimental source: strain H37Rv
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505
                                                                                                                        389
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                                                                                         STIEL----
                                                                                                                                                  GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADN 87
                           ---TRVVTHEMAHASV 135
                                                          QSTGLGYHYSSTTRNQHQHHWRNQSNASELSADGSEITHGVASPLVGGSSHARGASGGTS
                                                                                                                      GAGNNNNGSELASPDPNRGYFD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSALAGV-----VPQWGGGGNHNGGGNSSGPD---STLSIYQYGSANAALALQSDA 63
                                                                                                                                                                                    Conservative
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520
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                                                                                                                                                                                                Score 96; DB Pred. No. 1.8;
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Pred. No. 1
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                                                                                                                     -GASPPLPSSSHTTSTTYAGGHNGNGHGMRESVDS 444
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r;1451-1464/Region: zinc finger CCHC motif F;1478-1491/Region: zinc finger CCHC motif F;1501-1514/Region: zinc finger CCHC motif F;1501-1543/Region: zinc finger CCHC motif F;1535-1568/Region: zinc finger CCHC motif F;1579-1592/Region: zinc finger CCHC motif F;1602-1615/Region: zinc finger CCHC motif F;1602-1615/Region: zinc finger CCHC motif F;1602-1615/Region: zinc finger CCHC motif F;1626-1748/Region: glycine-rich
A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                            C/Species: Sinorhizobium meliloti
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 3:
C/Accession: E95965
R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.;
R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid
A;Reference number: A95842; MUID:21396508; PMID:11481431
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Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene
A;Reference number: $03650, MUID:88189811, PMID:3357771
A;Accession: $03650
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A;Title: Retroviral-type zinc fingers and glycine-rich repeats
A;Reference number: S42135; MUID:94051569; PMID:8233798
                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-2174 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain C;Species: Sinorhizobium meliloti
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A;Residues: 236-250,'I',252-255,'N',257-773
A;Cross-references: EMBL:X06462
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Best Local S
Matches 31
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                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
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Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-
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; Pred. No. 5.6;
11; Mismatches
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        A;Cross-references:
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nypothetical protein At2g15770 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: B84553
                                                                                                                                                                              R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P. Mol. Cell. Biol. 14, 6809-6818, 1994
A;Title: Multiple products from the shavenbaby-ovo gene A;Reference number: A56038; MUID:95021209; PMID:7935398
                                                                                                                                                                                                                                                                                                                                   DNA-binding protein ovo - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change
C;Accession: A56038
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A56038
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B84533
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A;Gene: At2g15770
A;Map position: 2
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                                A; Molecule type: mRNA
A; Residues: 1-1028 <GAR>
                                                                                                         A; Status: preliminary
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A; Residues: 1-301 <STO>
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                                                                                                                                                 A; Accession: A56038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           738 ----GGYANTANVGFKG-----LTLTTQG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 TITQSGYGNGADVGQGADNST----IELTQNGFRNNATIDQWNAKN-----SDITVGQYD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 SGSALA-----GVVPQWGGGGNH-NGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 TITQSGYGNGADVG-QGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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26.4%; Pred. No.
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Pred. No. 11;
L5; Mismatches
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PIDN: AAB60216.1;
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GB:U11383;

NID:g520526;

D 2 4 4	Search completed: March 11, 2004, 18:42:07 Job time : 11.3 secs	Qy 63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNS 111	QY 3 LLKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62	Query Match 11.7%; Score 91; DB 2; Length 1028; Best Local Similarity 31.2%; Pred. No. 6.7; Matches 34; Conservative 8; Mismatches 41; Indels 26; Gaps	C;Genetics: A;Gene: ovo A;Cross-references: FlyBase:FBgn0003028
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Title:
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No.
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.
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775
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GP63 LEIMA
DA6 CABEEL
SGG DROME
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P28307 escherichia
Q93u24 escherichia
D39828 escherichia
P55226 salmonella
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6 oryza sativ
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8 pepper mild
9 erwinia chr
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9 R S	"Comp	lete ge	nome s	equence	of Sal	monell	enteri	ca ser	ovar Ty	Typhimurium	cium	
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RA A	Krogh	ell T., 1 A., La	Hamli Irsen T	.S., Lea	aque A.	, Hien	e S., C	olroya O'Gaora	d S., Jagels a P., Parry C	rry C.		
<b>?</b>	White	head S.	Ruther:	ell B.G	.; Simmo	nds M.	Skeltc	on J.,	stevens	۶.,		
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"DNA-based diagnostic tests for Salmonella species
the structural gene for thin, aggregative fimbriae.
J. Clin. Microbiol. 31:2263-2273(1993).
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-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=94013373; PubMed=8104955;
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J. Bacteriol. 173:4773-4781 (1991).
-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUN
COILED SURFACE STRUCTURES THAT ASSEMBLE
TEMPERATURES BELOW 37 DEGREES CELSIUS. C
FIBRONECTIN.
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SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAIN=S7426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burli Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew (Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew (Riley M., Collado-Vides J., Glasner J.D., Rode M.A., Rose D
                                                                                                                                                                                 MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emoedy L., Trust T.J., "Purification and characterization of
                                                                                                                                                                                                                                                                                                                                       STRAIN=K12 / YMEL;

MEDLINE=93023873; PubMed=1357528;

Arnqvist A., Olsen A., Pfeifer J.

"The Crl protein activates cryptic

fibronectin binding in Escherichia

Mol. Microbiol. 6:2443-2452(1992).
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MEDLINE-97061202; PubMed=8905232;

Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Kashimoto K., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kinura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K. Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
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"A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
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MEDLINE=21218556; PubMed=11319125;
Whilch G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
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         MEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A. Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L. Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H
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STRAIN=0157:H7 / E
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SEQUENCE FROM N
STRAIN=0157:H7
Hammar M., Arngviet A., Bian Z., Olsen A., "Expression of two csg operons is required fibronectin- and congo red-binding curli po
                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
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"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
DNA Res. 8:11-22(2001).
-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CUI COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GITEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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STRAIN=K12 / MC4100;
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Escherichia coli O157:H7.
Bacteria; Proteobacteria;
Enterobacteriaceae; Escher
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                                                                                                                                                                            Armqvist A., Olsen A., Normark S.;

"Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coli can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";

Mol. Microbiol. 13:1021-1032(1994).

-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR TEMPERATURES STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H., Yasunag "Complete genome sequence of enterohemorrhagic Escherichia coli DNA Res. 8:11-22(2001).
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"A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland N. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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"Salmonella enteritidis agfBAC operon encoding thin,
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SPECIES=S
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                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SPECIES-S. typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
MEDLINE=98117058; PubMed=9457880;
"Curli fibers are highly conserved between Salmonella ty
Escherichia coli with respect to operon structure and re
                                                                                                                                     Nature 413:852-856(2001).
[3]
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01-OCT-1996
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Bacteriol. 178:662-667(1996).
FUNCTION: CURLIN IS THE STRUCTURAL
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FIBRONECTIN. THE MINOR SUBUNIT IS T
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                                                                                                                                                                                                                                                                                                                                                                                                                                               34, Last sequence update)
41, Last annotation updat
                                                                                                     STRAIN=27655-3B;
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POTENTIAL.
MINOR CURLIN SUBUNIT.
MW; B18D266B964014B8 CRC64;
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Pred. No. 0.
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            T ASSEMBLE CELSIUS. C
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RESULT
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Matches 34
substrate that
J. Biol. Chem.
[4]
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095271; 095272;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase I) (TNKS-1)
interacting ankyrin-related ADP-ribose polymerase).
TNKS OR TNKS1 OR TINI OR TINF1 OR PARPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
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PIR; JC6040; JC6040.
StyGene; SG10609; CBgB.
Fimbria; Signal; Complete proteome.
POTENTIAL.
                                                                                                 Smith S., de Lange T.;
"Cell cycle dependent localization of the
to nuclear pore complexes and centrosomes.
J. Cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions used by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                MEDLINE=20556282; PubMed=10988299; Chi N.-W., Lodish H.F.;
                                                                                                                                                                                     Smith S., Giriat I., Schmitt A., de Lange "Tankyrase, a poly(ADP-ribose) polymerase science 282:1484-1487(1998).
                                                                                                                                                                                                             MEDLINE=99040105; PubMed=9822378;
Smith S., Giriat I., Schmitt A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ002301; CAA05316.1; -. EMBL; AE008749; AAL20073.1; -.
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           "Tankyrase is a Golgi-associated mitogen-activated protein substrate that interacts with IRAP in GLUT4 vesicles."; J. Biol. Chem. 275:38437-38444 (2000).
                                                                                                                                                   MEDLINE=99454782; PubMed=10523501;
                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                               SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
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Pred. No. 0
                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                 telomeric
                                                                                                                                                                                                 T.; at human telomeres.";
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Phosphorylation; REPEAT
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PROSITE; PS501697; ANK REP REGION; 1.
PROSITE; PS50105; SAM DOMAIN; 1.
Transferase; GlycosylTransferase; NAD;
                                                                                                                                                                                                                                                                                                                PRINTS; PRO1415; ANKYRIN.
SMART; SM00248; ANK; 17.
SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 603303; -.

GO: GO:0000781; C:chromosome, telomeric regio
GO; GO:0003950; F:NAD ADP-ribosyltransferase
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007004; P:telomerase-dependent telome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF082556; AAC79841.1;
EMBL; AF082557; AAC79842.1;
EMBL; AF082558; AAC79843.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl}(N)-acceptor =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at human telomeres.";
Mol. Cell. Biol. 22:332-342(2002)
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HSSP; Q00420; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cook B.D., Dynek J.N., Chang W., Shost "Role for the related poly(ADP-Ribose)
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002110; ANK. InterPro; IPR001660; SAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOId=095271-2; Sequence=VSP 004538, VSP 004539;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Ubiquitous; highest levels in testis.
PTM: Upon insulin-stimulation, phosphorylated on serine reby MAPK kinases.
PTM: ADP-ribosylated (-tope of the PARP family.
SIMILARITY: Contains 15 ANK repeats.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nicotinamide + {ADP-D-ribosyl}(N+1)-acceptor.

SUBUNIT: Oligomerizes and associates with TMKS2. Interacts with the cytoplasmic domain of LNPEP/Otase in SLC2A4/GLUT4-vesicles. Binds to the N-terminus of telomeric TRF1 via the ANK repeats.

SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TMKS is found in the nucleus, associated with TRF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;
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Alternative
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polymerases tankyrase 1 and
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Matches 35
                                                                                   MEDLINE=91293102; PubMed=1712294; Mevel-Ninio M.T.M., Terracol R., Kafatos F.C.; "The ovo gene of Drosophila encodes a zinc finger protein required for female germ line development."; EMBO J. 10:2259-2266(1991).
                                                                                                                                                                                                                    MEDLINE=95021209; PubMed=7935398; Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavembaby-ovo gene region melanogaster: relationship to genetic complexity."; mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ovo protein (Shaven baby protein).
OVO OR SVB.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OVO DROME
P51521; Q9XZ
01-OCT-1996
01-OCT-1996
10-OCT-2003
                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Oregon-R;
                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Arthropoda, Hexapoda, Inse
Neoptera, Endopterygota, Diptera, Brachycera,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227,
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           TISSUE=Ovary;
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             FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF I
LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.
SUBCELLULAR LOCATION: Nuclear (Potential).
DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND
ACCUMULATES IN NURSE CELLS DURING OOGENESIS. STORED IN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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Pred. No. 3.3;
15; Mismatches
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H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1291.
          APPEARS IN THE GERMARIUM AND
DURING OOGENESIS. STORED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Missing (in isoform 2).
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      RESULT 8
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(Rel. 41, Created)
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PROSITE; PRO0028; ZÎNC FINGER C2H2 1; 3.

PROSITE; PRO0157; ZINC FINGER C2H2 2; 3.

Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;

Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS. SIMILARITY: Contains 4 C2H2-type zinc fingers.
                                                                                                            Similarity
                      ARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNS
                                                                    LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
                                              LQNAAAAYIMSAGSG-----GGGCTGNGGGGASGPGGGPSANSGGGGGGG
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C2H2-TYPE 1.
C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
A.-> R (IN REF. 2).
NW; D7068BB2BC0F6F77 CRC64;
                                                                                                                                             MW;
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Pred.
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POLY-GLN.
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No.
  LDGNNLLNFASVSNYNESNS
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                                                                                             41;
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STANDARD;

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Query Match
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the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 185:2330-2337 (2003).

-II- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLICOLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROTEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd I., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Chill M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Chill M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Churcher C., Mungall K.L., Bentley
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Enterobacteriaceae; Salmo
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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10-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - een the Swiss Institute of Bioinformatics are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURLIN MONOMERS.
141
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QSHMAIRVTQ 150
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                                                                                                                                                                                                                                                                                                                                                                                                                    151 AA;
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(Rel. 42, Last annotation update)
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16254 MW;
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Salmonella.
                                                                                                                                                                                                                                                                                                                                     11.7%;
25.4%;
                                                                                                                                                                                                                                                                                                          k; Score 90.5; Dk; Pred. No. 0.3617; Mismatches
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; 161C54326E573495 CRC64;
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                                                                                                       - AII OKGSGNKANI TOYGTOK - - -
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                                                                                                                                                                                                                                                                                                                                     .36;
                                                                                                                                                                                                                                                                                                                                                                 BB
                                                                                                                                                                                                                                                                                                                                                                 1; Length 151;
                                                                                                                                                                                                                                                                                                             43;
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RESULT 9
PER\_DROWI

EMBL;

AAB41367

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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       period length of circadian and ultradian rhythms; an increase in PER dosage leads to shortened circadian rhythms and a decrease leads to lengthened circadian rhythms. Essential for the circadian rhythmicity of locomotor activity, eclosion behavior, and for the rhythmic component of the male courtship song that originates in the thoracic nervous system. The biological cycle depends on the rhythmic formation and nuclear localization of TIM, which promotes complex. Light induces the degradation of TIM, which promotes elimination of PER. Nuclear activity of the heterodimer coordinatively regulates PER and TIM transcription through a negative feedback loop. Behaves as a negative element in circadian restrict transcriptional loop. Does not appear to bind DNA, suggesting indirect transcriptional inhibition (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93196482; PubMed=8450754;
Peixoto A.A., Campesan S., Costa R.H.,
"Molecular evolution of a repetitive r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Interspecific and intraspecific comparisons of the period locus the Drosophila willistoni sibling species.";
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PER DROWI STANDARD; PRT; 109
Q03297; 018421; O18422; P91721; P91722;
01-CCT-1993 (Rej. 27, Created)
                                                                                                                                                                           EMBL;
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MEDLINE=97357421; PubMed=9214747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 579-646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PER-TIM (BY SIMILARITY).

MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN ATLIXCO.
SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domai
SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translocates into the nucleus (By similarity).
SUBCELLULAR LOCATION: Nuclear at specific periods of the
First accumulates in the perinuclear region about one hou
translocation into the nucleus. Interaction with Tim is r
for nuclear localization (By similarity).
PTM: PHOSPHORYLATED WITH A CIRCADIAN RHYTHMICITY, PROBABL
DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLATION COULD BE IMPLI
THE STABILITY OF DER MONOMER AND IN THE FORMATION OF HETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Evol. 10:127-139(1993).
FUNCTION: Essential for biological clock functions.
                U51055;
U51056;
U51057;
U51059;
U51059;
U51060;
U51061;
U51062;
U51063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evol. 14:741-753 (1997)
                                                                  AAB41360.1;
AAB41361.1;
AAB41362.1;
AAB41363.1;
AAB41364.1;
AAB41365.1;
AAB41365.1;
AAB41366.1;
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                                                                                                                                                                                                                                                                                                   noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
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RESULT 10
VG38 BPT2
ID VG38 BPT2
AC . P07875;
DT 01-AUG-1988
DT 01-AUG-1998
DT 01-AUG-1990
DB Receptor recc
GN 38.
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Best Local S
Matches 26
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EMBL; U51066; AAB41371.1; --
EMBL; U51067; AAB41373.1; --
EMBL; U51068; AAB41373.1; --
EMBL; U51069; AAB41374.1; --
EMBL; U51070; AAB41375.1; --
EMBL; U51071; AAB41376.1; --
EMBL; U51072; AAB41377.1; --
EMBL; U51072; AAB41377.1; --
EMBL; L051072; AAB41372.1; --
EMBL; L051072; --
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Biological rhythms: PAS; 2.
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InterPro; IPR000114; PAS_domain.
Pfam; PF09989; PAS; 2.
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                  recognizing
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764
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                                                                                                                    STANDARD;
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                                   08, Created)
08, Last sequence 15, Last annotation
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27.7%;
                protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        115896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GUANA).

GUANA).

MISSING (IN STRAINS MANAUS 4, POI ALEGRE 1 AND PORTO ALEGRE 2).

S -> A (IN STRAINS GUADELOUPE AN MISSING (IN STRAIN MANAUS 3).

A -> T (IN STRAIN 0811.4).
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PAS 2.

PAC.

PAC 2.

PAC 3.

PAC 4.

PAC 5.

PAC 5.

PAC 6.

POLY-LYS.

POLY-GLY.

POLY-GLY.

POLY-GLY.

POLY-SER.

POLY-ALA.

T -> A (IN STRAIN 0811.4).

S -> F (IN STRAIN 0811.4).

G -> V (IN STRAIN GUANA).

G -> A (IN STRAIN GUANA).

G -> A (IN STRAIN GUANA).

G -> A (IN STRAIN GUANA).

G -> A (IN STRAIN SANTA MARIA).

MISSING (IN STRAIN PORTO ALEGRE 3).

MISSING (IN STRAIN PORTO ALEGRE 4).

MISSING (IN STRAIN PORTO ALEGRE 4).

MISSING (IN STRAIN SANAUS 1 AND MANAUS 3).

MISSING (IN STRAINS MANAUS 1 AND MANAUS 3).

MISSING (IN STRAINS MANAUS 1 AND MANAUS 3).
                                     annotati
                                                      sequence
                                                                                                                                                                                                                                                                                                                                                                   Score 90; DB:
Pred. No. 3.9;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                MW; AB6DE050267EC187 CRC64;
                (Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND CANO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G -> V (IN STRAIN PORTO ALEGRE 4).
MISSING (IN STRAINS GUADELOUPE, MA)
PORTO ALEGRE 2, PORTO ALEGRE 1 AND
                                                                                                                  PRT;
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                                                      update)
            update)
1 Gp38).
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3.9;
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PRINCE RELIGIOR OF THE PRINCE 
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Best Local Similarity
Matches 30; Conser
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PRFC_ERWCH STAN

P163T7

01-AUG-1990 (Rel. 1

01-NOV-1991 (Rel. 2

10-OCT-2003 (Rel. 4
                           MEDLINE=89255387; PubMed=2722818;
Delepelaire P., Wandersman C.;
                                                                     STRAIN=B374;
                                                                                            SEQUENCE OF
                                                                                                                                                                                      MEDLINE=91009140; PubMed=2211614;
Delepelaire P., Wandersman C.;
"Protein secretion in Gram-negative bacteria. The extmetalloprotease B from Brwinia chrysanthemi contains
                                                                                                                                                             secretion signal analogous
hemolvsin.";
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
Enterobacteriaceae; Pectol
                                                                                                                                                                                                                                                                                                                                                                                                            Erwinia chrysanthemi.
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                                                                                                                                                         nemolysin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87283911; PubMed=3302276;
Riede I., Drewler K., Eschbach M.L., Henning U.;
"DNA sequence of genes 38 encoding a receptor-recognizing bacteriophages T2, K3 and of K3 host range mutants.";
J. Mol. Biol. 194:31-39(1987).
-i- FUNCTION: V938 is at the tip of the long tail fibers a the phage recognition site for the cellular receptor.
-i- MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fiber
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use
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Pfam; PF05268; GP38; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Viruses, dsDNA viruses,
T4-like viruses.
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                                                                                                                                    Biol.
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S00275; S00275.
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20, Last sequence update)
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EMBL; M59229; AAA24860.1; -.
EMBL; J04736; AAA24862.1; -.
EMBL; J04736; AAA63638.1; -.
EMBL; M60395; AAA63638.1; -.
PIR; A38307; A38307.
PDB; 1GO7; 17-OCT-02.
PDB; 1GO8; 17-OCT-02.
PDB; 1K70; 20-OCT-02.
PDB; 1K70; 20-OCT-02.
PDB; 1K70; 19-OCT-02.
InterPro; IPR006134; Hemlysn_Ca_bind.
InterPro; IPR006025; Pept_M_Zn_BS.
InterPro; IPR006026; Pept_dase_M.
Pfam; PF00353; hemolysinCabind; 3.
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PROSITE; PS00330; HEMOLYSIN_CALCIUM; 1.
Hydrolase; Metalloprotease; Calcium-binding;
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SMART; SM00235; ZnMc; 1.
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264:9083-9089(1989).
3inds 1 zinc ion and 7 calcium ions per subunit (B)
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Q10778;
Q1-OCT-1996
15-JUL-1999
10-OCT-2003
                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1548c/MT1599,
RV1548C OR MT1599 OR MTCY48.17.
                                                                  Bacteria; Actinobacteria;
Corynebacterineae; Mycoba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; M08.001;
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SIMILARITY: Belongs to peptidase family M8.
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S19916; S19916.
P08148; 1LML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                     QYDQLVTRVVTHEMAHASVMVRQVGF 142
                                                                                                                                                                                                                                                                                                                                                                                                                     RYDQLVTRVVTHEMAHA-----VGF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Signal; Cell adhesion; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%;
larity 73.1%;
Conservative
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                                                                                                                                                                                                                                                                                              STANDARD;
                                                               Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69054 MW;
                                                                                    Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.

ACTIVATION PEDTIDE (POTENTIAL).

LEISHMANOLYSIN C1.

ZINC (CATALYTIC) (BY SIMILARITY).

BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

EXINC (CATALYTIC) (BY SIMILARITY).

EXINC (CATALYTIC) (BY SIMILARITY).

EXING (CATALYTIC) (BY SIMILARITY).

EX SIMILARITY.

EX SIMILARI
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                                                               Mycobacterium
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3.9;
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RESULT 14
GP63 LEICH
ID GP63 LEICH
AC P15706;
DT 01-APR-1990
DT 01-APR-1990
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Best Local S
Matches 34
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Pfam; PF01469; Pental
Pfam; PF00823; PPE;
Hypothetical protein
TRANSMEM 14
                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM CONFLICT
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22006494; PubMed=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S. Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical laboratory strains."; J. Bacteriol. 184:5479-5440(2002).
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Nature 393:537-544(1998)."
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TIGR; MT1599; -.
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EMBL; AE007026; AAK45866.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000030; Microbac_PPE.
InterPro; IPR002989; Mycobac_pentapep.
Pfam; PP01469; Pentapeptide_2; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TubercuList; Rv1548c;
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STRAIN=CDC 1551 /
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(Rel. 14, Created) (Rel. 14, Last seq
                                                                                                                                                                                                                                                                                                                                                                                        258
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
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                                               STANDARD;
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sequence
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Pred. No. 4.1;
10; Mismatches
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n N., Holroyd
, Murphy L.,
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Leishmanolysin
(Major surface)
                                                                                                                                                                                                                                                                                               PROPEP
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed during development of Leishmania promastigotes to an infectious form.";
J. Biol. Chem. 267:1888-1895(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; PeptIdase_M8.
Pfam; PF01457; Peptidase_M8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M80672; AAA29238.1;
EMBL; M28527; AAA29235.1;
PIR; A44951; A44951.
HSSP; P08148; 1LML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92112918; PubMed=1370484; Ramamoorthy R., Donelson J.E., Pa
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Mol. Biochem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller R.A., Reed S.G., Parsons M.; "Leishmania gp63 molecule implicated Arg-Gly-Asp sequence.";
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NCBI_TaxID=44271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90205976; PubMed=2320059; Miller R.A., Reed S.G., Parsons M
                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; M08.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Three distinct RNAs for the surface protease gp63 are differentially expressed during development of Leishmania donovani chagasi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
COFACTOR: Binds 1 zinc ion per subunit (By similarity).
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues
P1' and basic residues at P2 and P3'. A model nonapeptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3101. Chem. 267:1888-1895(1992). FUNCTION: Has an integral role during the infection of macrophages
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    adhesion;
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  asparagine
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(POTENTIAL).
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paragine (By
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RESULT 15
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Mailitscher J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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MEDLINE-22954850; PubMed=14593172;

MEDLINE-22954850; PubMed=14593172;

Yamada K., Lim J., Dale J.M., Chen M., Shinn P., Palm C.J.,

Yamada K., Lim J., Dale J.M., Chen M., Pham P.K., Cheuk R.F.,

Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyana K., Ansari Y.,

Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldamith A.D., Gurjal M., Hansen N.F.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Johnes T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 development.";
EMBO J. 17:170-180(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Columbia; TISSUB-Leaf;
MEDLINE=98090460; PubMed=9427751;
Bohmert K., Camus I., Bellini C.;
"AGO1 defines a novel locus of Ara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; eudicotyledons; eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Argonaute protein.
AGO1 OR AT1G48410 OR F11A17.3 OR T1N15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21016719; PubMed=11130712; Theologis A., Ecker J.R., Palm C.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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15-MAR-2004 (Rel.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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43, Last annotation updat
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of Arabidopsis controlling leaf
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Pred. No.
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746730AE8E2A2E7C
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edons; core eudicots; rosid
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Search completed: March 11, 2004, 18:34:54 Job time: 8.3 secs
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Matches 36
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EMBL; AC007932; AAD49755.1; -.

EMBL; BC020883; AAF79718.1; ALT SEQ.

EMBL; BC000941; AAN41341.1; -.

InterPro; IPR003100; PAZ.

InterPro; IPR003156; Piwi.

Pfam; PF02170; PAZ; 1.

Pfam; PF02171; Piwi; 1.

PROSITE; PS50821; PAZ; 1.

PROSITE; PS50822; PIWI; 1.

PROSITE; PS50821; PS5082; PAZ; 1.

Developmental protein; Alternative splicing.

DOMAIN 391 501 PAZ.
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome.";
Science 302:842-846(2003).
Science 302:842-846(2003).
-i- FUNCTION: Essential for proper development of leaves and floral organs, and formation of axillary meristems.
-i- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-i- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced. According to EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stages.
-!- SIMILARITY: Belongs to the argonaute family.
-!- SIMILARITY: Contains 1 PAZ domain.
-!- SIMILARITY: Contains 1 Piwi domain.
-!- CAUTION: Ref. 2 (AAP79718) sequence differs from that shown due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=004379-1; Sequence=Displayed;
-!- TISSUE SPECIFICITY: Widely expressed at low levels.
-!- DEVELOPMENTAL STAGE: Expressed throughout all developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Empirical analysis of transcriptional activity in the Arabidopsis
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                                                                   214 TITPEVTSRGVNRAVMKOLV 233
                                                                                                        121 LVTRVVTHEMAHASVMVRQV 140
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                                                                                                                                                                                                                                                    27 GGGGNHNGGGNSSGPDSTLSI------YQYGSANAALALQSDARKSETTITQSGYG 76
                                                                                                                                                                                                                                                                                                  36;
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                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                          EQLSVEQGAPSQAIQPIPSSSKAFKFPMRPGKGQSGKRCIVKANHFFAELPDKDLHHYDV 213
                                                                                                                                                                                                                   GGYGGGRGGGPSSGPPQRQSVPELHQATSPTYQAVSSQPTLSEVSPTQVPEPTVLAQQF-
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1048 AA; 116190 MW; 3E5146343A09C541 CRC64;
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                 11.0%;
                                                                                                                                                                                                                                                                                          ; Score 85.5; DB 1; Length 1048; ; Pred. No. 9.2; 17; Mismatches 60; Indels 27
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1: sp_archea:*
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5: sp_invertebrat:
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11: sp_virus:*
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16: sp_bacterias:
16: sp_archeap:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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033802 salmonella
07x243 citrobacter
07x240 citrobacter
08cw63 escherichia
07x237 enterobacte
054069 salmonella
09s3j5 escherichia
033801 salmonella
033801 salmonella
07x248 enterobacter
08eiha shewanella
07x241 citrobacter
08cw64 escherichia
07x244 citrobacter
07uc21 shigella fl
083ru7 shigella fl
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WNAKWSDITYGQYDQ 120 	SIYQYGSANAALALQ 60              SIYQYGSANAALALQ 60	152; ls 0; Gaps 0;				•	intestinal epithelial	h	Pfeifer J.D.,					Enceropacteriales;	•								

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Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Citrobacter
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515700; CAD56672.1; -.
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Bacteria; Proteobacteria; Gammar
Enterobacteriaceae; Citrobacter
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Pred. No. 1.7e
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        STRAIN=Fec39;
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                                                                                                                                  Enterobacteriaceae;
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Bacteria; Proteobacteria;
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MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Ro
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete ge
of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

EMBL; AE016759; AAN79779.1; -.
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"Virulence of Salmonella enteritidis in chickens correlates
colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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EMBL; AJ515702; CAD56678.1; -.
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                              Proteobacteria;
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   Eeria; Gammaproteobacteria;
Escherichia.
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Pred. No. 7e-28;
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                                  Enterobacteriales;
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RESULT 9 Q7X238

Q7X238

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O33801;
O1-JAN-1998
O1-JAN-1998
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Normark S.J., Rhen M.,
"Expression of thin, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99314153; PubMed=10386375;
La Ragione R.M., Collighan R.J., Woodward M.J.;
La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curlisation of Escherichia coli O78:K80 isolates associated with
IS1 inserti on in csgB and reduced persistence in poultry infection.";
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL, AJ131756; CAB45380.1; -.
NON_TER 29
                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                           Salmonella typhimurium
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Bacteria; Proteobacteria;
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EMBL; AJ000514;
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163
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AVVVQKQSHMAIRVTQ
                    RVVTHEMAHASVMVRQ
                                        GNSAAI-----SAAIIQKGSGNKANITQYGTQKTAVVVQKQSHMAIQANITQYGTQKT
                                                           GNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV------GQYDQLVT
                                                                                  GSKLLSVISQ-ERGGNNRAKVDQAGNYNFAYIEQTGNAN---
                                                                                                     GSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY
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; CAA04150.1; -.
                                                                                                                                                                                                                                        Lorentz R.G.,
                                                                                                                                                                  19318 MW;
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Salmonella.
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., "Genome sequence of the dissimilatory metal ion-reducing bacterium Nat. Biotechnol. 20:1118-1123(2002).
                                                                                                                                                                SEQUENCE 139 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gam
Alteromonadaceae; Shewanella.
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01-MAR-2003
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"Production of Cellulose and Curli Fimbriae by Members of tl
Enterobacteriaceae Isolated from the Human Gastrointestinal
Infect. Immun. 72:4151-4158(2003).

EMBL; AJ515702; CAD56677.1; -.
SEQUENCE 151 AA; 15985 MW; FOB82BD2A27882B7 CRC64;
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                                                                                                                          Similarity
                       NNATI DQWNAKNSDI TVGQYDQLVTRVVTHEMAHASVMVRQVGFGNNATANQY
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       NKASITQ-----
                                                 SGRDNLIDLVQQGTANQGIVFQSGSDNS-AYVTQAGNDNISLVTQIGTNNEVQLLQVGAQ
                                                                          $GPDSTLSIYQYGSANAALALQ$DARK$ETTITQ$GYGNGADVGQGADNSTIELTQNGFR
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                                                                                                            Conservative
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                                                                                                                                                                AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.9%; Score 107.5; D) 30.8%; Pred. No. 0.31; cive 14; Mismatches
-IGN-DNLVQ---LNQLGSGNFSIQQIADGAAISITQY
                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gammaproteobacteria; Alteromonadales;
                                                                                                        Score 105; DB 1.
Pred. No. 0.45;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last
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                                                                                                                                DB 16; Length 139;
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Q7X241
ID Q7X24
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DT 01-0C
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DT 01-0C
DT 01-0C
CHTC
GN CSGB.
OS Citrc
OC Enter
OC Enter
OC NCBI
RN [1]
RP SEQUE
RT EMBL,
RA Togad
RT EMBL,
SQ SEQUE
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Q8CW64
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Best Local
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                                                                                                                                                               EMBL; AEO:
Complete |
                                                                                                                                                                        "Extensive mosaic structure revealed by the complete of uropathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002). EMBL; AE016759; AAN79778.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8CW64;
Q8CW64;
01-MAR-2003
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                STRAIN=06:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., S Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mocaia transcriptions."
                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Minor curlin subunit precursor.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli 06.
                                                                                                                                                                                                                                                                                                                                                                                                             CSGB OR C1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zogaj X., Bokranz W., Nimtz M., Romling U.; "Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriacese Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515701; CAD56674.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Fec4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=546;
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66 SETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRV 125
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                                                                                                        Similarity
                           FAVNELSKSSFNQAAII----GQAGTNNSAQLRQGGSKLLTVVAQEGSSNRA-KIDQTGDY
                                                      FAAIVVSGSAL--AGVVPQWGGGNHNGGGNSSGPDSTLSIY-QYGSANAALALQSDARK 65
                                                                                                                                                 proteome.
160 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNGADVGQGADNSTIELTQNGFRNNATĮDQWNAKNSDITVGQYDQLVTRV
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                                                                                         Conservative
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3 (TrEMBLrel. 25, Last sequence update)
3 (TrEMBLrel. 25, Last annotation update)
component of curlin monomers.
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AA; 16149 MW;
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                                                                                    Score 104.5; DB
Pred. No. 0.58;
19; Mismatches
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Pred. No. 0.55
L3; Mismatches
                                                                                                                                              49F68448D979B986 CRC64;
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                                                                                                                DB 16;
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01-0CT-2003
01-0CT-2003
01-0CT-2003
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                                                                                                                                                                                                                        Q7X244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; SEQUENCE 502 AA; 57
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                        SEQUENCE FROM N.A.
STRAIN=Fec2;
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01-MAR-2003
  Enterobacteriaceae
                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                        Citrobacter sp.
                                                                                                                                                  Nucleation component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gam
Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
           Zogaj X., Bokranz W., Nimtz M., Romling U.; "Production of Cellulose and Curli Fimbriae
                                                                             NCBI_TaxID=213763;
                                                                                                Enterobacteriaceae;
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                                                                                                                                                                                                                      PRELIMINARY;
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  Isolated
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f curlin monomers.
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Pred. No. 2
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  Family ract.";
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Q7UCZ1;
01-OCT-2003
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EMBL; AE016981; AAP16542.1;
PROTENCE 151 AA; 15868 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of Shigella"
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EMBL; AJ515700; CAD56671.1; -.
SEQUENCE 151 AA; 16158 MW; BD0
                                                                                                                                                                                                                                                                                                                                                                                                                                flexneri serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).
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MEDLINE=22590274; PubMed=12704152;
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STRAIN=2457T / ATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shigella flexneri
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                                                                                                                                                                                                                                                                                                                                                                                      15868 MW;
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28.8%;
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geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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12.2	12.3	12.5	12.5	12.7	12.7	12.7	12.7	12.7	12.9	13.5	14.4	14.4	14.4	14.7	14.7	14.7	14.7	15.2	15.2
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AAB36331	ABU44579	AAE36890	ABR82647	AAB36328	AAB36336	AAB36323	AAE36891	AAW32312	ABR82645	ABR82649	AAB36319	AAB36324	AAB36340	AAB36337	AAB36327	AAB36322	AAB36342	AAB36320	AAB36339
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# ALIGNMENTS

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RESULT 1
AAB36348
WPI; 2000-672631/65.
N-PSDB; AAC64624.
                                                                                                                       White AP,
                                                                                                                                                                        12-OCT-2000.
                                                                                                                                                                                    WO200060102-A2
                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                            Salmonella enteritidis.
                                                                                                                                                                                                                              Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                      26-FEB-2001
                                                                                                                                                                                                                                                                 AAB36348;
                                                                                                                                                                                                                                                                              AAB36348 standard;
                                                                                                                                                05-APR-1999;
                                                                                                                                                           05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                        vaccine; immune response;
                                                                                                                                                                                                                                         AgfA::PT3#3 amino acid sequence
                                                                                                                                   (UYVI-) UNIV VICTORIA.
                                                                                                                       Doran JL,
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                99US-0127888P
                                                                                                                                                                                                                                                                              protein;
                                                                                                                       Collison
                                                                                                                                                                                                                        immunogen.
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                                                                                                                       Kay WW;
                                                                                                                                                                                                                                          NO:16
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaces for the production of Assembly; (2) and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

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RESULT 2
AAR74625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequences grown on a Salmonella, E. coil or acid sequence or sequences grown on a Salmonella, E. coil or acid sequence or sequences grown on a Salmonella, E. coil or acid sequence or sequences grown on a Salmonella, E. coil or acid sequence or sequences grown on a Salmonella, E. coil or acid sequence or sequences grown on a Salmonella, E. coil or acid sequence or sequences or sequences or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for cellciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the accemplification of the accemplification of the accemplification.
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                                                         Eliciting an immune respons strains, vector constructs,
                                                                                                        N-PSDB; AAQ87467
                                                                                                                                                                                                                                  26-APR-1993;
                                                                                                                                                                                                                                                                                           10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                     Salmonella;
                                                                                                                                                                                              (UYVI-) UNIV VICTORIA INNOVATION, &
                                                                                                                                                                                                                                                              26-APR-1994;
                                                                                                                                                                                                                                                                                                                          WO9425598-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    AgfA sequence
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26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR74625 standard; protein; 151 AA.
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                                                                                                                        1994-358275/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the present invention
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                                                                                                                                                                                      KING
                                                                                                                                                      Collinson
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                                                                                                                                                                                                                                                                                                                                                                                     AgfA; vaccine.
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                                                                       response
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Pred. No. 2.2e-67;
Mismatches 0;
                                                                       Salmonella
                                                                                                                                                    SC,
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                                                                                                                                                                                                CORP
                                                                                                                                                    Doran
                                                       using attenuated Salmonella
g. fimbrial type proteins.
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The

Salmonella AgfA protein and DNA are used

in vaccine

and genetic

Disclosure; Fig

7B;

95pp;

English. or

contg.

type

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RESULT 3
AAB36341
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               The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SER1/TMAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinantion of a recombinant gene back into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid polymer comprising a recombinant of the chromosome of the segment or segments of foreign amino acid polymer comprising a recombinant agfA protein containing a replacement segment or segments of foreign amino acid polymer comprising separation and the containing a recombinant segment or segments of foreign amino acid polymer comprising segments of foreign amino acid polymer comprising segments of foreign amino acid polymer comprising segments of foreign amino acid polymer comprising segments of foreign amino acid polymer comprising segments of foreign amino acid polymer comprising segments of segments of foreign amino acid polymer comprising segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments of segments segments of segments of segments of segments segments of segments segments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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N-PSDB; AAC64617.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151 AA;
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Pred. No. 1.6e-57;
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The present sequence represents agfA encoded derived from Salmonella enteritidis 27655-3b.
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Best Local S
Matches 135
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            The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described a sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinate companies.
                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                           Disclosure; Page 136; 139pp; English.
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protein useful for eliciting

immune response in animal

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RESULT 6
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Matches 131;
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WPI; 2000-672631/65.
N-PSDB; AAC64622.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑĄ;
                                                                                                                                                                                                       99US-0127888P
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76.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN
                                                                                    Collison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 618;
Pred. No. 1
                                                                                    SK,
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                                                                                 Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
.6e-53;
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Best Local Sim
Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                   against the inserted epitope, and hybrid fimbride are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 135; 139pp; English
                                               121
  121
                                                                                              61
                                                                                                                                         61
                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGFDSTLSIYQYGSANAALALQ
                                                                                                                                                                                          _
                                                                                                                                                                                                                                                                                                           Similarity
                                     NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                    SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                        76.6%;
80.1%;
                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                          Score 580; DB 3; L
Pred. No. 9.8e-50;
"" matches 23;
                                                                                                                                                                                                                                                                                                                       Length 151;
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                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               in
                                                                                       120
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RESULT 7
AAB36347
Escherichia
Synthetic.
                                                                    Salmonella enteritidis.
                                                                                 vaccine; immune response; immunogen.
                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin;
                                                                                                                                                         AAB36347 standard; protein; 151
                                                                                                           AgfA::PT3#2
                                                                                                                          26-FEB-2001
                                                                                                                                          AAB36347;
                                                           COLI
                                                                                                         amino acid sequence SEQ ID NO:14.
                                                                                                                         (first entry)
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epitope;

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA

05-APR-2000; 2000WO-CA000356

12-OCT-2000 WO200060102-A2

99US-0127888P.

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AAB36353
ID AAB3
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DE AgfA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC directing recombination of a recombinant gene into the chromosome of the back into the chromosome of the homologous species; (3) directing recombination of a replacing the native back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising a replacement segment or segments of foreign amino acid golymer comprising a recombinant AgfA content acid sequence or sequences grown on a Salmonella, E. coli or conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation conjunction, the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong communogenicity and adhesion properties relevant for an efficient live cagainst the inserted epitope, and hybrid fimbriae are usually strong construction which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and conversed to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151 AA;
                 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                            AgfA::PT3#8 amino acid sequence SEQ ID NO:26
                                                                                                           26-FEB-2001
                                                                                                                                                                                         AAB36353 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                     LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doran JL,
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                                                                                                      (first entry)
response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.4%;
80.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 578; DB 3;
Pred. No. 1.5e-49;
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                                                                                                                                                                                                                                                                                                                                        Matches 122;
                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
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                                                                                                                                                                                                                                                                                                                                                                               the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                  nexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
121
                                       121
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                                                                                                                                                                                                                                                                         Similarity
                                     NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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                                                                                                                                                                                                                                                                   76.2%;
80.8%;
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                                                                                                                                                                                                                                                                                                                                                                               present invention
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                                                                                                                                                                                                                                                   Score 577; DB 3; Length 151, Pred. No. 1.9e-49; 5; Mismatches 24; Indels
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cc back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA contein containing a replacement segment or segments of foreign amino card sequence or sequences grown on a Salmonella, E. coli or contein contein an animal in conjunction with a carrier or diluent. (1) is consecut the animal in conjunction with a carrier or diluent. (1) is consecut for the expression of recombinant AgfA protein which is useful for conjunction an animal. In a fimbrial presentation conjunction generally the hybrid fimbrin protein possesses both the conjunction properties relevant for an efficient live conjunction, the carrier fimbrial subunit proteins are usually strong conjunction, the carrier fimbrial subunit proteins are usually strong conjunction, the carrier fimbrial subunit proteins are usually strong the spans the inserted epitope, and hybrid fimbriae are easy and conjunction of the recent invention.
                                                                                       Matches
                                                                                                                         Query Match
                                                                                                                                                             Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                 the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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N-PSDB; AAC64628
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                                                                                                         Local
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                                                                                                       Similarity
                                 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                   76.0%;
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                                                                             Score 575; DB 3; 1
Pred. No. 3.1e-49;
5; Mismatches 23;
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CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for the pression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation conjunction which as the conjunction of conjunction with a carrier of the second of the celiciting an immune response in an animal. In a fimbrial pushers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the cimmunogenicity and adhesion properties relevant for an efficient live conjunction, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
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AAB36350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
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N-PSDB; AAC64626.
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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Matches 122;
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriacese for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologus fimbrin subunits, respectively; (2) directing recombination of a recombination of the homologous species; (3) directing recombination of a recombination of a recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
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N-PSDB; AAC64630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doran JL,
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Pred. No. 3.9e-49;
6; Mismatches 23
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RESULT 12
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Best Local S
Matches 121
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                                                                                                                             WPI; 2000-672631/65.
N-PSDB; AAC64627.
                                                                                                                                                                                                                                              05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement;
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                                                                                                                                                                                                                                                                                                                                           Escherichia
                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#6 amino acid sequence SEQ ID NO:22
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                                                                                                                                                                  Doran JL,
                                                                                                                                                                                                                                                                                                                                           coli.
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No. 1.5e-48;
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                                                                                                                                                                                                                                                                                                                                                                                               fimbrin; epitope;
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign DI sequence which encodes a foreign epitope or antigen. Also describe

Disclosure; Page 137; 139pp; English

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

N-PSDB; AAC64631.

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RESULT 13
AAB36355
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Best Local
WPI; 2000-672631/65
                                                                                       White AP,
                                                                                                                                                                                                                                                                           05-APR-1999;
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                                                                                                                                                                               (UYVI-) UNIV VICTORIA.
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                                                                                  Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.9%;
                                                                                  Collison
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Pred. No. 1.9e
5; Mismatches
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AgfA sequence

Salmonella; AgfA; vaccine

Salmonella enteritidis

10-NOV-1994 WO9425598-A2 27-AUG-2003 25-MAR-2003 26-JUN-1995

(revised)
(first entry) (revised) AAR62761;

AAR62761 ID AAR6

AAR62761 standard; protein; 120 AA

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CC directing recombination of a recombination of a recombination of the chromosome of the chomologous species; (3) directing recombination of a recombinant gene into the chromosome of the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant Agfa comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino caid sequence or sequences grown on a Salmonella, E. coli or an arrive control of the control of control of the animal in conjunction with a carrier or diluent. (1) is cuseful for the expression of recombinant Agfa protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation celiciting an immune response in an animal. In a fimbrial presentation celiciting an immune response in an animal. In a fimbrial presentation celiciting an immune response in an animal in conjunction with a carrier fimbrial subunit protein possesses both the immune, the carrier fimbrial subunit proteins are usually strong the immune response in an animal are usually strong and immune response in an animal are usually strong the immune response in an animal response in an animal conjunction an immune response in an animal conjunction and immune response in an animal conjunction and immune response in an animal conjunction and immune response in an animal conjunction and immune response in an animal conjunction and immune response in an animal conjunction and immune response in an animal conjunction and interction and immune response in an animal conjunction and immune res
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Matches 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant and the comprision of the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision and the comprision an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 139; 139pp; English
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                                               NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                            SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 2.4e-48;
5; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
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Matches 95
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                                                                                                          WPI; 1997-309886/28
N-PSDB; AAT74141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis 27655-3b InphoA mutant agfA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 7A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                         Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                         26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                          26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
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29-SEP-1997
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                                                                                                                                                                                                                                               (UYVI-) UNIV VICTORIA INNOVATION &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                             94US-00233788
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97.9%;
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Pred. No. 1.3e-40;
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                                                                                                                                                                                                                                                                              strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                          Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an agfA fragment encoded by an agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 7; 85pp;
                                                                                                                                                                                Local Similarity
                                       97
  76
                                                                             16
                                                                                                                                                             95;
                                                                                                      HASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
                                       FRNNATIDOWNAKNSDITYGOYGGNNAALVNOTASDS 133
                                                                               NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
FRNNATIDOWNAKNSDITYGOYGGNNAALVNOTASDS 112
                                                                                                                                                               Conservative
                                                                                                                                                                                64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                             2
                                                                                                                                                                                Score 487; DB 2;
Pred. No. 1.3e-40;
                                                                                                                                                               Mismatches
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64.3
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Copyright (c) 1993 - 2004 Compugen Ltd
US-08-233-788A-59
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US-09-477-135A-131
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US-09-252-991A-26438
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US-09-142-648B-7
US-08-614-377A-7
US-08-36-115C-3214
US-09-336-115C-12
US-09-336-115C-6
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US-09-336-115C-6
US-09-336-115C-6
US-09-336-115C-2
US-08-08-832-2
US-08-469-880-2
US-08-718-641-2
US-08-718-641-2
US-08-719-641-2
US-08-541-780-2
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Sequence 59, Appl
Sequence 57, Appl
Sequence 5434, Ap
Sequence 26438, A
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 69, Appli
Sequence 69, Appli
Sequence 2, Appli
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1 MKILKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ

60 0;

Query Match 86.3%; Score 653; DB 1; Length 151; Best Local Similarity 89.4%; Pred. No. 1.8e-60; Best Local Similarity 3; Mismatches 135; Conservative 3; Misma	US-08-233-788A-59 US-08-233-788A-59 US-08-233-788A-59 US-08-233-788A-59 US-08-233-788A-59 US-08-233-788A-59 US-08-233-788A-59 US-08-233-788A-59  US-08-233-788A-59  US-08-233-788A-59  US-08-233-788A-59  US-08-233-788A-59  US-08-233-788A-59	28 78 10.3 1864 2 US-08-804-227C-3 Sequence 29 77.5 10.2 518 3 US-09-043-123-2 Sequence 30 77.5 10.2 2314 4 US-09-252-991A-32096 Sequence 31 77 10.2 1612 1 US-08-169-277-2 Sequence 32 77 10.2 1612 1 US-08-169-277-2 Sequence 33 76.5 10.1 892 4 US-09-328-352-6467 Sequence 35 76 10.0 273 4 US-09-328-352-6467 Sequence 37 76 10.0 906 1 US-08-687-379-2 Sequence 38 76 10.0 906 1 US-08-687-379-2 Sequence 39 76 10.0 906 1 US-08-687-379-2 Sequence 40 76 10.0 906 1 US-08-687-379-4 Sequence 41 76 10.0 906 4 US-08-216-326-2 Sequence 42 76 10.0 906 4 US-08-216-326-2 Sequence 44 1 76 10.0 906 4 US-08-216-326-2 Sequence 44 1 76 10.0 906 4 US-08-216-326-2 Sequence 56 10.0 906 4 US-08-216-326-2 Sequence 57 10.0 943 4 US-09-056-556-204 Sequence 57 10.0 943 4 US-09-072-967-204 Sequenc
151 18	ECTION	Sequence 3, Appli Sequence 2, Appli Sequence 49, Appli Sequence 32096, Appli Sequence 3159, Ap Sequence 5, Appli Sequence 6167, Ap Sequence 7854, Ap Sequence 7854, Ap Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 204, Appli

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                                          US-09-543-681A-5434
                                                           RESULT 3
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US-08-233-788A-57
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Sequence 5434, Application US/09543681A Patent No. 6605709 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: METHODS AND C
TITLE OF INVENTION: OF SALMONELLA
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                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 35,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01
FILING DATE: 26-APR-1994
                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                 FRNNATIDQWNAKUSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                     NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
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William W.
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                                                                                                                                                                                                                  Score 487; DB 1;
Pred. No. 2.5e-43;
2; Mismatches 0
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; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-477-135A-131
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GENERAL INFORMATION:
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PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60//
PRIOR FILING DATE: 1995-06-15
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CURRENT APPLICATION NUMBER: US/09/477,135A
CURRENT FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08990823
PRIOR FILING DATE: 1997-12-15
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TITLE OF INVENTION: Mycol
TITLE OF INVENTION: immur
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIT
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2:
TYPE: PRT
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                                                                                                      57 L----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
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1 Similarity 28.0%;
37; Conservation
                                                                                                                                                                                                                                                Similarity
                                                                                                                                            ALFVSLVVSNLLGQNAPAIAATEAAYEQMWAQDVAAMFGYHAGASAAVSALTPFGQALPT 155
                                                                                                                                                                               AAFAAIVVSG-----SALAGVYDQLVTRVVTHEMAHASGPDSTLS-IYQYGSANAA 56
                                                                        VAGGGALVSAAAAQVTTRVFRNLGL-ANVGEGN
IGSGNIGSSNIGFGN-VGPGLTAALNNIGFGNTGSNN 243
                                   ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                          11.4%; Score 86.5;
24.8%; Pred. No. 2.
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Pred. No.
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RESULT 6
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APPLICANT: Marc J. R.
TITLE OF INVENTION: N
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GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garvey, George A
REGISTRATION NUMBER: 1737
REFERENCE/DOCKET NUMBER: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1415
                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Smit, John
APPLICANT: Bingle, Wade H
TITLE OF INVENTION: Bacterial surface protein expression
NUMBER OF SEQUENCES: 10
                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELEPHONE:
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                                                                                                                                           FILING DATE:
                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                             ITY: Arlington
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WENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

WENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                             Virginia
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                                                                                                                                                                                                                                                                                                                                                                                3000 South Eads Street
  703-684-5600
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                                                                                                                                      09-FEB-1994
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25.6%;
                                                                                                                                                         US/08/194,290
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                                        5946-1
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                                                                                                                                                     TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34053
REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/194,290
FILING DATE: 09-FEB-1994
                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TBAO, Y. ROCKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURENT APPLICATION DATA: APPLICATION UMBER: US/08/614,377A FILING DATE: 12-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
TYPE: amino STRANDEDNESS:
                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                             ENGTH:
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                                                                             1026 amino acids
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225 Franklin Street
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No. 5976864ellini, John F.

VENTION: EXPRESSION AND SECRETION OF

VENTION: TOTAL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
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RESULT 9
US-09-134-001C-3214
    Sequence 3214, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: LYIN DOUCETTE STARM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
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US-09-142-648B-7
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Best Local
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SEQ ID NO 7
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Patent No. 6210948
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PRIOR TILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1996-03-12
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 08106/002002
CURRENT APPLICATION NUMBER: US/09/142,648B
CURRENT FILING DATE: 1999-03-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Caulobacter crescentus
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                                                                                                                                                                                                                               TASSTIASLVAADATTL 590
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                                                                                                                                                                                                                                                                              TTVNLSGTGTSLGIGRGALTATPTANTLTLNVNGLTTTGAITDSEAAADDGFTTINIAGS
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                                                                                                                                                                                                                                                                                                        TTITQSGYGNGADYGOGA-----DNSTIELTQNGFRNNATI-DQWNAKNSDITYGQYGGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 4.0
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No. 6210948ellini,
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1UMBER: US 07/614,377
                                                                                                                                                                                                                                                                                                                                                                                                                 10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.8%; Score 82; DB 24.8%; Pred. No. 7.9; tive 28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                             Score 82; DB 3; Length 1026; Pred. No. 7.9; 8; Mismatches 55; Indels
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US-09-336-115C-12
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Sequence 12, Application US/09336115C Patent No. 6576244 GENERAL INFORMATION:
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Patent No. 6
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US-09-336-115C-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weltzin, Richard A.
APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immuni
TITLE OF INVENTION: Methods Against Helicobacter
FILLE REFERENCE: 06132/055002
CURRENT FILING DATE: 1999-06-18
CURRENT FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/100,258
PRIOR FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 24
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NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3214
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SIGNAL
LOCATION: (1)...(18)
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Helicobacter
                                                                                                                                                                                                                                                                Local Similarity
213 NNIIEHYYTENGKEIPVSYSGGSSFSPTIQLTYHNNAENLLQQAATIMQVLITQ 266
                                                                          159 GILSIDEYQKLNQAYQI-----IQTALNQNQGGGMPALNDTTKTGVVNIQQTNYRTTTQ 212
                                           99 NNATIDQWNAKNSDITVGQYGG-----
                                                                                                               43 STĻSIYQYGSAŅAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR----
                                                                                                                                                      99 AYQAVALALNAAVGMWQVIALFIGCGPGPTNNQSYQSFGNTPALNGTTTTCNQAYGTGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           612 GFSPEYTMSVWMGFNK---VKQYGTNS 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566 KAYGSAYGH------GVSGVNMGAKTGTGTYGQEIYEKYNLPDNAAKDVWIN 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 SAFAAI-----ANGGTYNNAHSIQKVVTHEGDTIBYEHTSHKAMKDYTSYMLABILKGTF 565
                                                                                                                                                                                                8 AFAAIVVSGSALAGVYDQLVTRV----------
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19.0%; Pred. No...
ative 27; Mismato
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Pred. No. 5.7;
12; Mismatches
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                                       ----NNAA-LVNQTASDSSVMVRQ 139
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                                                                                                                  Query Match
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Best Local Similarity
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LENGTH: 691
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: US 09/100,258
PRIOR PILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
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TITLE OF INVENTION: HI and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
PILE REFERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: US 09/100,258
PRIOR PILING DATE: 1998-06-19
PRIOR PILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                                                                                                                                    NAME/KEY: SIGNAL LOCATION: (1)...(20)
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ORGANISM: Helicobacter pylori
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                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                              OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                               NAME/KEY: VARIANT
LOCATION: 721
                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                 ORGANISM: Helicobacter pylori
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                                     31 VTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYGQGADNSTI 90
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                                                                                                 Similarity
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ITCNRFESTGPGKSMSIDEFKKLNEAYQIIQQALKNQSGFPELG-GNGTKV---SVNYNY 207
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                                                                                               10.7%;
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19.0%; Pred. No.
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                                                                          18; Mismatches
                                                                                               Score 81;
Pred. No.
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SEQ ID NO 69
LENGTH: 1095
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Best Local
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ZIP: 22202-0286

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High TITLE OF INVENTION: Molecular Weight Proteins FILE REFERENCE: 1038-861 MIS:jb CURRENT APPLICATION UNMBER: US/09/206,942 CURRENT FILING DATE: 1998-12-08 EARLIER APPLICATION NUMBER: 09/167,568 EARLIER FILING DATE: 1998-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Loosmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                        ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                     ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             840 NTVNVTANAGDLTV-----GNGAEIN 860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAALVNOTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITOSGYGNGADVGQGADNSTIEL-----TQNGFRNNATIDQWNAKNSDITVGQYGGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGSILGGIESSSGSVTLTATEGALAVSNISG--NTVTVTANSGALTTLAGSTIKGTESVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08038682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
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                                                                                                                                                                                                                                                                                                                                                                                                             BARENKAMP, STEPHEN J
ST. GEME III, JOSEPH W
VENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.6%; Score 80.5;
26.4%; Pred. No. 12;
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                                                                      Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                      #1.25
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ATTORNEY/AGENT INFORMATION:

NAME: BERKSTRESSER, JERRY W REGISTRATION NUMBER: 22,651 REFERENCE/DOCKET NUMBER: 10:

1038-293

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RESULT 15
US-08-302-832-2
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                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,832
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08302832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US pct/us93/02166
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5603938-Typeable Haemophilus
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
STRANDEDNESS: single
TOOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                   NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1168 TGSILGGIESSSGSVTLTATEGALAVSNISG--NTVTVTANSGALTTLAGSTIKGTESVT 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1226 TSSOSG-----DIGGTISGGTVEVKATESLTTOSNSKIKATTGEANVTSATGTIGGTISG 1280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 SGSALAGVYDQ--LVTRVVTH---EMAHASGPDSTLSIYQYGSANAALALQS-DARKSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
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Similarity 26.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virginia : U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B: Shoemaker and Mattare, Ltd.
2001 Jefferson Davis Hwy., 1203 Crystal plaza
Bldg. 1
                     (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                     Version #1.30
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                                                                                                                                                                                                                                Query Match
10.6%; Score 80.5;
Best Local Similarity 26.4%; Pred. No. 20;
Matches 39; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1536 amino ac
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
1281 NTVNVTANAGDLTV-----GNGAEIN 1301
                                                                     1226 TSSÓSG-----DIGGTISGGTVEVKATESLTTÓSNSKIKATTGEANVTSATGTIGGTISG 1280
                                                                                                                                                 1168 TGSILGGIESSSGSVTLTATEGALAVSNISG--NTVTVTANSGALTTLAGSTIKGTESVT
                                     122 NAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                        69 TITQSGYGNGADVGQGADNSTIEL-----TQNGFRNNATIDQWNAKNSDITVGQYGGN 121
                                                                                                                                                                                       15 SGSALAGVYDQ--LVTRVVTH---EMAHASGPDSTLSIYQYGSANAALALQS-DARKSET 68
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                   DB 1;
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1225

Search completed: March 11, 2004, 18:44:50 Job time: 17.4 secs

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Regult
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                 Score
                     113.5
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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757
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     GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
       182
597
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                                                     15 US-10-369-493-20638

16 US-10-238-075-1549

3 US-99-793-306-146

3 US-99-996-634-131

10 US-09-997-182-131

10 US-09-997-181-131

10 US-09-9984-334-1

14 US-10-004-115A-34

14 US-10-327-108-1

14 US-10-156-761-9411

14 US-10-185-990-11
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   US-09-996-194-16
US-10-156-761-13173
US-10-369-493-20096
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Sequence 20638, A
Sequence 1549, Ap
Sequence 146, App
Sequence 131, App
Sequence 131, App
Sequence 131, App
Sequence 131, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 9411, App
Sequence 10, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
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45	44	43	42	41	40	39	38	37	36	<b>3</b> 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
76	76	76	76.5	76.5	77	77	77	77.5	77.5	77.5	78	78	78	78.5	79	79.5	80	80	80	80.5	80.5	0	81	81	81	82	82	82	82
10.0	10.0	10.0	10.1	10.1	10.2	10.2	10.2	10.2	10.2	10.2	10.3	10.3	10.3	10.4	10.4	10.5	10.6	10.6	10.6	10.6	10.6	10.6	10.7	10.7	10.7	10.8	10.8	10.8	10.8
943	906	210	892	388	565	495	495	518	404	395	1376	310	278	385	552	354	814	503	481	1536	1536	1095	745	691	691	1236	1026	1026	534
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US-10-193-002-199	US-10-251-661-2	US-10-369-493-20095	US-09-952-267-5	US-09-738-626-5044	US-10-389-566-1717	US-10-369-493-7187	US-10-369-493-4429	US-09-976-297-2	US-10-389-566-1029	US-10-369-493-18788	US-10-238-075-560	US-09-815-242-13976	US-09-810-264-28	US-10-156-761-13909	US-10-369-493-3745	US-09-820-843A-21	-10	US-10-153-668-230	US-10-153-668-352	US-10-193-764-63	US-10-092-880-2	US-10-193-764-65	US-08-834-666A-6	US-08-834-666A-22	US-08-834-666A-12	US-09-769-787-109	US-10-223-597-7	US-09-379-931-7	US-10-369-493-5343
199	2, A	200	ø	Sequence 5044, Ap	1717,	7187,	129	2, Appl	Sequence 1029, Ap		æ		Sequence 28, Appl			Sequence 21, Appl	Sequence 3951, Ap					ø	_				Sequence 7, Appli	Sequence 7, Appli	Sequence 5343, Ap

## ALIGNMENTS

US-10-369-493-20638

Sequence 20638, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
INUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                      Matches
                                                                                                                                                       Query Match
Best Local
                    59
                                                                                                                                  46;
                                                                                                                                                         Similarity
                -----LQSDARKSETTI-----
                                                         LFFVTASVLVLSSSAAFAADSNTVY------LNQTGNDQQANITQSGNGNSVGA
                                                                                           LLKVAAFAAIVVSGSALAG----VYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALA 58
                                                                                                                                      Conservative
                                                                                                                                                         15.0%; Score 113.5; DB 1 25.0%; Pred. No. 0.00077;
                                                                                                                                    18;
                                                                                                                                    Mismatches
-----TQSGYGNGADVGQGADNSTIELT 93
                                                                                                                                                                         DB 15;
                                                                                                                                      63;
                                                                                                                                    Indels
                                                                                                                                                                         Length 445;
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                                                                                                                                      57;
                                                                                                                                    Gaps
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RESULT 3
US-09-793-306-146
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US-10-238-075-1549
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US-10-238-075-1549
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                SEQ ID NO 146
LENGTH: 597
                                               APPLICANT: COTIAS COrporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: 0f Tuberculosis
FILE REFERENCE: 014058-08740US
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTMARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1549
LENGTH: 182
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Publication No. US20030148324A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                APPLICANT: Campos-Neto, Antonio
APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
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CURRENT FILING DATE: 2002-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and cFILE REFERENCE: BLANDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: I.N.S.E.R.M.
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                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LALQSDARKSETT----ITQSGYGNGADVGQGA-----DNSTIELTQNGFRNNATIDQWNA 108
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                                                                                                                                                                                                                                                                                                      Jen, Shyian
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                                                                                                                                                                                                                                                                                  Lodes, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNGFRNNATIDQWNAKN-----
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24.5%;
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0.11;
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CURRENT APPLICATION NUMBER: US/09/997,182
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US-09-997-182-131
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Sequence 131, Application US/09997182
Publication No. US20030049263A1
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences:
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 1097-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR FILING DATE: 1996-06-14
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; ORANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mTTC#3-His
US-09-793-306-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. SEQ ID NO 131
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Best Local (
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GENERAL INFORMATION:
APPLICANT: Nano, FI
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PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 943
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es 39; Conserv
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                                                                                                                                                                                                                                                                     113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                               156 VAGGGALVSAAAAQVTTRVFRNLGL-ANVGEGN-----VGNGNVGNFNLGSANIGNGN
                                                                                                                                                                                                                                                                                                                                                  57 L----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
                                                                                                                                                                                                                                                                                                                                                                                               96 ALFVSLVVSNILGQNAPAIAATEAAYEQMWAQDVAAMFGYHAGASAAVSALTPFGQALPT 155
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35.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 86.5; DB Pred. No. 1.9; 22; Mismatches
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CURRENT FILING DATE:

2001-11-28

APPLICATION NUMBER: 09/447,135 FILING DATE: 2000-01-03

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LENGTH: 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 131, Appropriate Publication No.
                                                                                                                                                         Query Match 11.4
Best Local Similarity 24.8
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 39; Conservative
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                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis -09-997-181-131
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                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/447, 135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990, 823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: 05/000, 254
PRIOR APPLICATION NUMBER: 60/000, 254
                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/997,181
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding TITLE OF INVENTION: immunostimulatory Peptides
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PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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156 VAGGGÁLVSAÁAAQVTTRVFRNLGL-ÁNVGEGN-----VGNGNVGNFNLGSANIGNGN
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                                      57 L----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
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                                                                                                                     7 AAFAAIVVSG-----SALAGVYDQLVTRVVTHEMAHASGPDSTLS-IYQYGSANAA 56
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                                                                            ALFVSLVVSNILGONAPAIAATEAAYEOMWAQDVAAMFGYHAGASAAVSALTPFGQALPT 155
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24.8%; Pred. No. 1.9;
                                                                                                                                                         11.4%; Score 86.5; Di
24.8%; Pred. No. 1.9;
Live 22; Mismatches
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US-09-984-334-1
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                                                                                   US-10-004-115A-34
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SEQ ID NO 1
LENGTH: 385
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                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 34
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Query Match
Best Local Similarity
Matches 30; Conserv
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Best Local
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CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD FOR PRODUCING 4-CYANO-3-OXOBUTANOATE AND TITLE OF INVENTION: 4-CTANO-3-HYDROXYBUTANOATE
                                                                                                                                                                                                      PRIOR FILING DATE: 2001-06-11 NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 2001-006144 PRIOR FILING DATE: 2001-01-15 PRIOR APPLICATION NUMBER: JP 2001-026594
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE FILE REFERENCE: 7372-72249
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PRIOR APPLICATION NUMBER: JP 2001-175175
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CURRENT FILING DATE: 2002-10-23
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                                                                                                  ORGANISM: Corynebacterium sp
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                                                                                                                         TYPE:
                                                                                                                                            LENGTH: 385
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SHIMIZU, MASATOSHI
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    Conservative
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                       25.9%;
                       11.1%; Score 84; D
25.9%; Pred. No. 1;
    21;
    Mismatches
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                                        DB 14; Length 385;
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RESULT 10
US-10-156-761-9411
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SEQ ID NO 941:
LENGTH: 356
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                                                                                                 CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29 PRIOR APPLICATION NUMBER: JF 2001-204089
                                  NUMBER OF
                                                       PRIOR FILING DATE:
                                                               PRIOR APPLICATION NUMBER: JP 2001-272697
                                                                                           PRIOR FILING DATE:
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APPLICANT:
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PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: JP 2001-395885
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: JP 2002-107648
PRIOR FILING DATE: 2002-04-10
NUMBER OF SEQ ID NOS: 15
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PPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHOD FOR PRODUCING OPTICALLY ACTIVE TITLE OF INVENTION: 2-HYDROXYCYCLOALKANECARBOXYLIC ACID ESTER FILE REFERENCE: 073517
CURRENT APPLICATION NUMBER: US/10/327,108
CURRENT FILING DATE: 2002-12-24
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ORGANISM: Corynebacterium pseudodiphtheriticum
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APPLICANT: WAKITA, RYUHI
APPLICANT: ITOH, NOBUYA
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                                  SEQ ID NOS:
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HORIKAWA, HIROSHI
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RESULT 12
US-10-185-990-11
Sequence 11, Application US/10185990
Publication No. US20030073109A1
GENERAL INFORMATION:
APPLICANT: Pan, Jae-Gu
ITILE OF INVENTION: JAE GU PAN ET AL
FILE REFERENCE: 02589.000100
CURRENT APPLICATION UNMBER: US/10/185,990
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
LENGTH. 167.
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US-10-185-990-10
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Best Local Similarity
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                                  LENGTH: 16
TYPE: PRT
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ORGANISM: Bacillus subtilis
10-185-990-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 02589.000100
CURRENT APPLICATION NUMBER: US/10/185,990
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pan, Jae-Gu
TITLE OF INVENTION: JAE GU PAN ET AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 1621
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                                                                                                                                                                                                                                                                                                                               516 ---SGSESSLTAG-YGS-----TQTAQQGSVLTS--GYGSTQTA 548
                                                                                                                                                                                                                                                                                                                                                              104 DQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                     469 -----GSESSLT-AGYGSTQTAREGSTLTAGYGSTGTAGADSSLIA---
                                                      1626
                                                                                                                                                                                                                                                                                                                                                                                                                                      58 ALQSDARKSETTITQSGYGN------GADVGQGADNSTIELTQNGFRNNATI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PVTTGGQESQWTALPSDTRDGE--ARNGAADPSGAAD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VAAFAAIVVSG--SALAGVYDQLVTR-----VVTHEMAHASGPDSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 IEAGPQSSEETEAOLRLGGNDDAGAAADGETARMPSDGDFDGGATGAAGPPAQWEVDGQC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 -----RKSETTITQSGYGNGADVGQGADNSTIELTQNG-FRNNAT-----ID---- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AIVVSGSALAGVYDQLVTRVVTHEMAHASGPDS-----TLSIYQYGSANAALALQSDA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAGYGSTQTSGSDŠÁLTAGYGSTQTAQEGSNLTAGYGSTGTAGADSSL-IAGYGSTQTS- 468
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26.7%; Pred. No. 8.6;
tive 21; Mismatches
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28.0%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1621;
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                               APPLICANT: INTERMA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SKAKXI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
PILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 16
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 65
TYPE: PRT
                                                                                                                                                                                                                                                            Sequence 13173, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                             APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/250,338 PRIOR FILING DATE: 2000-11-30
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PRIOR APPLICATION NUMBER: 60/253,878
PRIOR FILING DATE: 2000-11-29
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/250,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 35800/240590
CURRENT APPLICATION NUMBER: US/09/996,194
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bandaru, Rajasehkar
TITLE OF INVENTION: 84242, 8035, 55304, 52999, and 21999,
TITLE OF INVENTION: No. US20020151696A1el Human Proteins and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
APPLICATION NUMBER: JP 2001-204089 FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 DOWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATA 148
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ilarity 88.9%;
Conservative
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Pred. No.
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; LICATION: (1)..(273)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-20096
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
Chen, Xianfeng
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US-10-369-493-20096
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20096
LENGTH: 273
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LENGTH: 594
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052)8 CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: No. US20030233675Altoc punctiforme
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                         151
209
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                                     141 GFGNN 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                               84
                                                                                                                                                                                  43 STLSIYQYGSANA-ALALQS------DARKSETTITQSG-----YGNGADVGQ 83
                                                                                                                                                  92 TTLDL-QFGSTNSDDVTLKPNQTLFAGDGADFVEGTKGNTIVTGNGEDTVLVGSGSSVST 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 TQSGYGNGADVGQG---ADNSTIELTQNGFRNNATIDQWNAKNSDIT----
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SFGGS 213
                                                                         GDGNDQVFIGVNSPASNTSADGGNG-NDEVTVVEANGSN-NLFGGAGADTLTVVEGSRQL
                                                                                                           GADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMV----RQV
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Pred. No. 0.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                        PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             March 11, 2004, 18:24:14; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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757
                                                                                                                                                                                                                                                                                                                                                                                                                                                   283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                             283366
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Result No.	Score	Query Match	% Query Match Length	BQ	ID	Description
1	859	86.9	151	ν :	JC6039	fimbrin protein ag
2	658	86.9	151	N	AI0635	major curlin chain
w	484	63.9	151	N	S70788	curlin protein cag
4	474.5	62.7	152	N	D90806	curlin major subun
G	474.5	62.7	152	N	H85665	hypothetical prote
σ	118.5	15.7	151	N	S70787	curlin nucleator p
7	118.5	15.7	151	N	C90806	minor curlin subun
œ	118.5	15.7	151	N	G85665	curlin minor chain
9	111.5	14.7	151	N	JC6040	fimbrin protein ag
10	111.5	14.7	151	N	AH0635	nucleation compone
11	101.5	13.4	590	ш	A45621	leishmanolysin (EC
12	101	13.3	599	N	B42049	
13	101	13.3	599	ν	A44951	
14	99.5	13.1	582	Ν	F70675	probable PPE prote
15	99.5	13.1	646	۳	S19916	leishmanolysin (EC
16	98	12.9	145	N	AD3143	conserved hypothet
17	98	12.9	145	N	H98144	hypothetical prote
18	97.5	12.9	1034	N	JC2143	ice nucleation act
19	96.5	12.7	602	<u></u>	PL0221	leishmanolysin (EC
20	96	12.7	1651	N	JC1340	outer membrane pro
21	95.5	12.6	1258	N	JQ0188	ice nucleation pro
22	94.5	12.5	1322	N	807053	ice nucleation pro
23	93.5	12.4	1567	N	S11672	ice nucleation pro
24	91.5	12.1	1655	N	E97835	hypothetical prote
25	89.5	11.8	552	N	D70604	probable PPE prote
26	89.5	11.8	639	N	C42049	leishmanolysin (EC
27	88.5	11.7	590	N	E70946	probable PPE prote
28	87	11.5	329	N	S23247	outer membrane pro
3	87	11.5	331	N	S21406	outer membrane pro

4 4 4 5 4 8	410	338 398	2 2 4 2 2 4 2	30
81.5 81.5	882	83 · 5 82 82	86.5 85.5 84	87 87
10.8	10.8	11.1 11.0 10.8	11.5 11.4 11.3	11.5
4776 760 760	1026 1073 1635	3716 1200 528 534	573 3300 1210 823	331 455
N N N	N N N	22L8	2222	NN
E95206 C90739 E85589	A48995 C87374 AI0452	E70969 SNPSO S69589 T32020	C86266 D70575 A25547 S14055	S21408 C29349
cell wall surface hypothetical prote hypothetical prote	paracrystalline su S-layer protein Rs hemolysin [importe	probable PPE prote ice nucleation pro hypothetical prote hypothetical prote	F3F19.21 protein - probable PPE prote ice nucleation pro nucleoskeletal-lik	outer membrane pro hypothetical prote

## ALIGNMENTS

Oy 121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151	SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG	Ov 61 SDARKSETTTTOSGYGNGADVGOGADNSTTELTONGFRNNATTDOWNAKNSDITVGOYGG 120	Db 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSAN	Query Match  86.9%; Score 658; DB 2; Length 151;  Best Local Similarity 90.1%; Pred. No. 7.5e-52;  Matches 136; Conservative 3; Mismatches 12; Indels 0; Gaps 0;	F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>	A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C:Karwords: fimbria		A;Note: sequence extracted from NCBI backbone (NCBIP:45936)	A; Molecule type: protein	A;Accessiui: A++070 A;Status: Dreliminary	A;Contents: 27655	7357	A: Triffication and characterization of thin, aggregative fimbriae from Salmonell.	R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W.	lated the codon ACG for residue	A, Experimental source: strain 27655-3b	A; MOLECULE Type: protein	A;Cross references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714	A;MoJecule type: DNA A:Residines: 1-151 <coi:></coi:>	A;Accession: JC6039	A; reference number: JC6039; MUID: 96146512; PMID: 8550497	J. Bacteriol. 178, 662-667, 1996	R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.	C;Date: 31-Dec-1996 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999 C:Accession: TC6039: PC6015: A44898	C;Species: Salmonella enteritidis	fimbrin protein adfA precursor - Salmonella enteritidis	RESULT 1

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N;Alternate names:
C;Species: Escheric
C;Date: 12-Feb-1998
C;Accession: S70788
                                                                                                                                                                                                                    A;Cross-references: EMBL:X90754; NID:gl147558; PIDN A;Experimental source: strain Kl2, substrain W3110 A;Note: the nucleotide sequence was submitted to the R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; PeA.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
    A;Cross-references: GB:AB000205; GB:U00096; NID:g1787265; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Norn Mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01
C;Accession: S70788; G64846; $\overline{3}\) 321202; $34560; $34559
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production
A;Reference number: $70783; MUID:96414468; PMID:8817489
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A; Residues: 1-151 <HAM>
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AI0635
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, th, T. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-151 < PAR>
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
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                                                                                                Molecule type: DNA
Residues: 1-151 <BLAT>
                                                                                                                                   Status: nucleic acid sequence not shown; translation
                                                                                                                                                                          ;Title: The complete genome sequence of Escherichia coli K-12;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                   Accession: G64846
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Matches 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKLLKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSTYQYGSANAALALQ
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Pred.
                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, Au Bloch, C.A.; Perna, N.T.; Burland, V.;
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Davis,
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No. 7.5e-52;
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                         S.; Normark,
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ies, R.M.; Dowd,
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V.; Riley,
                                                                PID:g1787279
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ey, M.;
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A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424; PIDN:AAA23616.1;
A;Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 21-42;44-50 <OLS2>
R; Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library,
A; Reference number: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-6,'V',8-151 <OLS1>
A;Cross-references: EMBL:L04979
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;Function:
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                         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                 MKLLKVAATAATVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQ 60
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GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                TDARNSDLTÍT QHÓGGNGAÐVGQGSDÐSSIÐLT QRGFGNSATLÐQWNGKNSEMTVKQFGG
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Pred. No. 2.7e-36;
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, N.; LBHIL, N.; Shipasayara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shi DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D99806
                                                                                                                                                                        A;Cross-references: GB:BA000007; PIDN:BAB34843.1; A;Experimental source: strain O157:H7, substrain R C;Genetics:
                                                                                                                                                         A;Gene:
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-152 < HAY>
                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: D90806
                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Escherich
C; Date: 18-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  curlin major subunit CsgA [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D90806
                                                                                   Matches
                                                                                                                    Query Match
                                                                                                    Local
                                                                                   100;
                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
                                                                                                  Similarity
MKLLKVAATAATVFSGSALAGVVPQYGGGGGNHGGGGGNNSGPNSELNTYQYGGGNSALAL
                                    MKILKVAAFAAIVVSGSALAGVYDQLVTRVVTH-EMAHASGPDSTLSIYQYGSANAALAL
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                              62.7%;
                                                                             19;
                                                                           Score 474.5; DB 2;
Pred. No. 2e-35;
9; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                        ; PID:g13360880; GSPDB:GN00154
RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                  coli
                                                                           Indels
                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                 , K.; Yokoyama,
M.; Shinagawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                              O157:H7, substrain
                                                                                                                                                                                                                                                                                                                    coli
                                                                         Gaps
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QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG

119

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A;Experimental source: Strain K[2], substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Aug R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64846
                                                                                                                                                                                                                                                                                                                                                                   R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: csgB prot
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      curlin nucleator protein csgB precursor - Escherichia coli (strain K-12)
N;Alternate names: csgB protein; curlin nucleation component; minor curl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iller, L.; Grotbeck, E.J. Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: H85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S70787; F64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
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                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62281.1; PID:g1147563
                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
                                               Molecule type: DNA
                                                                     Status: nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QADARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKDSHMTVKQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAATAATVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNTYQYGGGNSALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTH-EMAHASGPDSTLSIYQYGSANAALAL
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                          <BLAT>
       G
    AE000205;
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                                                                     not shown;
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    GB:U00096;
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Pred. No. 2e-3
L9; Mismatches
                                                                     translation not
NID:g1787265;
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    PIDN: AAC74125.1;
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  PID:g1787278;
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                                                                                                                                iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enter
                       A; Molecule type: DNA
A; Residues: 1-151 < STO>
                                                                     A;Status: preliminary
                                                                                        A; Reference number: A85480; A; Accession: G85665
                                                                                                                                                                                  R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
                                                                                                                                                                                                                                C;Date: 16-Fe
C;Accession:
                                                                                                                                                                                                                                                                           C; Species: Escherichia coli
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gasawara, N.; Yasunaga, T.; Kunara, J., .....
gasawara, N.; Yasunaga, T.; Kunara, J., ....
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
                                                                                                                                                                                                                                                                                                                        A;Bolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Cross-referencal source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: C; Genetics:
curlin minor chain precursor, CsgA homolog
                   G85665
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A;Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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Best Local
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N.; Yasunaga, T.; Kuhara,
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37; Conser
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                                                                                                                               NGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                  IAAAAGYDLANSEYNF----AVNELSKSSFNQAAIIGOAGTNNSAQLROGGSKLLAVVAQ
                                                                                                                                                                                                         MAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQ
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                                                                                         EGSSNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGSSNRAKIDOTGDYNL-AYIDOAGSANDASISOGAYGNTAMIIOKGSGNKANITOY 129
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                                                                                                                                                                                                                                                Conservative
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Pred. No. 0.0014;
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[imported] - Escherichia coli (strain
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;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001 ;Accession: G85665

enterohemorrhagic Escherichia MUID:21074935; PMID:11206551

coli

O157:H7

D.J.; Mayhew K.; Apodaca,

GB:AE005174;

NID:g12514573;

PIDN: AAG55787.1;

GSPDB:GN00145;

UWGP: Z16

Gaps

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129

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73 94

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C;Spec...
A;Note: this spec...
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomas
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, ...
S; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Athors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, ...
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0635
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C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-196
C;Accession: JC6040
R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996
J. Bacteriol. 178, 662-467, 1996
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A;Experimental source: strain 276755-3b
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A; Residues: 1-151 < COL>
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Pred. No. 0.0014;
3; Mismatches 6
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                                                                                                                                                                    leishmanolysin (EC 3.4.24.36) precursor, stationary phase - N;Alternate names: glycoprotein gp63, stationary phase; surf C;Species: Leishmania chagasi C;Date: 10-Mar-1994 #sequence_revision 07-Apr-1994 #text_chaC;Accession: B42049
                                                                                                                                                                                                                                                                                                                                                             B42049
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
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F;48.251,255,321/Binding site: zinc, catalytic (Cys, His, His, His, His) (inhibited) #status
F;112-129,178-217,301_373,301-473,402-477,454-498,503-553,523-546/Disulfide bon
F;251,255,321/Binding site: zinc, catalytic (His) (active) #status predicted
F;252/Active site: Glu #status predicted
F;287/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Description: catalyzes the hydrolysis of peptide bonds between two hydrophobic A;Note: the activated form can activate the proenzyme form C;Superfamily: leishmanolysin C;Keywords: blocked carboxyl end; cell adhesion; glycoprotein; hydrolase; lipopro F;1-39/Domain: signal sequence #status predicted <SIG>F;40-87/Domain: activation peptide #status predicted <ATP>F;88-565/Product: leishmanolysin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;287/Binding site: carbohydrate (ASD) (COVALUM, FULLY FULLY FILES) (in mature F;565/Modified site: GPT anchor ethanolamine amidated carboxyl end (ASD) (in mature
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A; Accession: A45621
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Mol. Biochem. Parasitol. 48, 173-184, 1991
A;Title: Heterogeneity of the genes encoding the major surface glycoprotein A;Reference number: A45621; MUID:92107220; PMID:1762629
A;Reference number: A45621; MUID:92107220; PMID:1762629
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A; Residues: 1-590 <WEB>
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSDITVGQYGGNNAALVNQTA---SDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SETTITQS--GYGNGA-----DVGQGADNSTIELTQNGFRNNATIDQWNAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGYYSALTMAIFODLGFYQADFS-KAEEMPWGRNA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from NCBI backbone (NCBIN:74958, NCBIP:74959)
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C;Superfamily: leishmanolysin
C;Reywords: cell adhesion; glycoprotein; hydrolase; membrane bound; metalloproteinase;
C;Reywords: cell adhesion; glycoprotein; hydrolase; membrane bound; metalloproteinase;
F;1-39/Domain: signal sequence #status predicted <SIG>
F;40-97/Domain: activation peptide #status predicted <ATP>
F;40-97/Domain: activation peptide #status predicted <MAT>
F;98-599/Product: leishmanolysin #status predicted <MAT>
F;48.261,265,331/Binding site: zinc, catalytic (Cys, H1s, His, His) (inhibited) #status
F;122-139,188-227,311-383,390-451,403-422,412-486,463-507,512-562,532-555/Disulfide bound;
F;261,265,331/Binding site: zinc, catalytic (His) (active) #status predicted
F;261/Active site: Glu #status predicted
F;267/Active site: carbohydrate (Asn) (covalent) #status predicted
F;1-39/Domain: signal sequence #status predicted <SIG>
F;10-99/Domain: activation peptide #status predicted <ANT
F;40-97/Domain: activation peptide #status predicted <ANT
F;98-574/Product: leishmanolysin #status predicted <MAT>
F;575-599/Domain: carboxyl-terminal propeptide #status pr
F;48,261,265,331/Binding site: zinc, catalytic (Cys, His
                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M80672; NID:g159328; PIDN:AAA29238.1; PID:g159329
A;Note: sequence extracted from NCBI backbone (NCBIN:76040, NCBIP:76041)
A;Note: the source is designated as Leishmania donovani chagasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M28527; NID:g159322; PIDN:AAA29235.1; PID:g159323 R;Ramamoorthy, R.; Donelson, J.E.; Paetz, K.E.; Maybodi, M.; Roberts, S.(J. Biol. Chem. 267, 1888-1895, 1992 A;Title: Three distinct RNAs for the surface protease gp63 are different: A;Reference number: A42049; MUID:92112918; PMID:1370484 A;Accession: A42049
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Mol. Biochem. Parasitol. 39, 267-274, 1990
A;Title: Leishmania gp63 molecule implicated in cellular A;Reference number: A44951; MUID:90205976; PMID:2320059
A;Accession: A44951
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                                                                                                                                                                                                      A; Note: the C; Superfamil
                                                                                                                                                                                                                                 A;Description: catalyzes the hydrolysis of peptide bonds between A;Note: the activated form can activate the proenzyme form
                                                                                                                                                                                                                                                                                                         C; Function:
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A; Residues: 1-599 <MIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-599 < RAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leishmanolysin (EC 3.4.24.36) precursor, log phase - Leishmania chagasi
N;Alternate names: glycoprotein gp63; surface metalloproteinase, log ph
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                                                                                                                                                                    ;Note: the activated form can activate the proen;Superfamily: leishmanolysin;Keywords: blocked carboxyl end; cell adhesion;
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.Title: Three distinct RNAs for the surface protease gp63 are differentially expressed;Reference number: A42049; MUID:92112918; PMID:1370484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: A44951; A42049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Leishmania chagasi
Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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Pred. No. 0.27;
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   #status pre
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                              leishmanolysin (EC 3.4.24.36) precursor - Leishmania mexic NyAlternate names: surface metalloproteinase glycoprotein C;Species: Leishmania mexicana C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_c C;Accession: S19916; A48564 R;Medina-Acosta, E.; Karess, R.E.; Russell, D. submitted to the EMBL Data Library, February 1992 A;Description: Structurally distinct genes for the surface A;Description: Structurally distinct genes for the surface
                                                                                                                                                                                                                                                                                                         RESULT
S19916
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296

GNTGSSNWGFGNNGIGN 312

Leishmania mexicana

#text\_change

10-Sep-1999

**surface** 

protease

(gp63) of

Leishmania

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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: F70675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:Z82098; GB:AL123456; NID:g3261664; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-582 < COL>
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Matches 32
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Best Local
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                                                                                       ---GADNSTIEL----TQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASD---
                                                                                                                                                                               -TLSIYQYGSANAALALQSDARKSETTI--TQSGYGN-----
                                                                                                                                                                                                                           AFAQLVMSNWFGLNAPLIAAVEGAYEQMWAADVAAMVGYHSGASAAAEQLVPFQQALQQL
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  SSVMVRQVGFGNNATAN 149
                                                GNFGSGNGRAGLPGSGNVGNGNLGNSNLGSGNTGNSNVGFGNTGNNNVGTGNAGSGNIGA
                                                                                                                                     PNLGI GNI GNANLGGGNTGDLNTGNGNI GNTNLGSGNRGDANLGSGNI GNSNVGGGNVGN
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23.4%;
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Holroyd,
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Search completed: March 11, 2004, 18:42:08 Job time: 11.3 secs
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R;Medina-Acosta, E.; Karess, R.E.; Russell, D.G.
MOl. Biochem. Parasitol. 57, 31-45, 1993
A;Title: Structurally distinct genes for the surface protease of Leishmania mexicana are A;Reference number: A48564; MUID:93149206; PMID:8426614
A;Accession: A48564
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A;Molecule type: mRNA
A;Residues: 1-646 <MED>
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A;Map position: 700kb chromosomal band
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Local Similarity 30.8%; Pred. No. 0.4;
hes 40; Conservative 15; Mismatches 66; Indels 9
                                                                                                                                            357 TALTMAVFQD 366
                                                                                                                                                                                                              123 AALVNOTASD 132
                                                                                                                                                                                                                                                                                    297 NVSVITSSTVVAKAREQYGCNSLEYLEIEDQGGAGSAGSHIKMRNAKDELMAPAASAGYY 356
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
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seq length: 2000000000
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J. Bacteriol. 173:4773-4781(1991).
-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY ASTEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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MEDLINE=97426617; PubMed=9278503;
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Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
Mau B., Shao Y.;
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MEDLINE=93211294; PubMed=8459772;
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      WEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
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Welch R.A., Blattner F.R.;
"Genome sequence of enterohamments."
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                                                                                                                                                        STRAIN=0157:H7 / ATCC 43895;
MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
Uhltations in the cegD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7.TAppl. Environ. Microbiol. 67:2367-2370(2001).
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Escherichia coli O157:H7.
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X90754; CAA62282.1; -.
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X MARY A. Ishi K., Vokoyama K., Murata T., Tanaka M., Tobe T.,

A Han C., -G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.

A Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli

T "Complete genome sequence of enterohemorrhagic Escherichia coli

T 0157:H7 and genomic comparison with a laboratory strain K-12.";

L DNA Res. 8:11-22(2001).

L DNA Res. 8:11-22(2001).

DNA Res. 8:11-22(2001).

C -!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI

C COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWT

TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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Best Local Similarity
Matches 100; Conserv
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P39828;
01-FEB-1995
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SEQUENCE
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01-OCT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Hammar M., Arnqvist A., Bian Z., Olsen A., "Expression of two csg operons is required fibronectin- and congo red-binding curli po
                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=K12 / MC410
                                                                                                                                                                                                                                                                                                       Escherichia coli, and
Escherichia coli O157:H7.
Bacteria; Proteobacteria;
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EMBL; AE005315; AAG55788.1;
EMBL; AP002554; BAB34843.1;
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                                                                                                       STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
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ka M., Tobe .
<sup>N</sup>., Yasunaga '
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This SWI
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-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENTS.
                                                                 use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
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MEDLINE=21074935; PubMed=11206551;

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"Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
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"A 718-kb
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
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                                              an email to license@isb-sib.ch).
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M., Tobe T.,
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Matches 37
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EMBL; D90741; BAA35831.1; -
EMBL; AE005315; AAG55787.1; -
EMBL; AP002554; BAB34842.1; -
PIR; G85665; G95665.
PIR; G85665; G95665.
PIR; G85665; G708787.
PIR; G70787; S70787.
                                                                                                                                        STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
                                                                           J. Bacteriol. 185:2330-2337(2003).
-i- FUNCTION: CURLIN IS THE STRUCTURAL-
COILED SURFACE STRUCTURES THAT ASSE
TEMPERATURES BELOW 37 DEGREES CELSI
FIBRONECTIN. THE MINOR SUBUNIT IS T
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28-FEB-2003 (Rel. 41, Last
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Minor curlin subunit precur
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                                                 CURLIN MONOMERS.
SIMILARITY: BELONGS
SWISS-PROT entry is copyright.
een the Swiss Institute of Bioi
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Pred. No. 0.
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RESULT 6
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SPECIES=S.typhimurium; STRAIN=SR-11;

SPECIES=S.typhimurium; STRAIN=SR-11;

MEDLINE=98117058; PubMed=9457880;

Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;

"Curli fibers are highly conserved between Salmonella typhil

Escherichia coli with respect to operon structure and regul

J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P55276;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGPB OR STM1143.
                                                                                                                                                                                                                                                                                                                                                                 McClelland M., Sanderson K.E., Spleth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella typhimurium, and Salmonella enteritidis.
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                                                                                                                                             MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                 SPECIES=S.enteritidis; STRAIN=27655-3B;
                                                                                                                                                                                                                                                                                                                                                 Ryan E., Sun H., Florea L.
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720, MEDLINE=21534948; PubMed=11677609;
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. BACTERIOI: 178:662-667(1996).
. BACTERIOI: CURLI IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE I- FUNCTION: CURLI IS THE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR CURLIN MONOMERS.
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an email to license@isb-sib.ch).
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Fimbria;
                                                                                                                                                                                                                   Webb J.R., Button L.L., McMaster R.W.;
"Heterogeneity of the genes encoding the n
of Leishmania donovani.";
Mol. Biochem. Parasitol. 48:173-184(1991).
-!- FUNCTION: Has an integral role during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
SEQUENCE
          EMBL;
                                                                                                            This
                                                                                                                             in the mammalian host.

-!- CATALYTIC ACTIVITY: Preference for hydrophobic P1' and basic residues at P2 and P3'. A model n cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
-!- COFACTOR: Binds 1 zinc ion per subunit (By simi-
-!- SUBCELLULAR LOCATION: Attached to the membrane
-!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                Leishmania donovani.
Eukaryota; Euglenozoa;
NCBI_TaxID=5661;
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EMBL; AE008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
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; M60048;
; P08148;
                                                                                              SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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Signal; Complete proteome
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(Rel. 20, Last sequence update)
(Rel. 42, Last annotation update)
(Rel. 42, Cast annotation (Cell
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                                             license agreement
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"Three distinct RNAs for the surface protease gp63 are differentially promastigotes to an infectious form.";
J. Biol. Chem. 267:1888-1895(1992)

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FUNCTION: Has an integral role during in the mammallan host.

CATALYTIC ACTIVITY: Preference for hyder and basic residues at P2 and P3'.

Cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.

COFACTOR: Binds 1 zinc ion per subunit

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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/

There are no rest

restrictions

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EMBL

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collaboration outstation

SUBCELLULAR LOCATION: Attached to the membrane SIMILARITY: Belongs to peptidase family M8.

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P15706;
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SEQUENCE FROM N.A.
MEDLINE=92112918; PubMed=1370484;
Ramamoorthy R., Donelson J.E., Paetz
Wilson M.E.;
                                                                                                                                   Leishmania chagasi.
Eukaryota; Eugleno:
NCBI_TaxID=44271;
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01-APR-1990 (Rei. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (1
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InterPro; IPR001577; Peptidase M8.
Pfam; PF01457; Peptidase M8; 1.
PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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                                                                                                                  Biochem.
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PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptidase_M8.
InterPro; Peptidase_M8.
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HSSP; P08148; 1LML.
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adhesion; GPI-anchor; Lipoprotein.
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Leishmanolysin (
(Major surface gendopeptidase).
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InterPro; IPR006025; Pept M Zn I
InterPro; IPR001577; PeptIdase_I
Pfam; PF01457; PeptIdase M8; 1.
PRINTS; PR00782; LSHMANOLYSIN.
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Eukaryota; Euglenozoa;
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STRAIN=MNYC/BZ/62/M379;
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SIMILARITY: Belongs to peptidase
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COPACTOR: Binds 1 zinc ion per subunit (By simi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE:
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(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
sin Cl precursor (EC 3.4.24.36) (Clase glycoprotein) (GP63 protein) (GP63)
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                                           ACTIVATION PEPTIDE (POTENTIAL).

LEISHMANOLYSIN C1.

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                (GLCNAC. .
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MRL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
-ISTRUCTURAL PROTEIN WHICH WAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMPB_RI
                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia japonica.
                                                                                                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               japonica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
SUBCELLULAR LOCATION: Cell wall.
layer with hexagonal symmetry.
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                                                                                                                                                                                                                                              PF03797;
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                                                                                                                                                                                           S-layer;
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                                                                                                                                                                                                                                                                IPR006315; Autotransport. IPR005546; Autotransporter.
                                                                                                                                                                                                                  TIGR01414; autotrans_barl;
                                                                                                1656
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POLY-GLY.
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32 kDa BETA PEPTIDE.
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                                                DB 1;
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.33;
                                                                                                                                                PEPTIDE.
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                                                Length 1656;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
Enterobacteriaceae; Panto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997
16-OCT-2001
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Q47879;
                                                                                                                                                                                   HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

    -!- FUNCTION: Ice nucleation proteins enable

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                                                                                                                                                                                                                                                                                                                                                                                             CTYSTAllization in supercooled water.
SUBCELLULAR LOCATION: Outer membrane.
DOMAIN: CONTAINS IMPERFECT REPEATS OF A C
A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE
                                                                                                                                                                                                                                                                                                                                                          PERIODICITY IS SUPERIMPOSED.

MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH TH NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF
                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleation protein
161
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                                                                                                                                                                                              D14992; BAA03636.1;
JC2143; JC2143.
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                       12
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                                                                                                                                                                                                                                    s requires a license agreement (S an email to license@isb-sib.ch).
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biotechnol. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and sequencing
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IATYGSTLSGTHQSQLIAGYGSTETA---
                      IVVSGSALAGVY-DQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTI
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                                                                                              1034 AA;
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35, Last sequence update)
40, Last annotation updat
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                                                         12.9%;
28.7%;
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P08148; P15906;
01-AUG-1988 (Rel
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Button L.L., Morney
"Molecular cloning of the """
"Molecular Cloning of the """
Med. 167:724-729(1988)
                 between
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Schlagenhauf E., Btges R., Metcalf P.;
"The crystal structure of the Leishmania
leishmanolysin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schneider P., Ferguson M.A.J., McConville M.J.,
Homans S.W., Bordier C.,
"Structure of the glycosyl-phosphatidylinositol
"Structure of the glycosyl-phosphatidylinositol
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NCBI_TaxID=5664;
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"Crystallization and preliminary X-ray
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(Major surface
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                                                                                                                                                                                                                                                      FUNCTION: Has an integral role in the mammallan host in the mammallan host CATIALYTIC ACTIVITY: Preference P1' and basic residues at P2 an cleaved at -Ala-Tyr-|-Leu-Lys-L
s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no wa
                                                                                                                      Cleaved at -Ala-Tyr-|-Leu-Lys-Lys-COPACTOR: Binds 1 zinc ion per subunit.

COPACTOR: Binds 1 zinc ion per subunit.

SUBCELLULAR LOCARION: Attached to the membrane by a GPI-anchor.

BTM: THE PHOSPHATIDYLINGSITOL MOIETY OF THE GPI-ANCHOR CONTAINS

FULLY SATURATED, UNBRANCHED 1-O-ALKYL CHAIN (MAINLY C24:0) AND A

MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0,

C14:0, C16:0, AND C18:0)
                                                                                                    SIMILARITY: Belongs to peptidase family M8.
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(Rel. 14, Last sequence update)
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(sin precursor (EC 3.4.24.36) (Cell
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171:589-589(1990)
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PROSITE; PS00142; ZINC PROTEASE; 1.

Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;

Zymogen; Signal; Cell adhesion; GPI-anchor; 3D-structure; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; PeptIdase_M8.
Pfam; PP01457; PeptIdase_M8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y00647; CAA68673.1; -. PIR; PL0221; PL0221. PDB; 1LML; 17-SEP-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; M08.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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AC P16239;
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DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
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        Erwinia herbicola.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
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                                                                                                                                         8 AFAAIVVSGSALAGVYDQLVTRVVTHEMAHA---SGP
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Pred. No. 0.56
3; Mismatches
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              SEQUENCE FROM N.A.
MEDLINE=90092494; PubMed=2599095;
Abe K., Watabe S., Emori Y., Watan
                                                                 NCBI_TaxID=553;
                                                                              Enterobacteriaceae;
                                                                                         Pantoea ananas (Erwinia uredovora)
Bacteria; Proteobacteria; Gammaprot
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Pfam; PF00818; ICe nucleation; 65.
PRINTS; PR00327; ICENUCLEATION; 45.
PROSITE; PS00314; ICE_NUCLEATION; 45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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PIR; JQ0188; JQ0188.
                                                                                                                                                                                               CEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
STRAIN=M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   herbicola,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Warren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90152370;
                                                                                                                             nucleation protein inaA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYPSTAllization in supercooled water.
SUBCELLULAR LOCATION: Outer membrane.
DOWALN: CONTAINS 126 IMPERFECT REPRATS OF A CONSENSUS OCTA
A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48
PERIODICITY IS SUPERIMPOSED.
MISCELLAMEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH TH
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF
SIMILARITY: Belongs to the bacterial ice nucleation protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleation; Repeat; Outer membrane.
AIN 162 1217 OCTAPEPTIDE PERIODICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                              PANAN
                                                                                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                             257
                                                                                                                                                                                                                                                                                                                                                               161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85:239-242 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consensus sequence of ice nucleation proteins from Erwinia
                                                                                                                                                                                                                                                                                                                                      71
                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P06620; 1INA.
                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G.J.,
     nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                  V-----NOTASDSSVMVRQVGFGNNATANO 150
                                                                                                                                                                                                                                                                                                           V-AGYGSTQTAGEESSQMA----GYGSTQT---
                                                                                                                                                                                                                                                                                                                               TQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG----
                                                                                                                                                                                                                                                         IAGYGSTQTAGEDSSLT--AGYGSTQTAQK 284
                                                                                                                                                                                                                                                                                                                                                           IATYGSTLSGTHQSQLIAGYGSTETA---GDSSTL-IAGYGSTGTAGA---
                                                                                                                                                                                                                                                                                                                                                                                  IVVSGSALAGVY-DOLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas fluorescens and
                                                                                                                                      (Rel. 17, Created)
(Rel. 17, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                             STANDARD;
   active
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                                                                               Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                         12.6%;
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   gene
                                                                                       Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                             24;
  Watanabe M.,
ne of Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                          Score 95.5; DI
Pred. No. 1.6;
24; Mismatches
                                                                                                                                                                                             PRT;
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                                                                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                                                                                                         1.6;
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  Arai S.;
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Sequence similarity
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICEN XANCT
P18127;
Xanthomonas campestris pv. translucens.";

Mol. Gen. Genet. 223:163-166(1990).

-i-FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.

-i- SUBCELLULAR LOCATION: Outer membrane (By similarity).

-i- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XANCT
                                                                                                                                                                      Zhao J.,
                                                                                                                                                                                          MEDLINE=91080859;
                                                                                                                                                                                                                     STRAIN=X56S;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel.
01-NOV-1990 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                           Zhao J., Orser C.S.; "Conserved repetition in the ice nucleation
                                                                                                                                                                                                                                                                                   NCBI_TaxID=343;
                                                                                                                                                                                                                                                                                                                                                              Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ice nucleation; Repeat; Outer membrane.
162 1281 OCTAPEPTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S07053; S07053.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license
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FEBS Lett. 258:297-300(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                        nucleation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTYSTALLIZATION IN SUPERFOOLED WATER.
SUBCELLULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSEN
OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Ice nucleation proteins enable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED SIMILARITY: Belongs to the bacterial ice nucleat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pro; IPR000258; Ice_nucleatn.
PF00818; Ice_nucleation; 69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P06620; 1INA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    16, Created)
16, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                          PubMed=2259339;
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131094 MW; 89B0EE24AA837039 CRO
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Pred. No. 2.1;
20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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(See http://www.isb-sib.
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OF THE CONSENSUS
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Search completed: March 11, 2004, 18:34:55 Job time: 7.3 secs
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Best Local Similarity
Matches 43; Conserv
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HSSP; P06620; IINA.
InterPro; IPRO00258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR0037; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MISCELLANEOUS: A STRUCTURAL MODEL IS SUBDRIMPOSED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
SIMILARITY: Belongs to the bacterial ice nucleation protein
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29.9%; Pred. No. 3;
ative 26; Mismatches
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Maximum DB
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q9cw63 escherichia
Q7x237 enterobacte
Q54069 salmonella
Q8eih4 shewanella
Q8eih4 shewanella
Q8cw64 escherichia
Q83ru7 shigella fl
Q7ucz1 shigella fl
Q8eji3 bradyrhizob
Q8eji4 bradyrhizob
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Q8eih3 shewanella
Q8eih3 shewanella
Q8eji4 bradyrhizob
Q7x244 citrobacter
Q8eji5 bradyrhizob
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Q7x243 citrobacter
Q7x240 citrobacter
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12.6	12.6	12.6	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.7	12.8	12.8	12.9	12.9	13.0	13.1	13.1	13.1	13.1	13.1	13.1	13.3	13.4	13.5	13.9
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Q9kkb2 israeli tic	Q94593 leishmania	O33801 salmonella	Q8mnz5 leishmania	Q8mnz4 leishmania	· Q8mnz3 leishmania	Q8mm48 leishmania	Q8mnz2 leishmania	Q25275 leishmania	Q9bit0 plectreurys	$\mathbf{r}$	יטי	O43994 leishmania	093397 cyprinus ca	Q7x5n9 rickettsia	Q840u6 rickettsia	Q88hg0 pseudomonas	Q8u6n9 agrobacteri	Q7x238 enterobacte	Q9kkb1 rickettsia	Q840u5 rickettsia	Q8mnz1 leishmania	Q8mnz0 leishmania	Q7tw98 mycobacteri			Q8mvw7 naegleria g	-	Q9s3j8 escherichia

## ALIGNMENTS

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01-OCT-2003
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"Production of Cellulose and Curli Fimbriae by Members of the
Enterobacteriaceae Isolated from the Human Gastrointestinal Tr
Infect Immun: 72:4151-4158(2003).
EMBL; AJ515701; CAD56675.1; -.
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                             STRAIN=Fec4;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Enterobacteriaceae; Citrol
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515700; CAD56672.1; -.
SECHEMPE 150.3.
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01-OCT-2003
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Bacteria, Proteobacteria,
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                                                                        Conservative
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                                                                                                                                                              AA;
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                                                                                                                                                            15260 MW;
                                                                                                                                                                                                                                                                                                                                                                               Citrobacter.
                                                                                            69.2%;
72.8%;
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                                                                                                                                                                                                                                                                                                                                                                                               Gammaproteobacteria; Enterobacteriales;
                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                   Score 524; DB
Pred. No. 1.2e-
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Last sequence update)
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l; Mismatches
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                                                                                                                                                            946DD52017F648FD CRC64;
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                                                                                                               DB
                                                                                            .2e-34;
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01-MAR-2003
01-MAR-2003
                              SEQUENCE FROM N.A. STRAIN=Fec39;
                                                                                                                     Enterobacteriaceae;
NCBI_TaxID=28141;
                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                          Curlin-csgA
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SEQUENCE
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                                                                                                                                                                                                                          Enterobacter sakazakii.
                                                                                                                                                                                                                                                               CSGA.
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Enterobacteriaceae; Esche
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MEDLINE=22388234; PubMed=12471157;
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Bokranz
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Q54069;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                    Bacteria;
                                             Shewanella oneidensis.
                                                                                    Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cox J.M., Eglezos S., Woolcock J.B.;
"Virulence of Salmonella enteritidis in chickens correlates
colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Production of Cellulose and Curli Fimbriae by Members of th Enterobacteriaceae Isolated from the Human Gastrointestinal Infect. Immun. 72:4151-4158(2003).

EMBL; AJ515702; CAD56678.1;
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  Proteobacteria; Gammaproteobacteria; Alteromonadales;
adaceae; Shewanella.
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7704 MW;
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SEQUENCE
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Q8CW64;
01-MAR-2003
                                                                                                                             STRAIN=O6:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Rc

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete ge
of uropathogenic Escherichia coll.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

EMBL; AB016759; AAN79778.1; -.
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Heidelberg J.F., Pauleen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium Characterian and the sequence of the dissimilatory metal ion-reducing bacterium
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SEQUENCE 5
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Enterobacteriaceae;
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                  Escherichia coli 06
                                                                                                                                                                                                                                                                                                                                                  CSGB OR C1305.
                                                                                                                                                                                                                                                                                                                                                              Minor curlin subunit
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37; Conser
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                           VYDQ----
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MYDQVQGDNMKNKLLFMMLTILGAPGIAAAAGYDLANSEYNF---
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                                                                                                      160 AA;
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502 AA; 52441 MW;
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                                                   Conservative
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                                                                                                       16963 MW;
                                                                                                                                                                                                                                                                                                           teria; Gammaproteobacteria;
Escherichia.
                          -----LVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSET
                                                              15.9%;
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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SEQUENCE FROM N.A.
STRAIN=2457T / ATCC 700930
MEDLINE=22590274; PubMed=1:
                                                                                                               Bacteria; Proteobacteria;
Enterobacteriaceae; Shige
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CSGB OR S1108.
                                                                                            NCBI_TaxID=623;
                                                                                                                                                           Shigella flexneri.
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01-JUN-2003
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang Yang J., Yang G., Wu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
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CSGB OR SF1035.
Shigella flexneri
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Enterobacteriaceae; Shigella.
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n subunit precursor, similar ro CsgA.
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PubMed=12704152;
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STRAIN-USDA 110;
MEDLINE=22484998; PubMed=12597275;
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Bacteria; Proteobacteria; Alphaproteobacteria;
Bradyrhizobiaceae; Bradyrhizobium.
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"Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).
EMBL; AE016981; AAP16542.1; -.
SEQUENCE 151 AA; 15868 MW; 5D5D266B964014A0 CRC64;
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.., Idesawa K., Iriguchi M., Kawashima K.,
, Shimpo S., Tsuruoka H., Wada T., Yamada
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Bacteria; Proteobacteria; Alphapro
Bradyrhizobiaceae; Bradyrhizobium
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamad
                                                                                                                                                                                                                                              "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
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NCBI_TaxID=70863;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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OR BLL5300.
                                                                                                                                                                                                                Biotechnol.
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                                                                                                                                                                  S00866; -
                                                                                                                                                                                        AE015532; AAN53942.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 AALALQSDARKSETTIT-QSGYGNGADVGQ-GADNSTIELTQNGFRNNATIDQWNAKNSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
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139 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVLALSSAAQAANTSTTVQVGLVNGSSVTQNGLTNDSSSTTQIGILNGASTMQGTSSPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 AA;
          Conservative
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                                                                                                               14811 MW;
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                                15.2%;
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             23;
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Last annotation update)
          Score 115; DB
Pred. No. 0.07
23; Mismatches
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Pred. No. 0.
                                                                                                               41EC1CFA76957920 CRC64;
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1.077;
52;
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Best Local
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01-OCT-2003
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Q89JI4;
Q1-JUN-2003
Q1-JUN-2003
Q1-JUN-2003
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Ucl
Kasamoto S., Watanabe A., Idesawa K., Iriguchi M.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Watana S.;
                                                                                                                                                                                                                                                                                                                                                                           "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                      Nucleation
                                                                                                                          Q7X244
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                                                            CSGB.
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                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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                                                                      component
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
component of curlin monomers.
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Citrobacter sp.

Bacteria;

Proteobacteria;

ceria; Gammaproteobacteria; Enterobacteriales; Citrobacter.

Fec2.

Enterobacteriaceae;

NCBI\_TaxID=213763;

SEQUENCE

FROM N.A.

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Result
No.
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Maximum
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Perfect score:
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length: 2000000000
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Maximum Match 10
Listing first 45
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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| Salmonell
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
91.5	92	92	93	93.5	95	96	96	96	98	101	102	106.5	107.5	109	111	111	. 111	115	115
11.7	11.8	11.8	11.9	12.0	12.2	12.3	12.3	12.3	12.6	12.9	13.1	13.7	13.8	14.0	14.2	14.2	14.2	14.7	14.7
580	975	23	974	287	24	19	19	19	26	262	26	151	151	24	22	22	22	22	22
v	σ	ω	σ	4.	7	W	w	w	7	4	7	w	w	7	w	w	w	w	u
AAG66008	ADA33477	AAB36331	ABU17075	ABB66343	ABR82647	AAB36328	AAB36336	AAB36323	ABR82645	ABB66342	ABR82649	AAB36342	AAB36344	ABR82644	AAB36337	AAB36327	AAB36322	AAB36320	AAB36339
Aag66008	Ada33477	Aab36331	Abu17075	Abb66343	Abr82647	Aab36328	Aab36336	Aab36323	Abr82645	Abb66342	Abr82649	Aab36342	Aab36344	Abr82644	Aab36337	Aab36327	Aab36322	Aab36320	Aabs6339
F. necrop	Acinetoba	Escherich	Protein	Drosophi	E. coli	Salmonel	Salmonel	Salmonel	E. col	Drosophil	E. coli	Salmonell	Escherich	E. coli	Salmonel	Salmonel	Salmonel	Salmonel	Saimonei

# ALIGNMENTS

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RESULT 1
AAB36349
ID AAB3
WPI; 2000-672631/65.
N-PSDB; AAC64625.
                                                                                                                        White AP,
                                                                                                                                                             05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                             Salmonella enteritidis
                                                                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                05-APR-1999;
                                                                                                                                                                                     WO200060102-A2
                                                                                                                                                                                                                          vaccine; immune response;
                                                                                                                                                                                                                                            AgfA::PT3#4 amino acid sequence SEQ
                                                                                                                                                                                                                                                        26-FEB-2001
                                                                                                                                                                                                                                                                     AAB36349;
                                                                                                                                                                                                                                                                                AAB36349 standard;
                                                                                                                                     (UYVI-) UNIV VICTORIA.
                                                                                                                                                                         12-OCT-2000.
                                                                                                                                                                                                        Escherichia coli.
                                                                                                                       Doran JL,
                                                                                                                                                                                                                                                        (first
                                                                                                                                                 99US-0127888P
                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                        entry)
                                                                                                                        Collison
                                                                                                                                                                                                                          immunogen.
                                                                                                                                                                                                                                                                                 151
                                                                                                                        SK,
                                                                                                                                                                                                                                                                                 ₹
                                                                                                                                                                                                                                            ID NO:18
                                                                                                                        Kay WW;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria mubunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene

into the

chromosome

o H

the

homologous

species,

recombinant gene

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

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RESULT 2
AAR74625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant Agfa (CC protein containing a replacement segment or segments of foreign amino (CC acid sequence or sequences grown on a Salmonella, E. coli or (CC eliciting the expression of recombinant Agfa protein which is useful for the expression of recombinant Agfa protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation (CC system the heterologous antigens are presented in high numbers (up to accine, the carrier fimbrial subunit protein possesses both the carrier fimbrial subunit proteins are usually strong (CC immunogenicity and adhesion properties relevant for an efficient live against the inserted epicope, and hybrid fimbriae are usually strong (CC inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Disclosure; Fig 7B; 95pp; English.
                                              strains,
                                                          Eliciting an
                                                                                     WPI; 1994-358275/44.
N-PSDB; AAQ87467.
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Best Local :
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                                                                                                                                           Kay ww,
                                                                                                                                                        (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING {\tt J}.
                                                                                                                                                                                                                                                26-APR-1994;
                                                                                                                                                                                                                                                                                 10-NOV-1994.
                                                                                                                                                                                                                    26-APR-1993;
                                                                                                                                                                                                                                                                                                              WO9425598-A2
                                                                                                                                                                                                                                                                                                                                              Salmonella.
                                                                                                                                                                                                                                                                                                                                                                   Salmonella; AgfA; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                         AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR74625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR74625 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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                                                                                                                                Collinson SK,
                        an immune response to Salmonella - using vector constructs, or compsns. contg. fimt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNAAL VNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGERNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 780; DB 3; ilarity 100.0%; Pred. No. 1.7e-67; Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                              93US-00054452
                                                                                                                                                                                                                                           94WO-IB000207
                                                                                                                           Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
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                                                                                                                         Doran
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                  sing attenuated Salmonella fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 151;
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ACC X S S X P P F X X P F X X P P X X

The Salmonella AgfA protein and DNA are used in vaccine

and genetic

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The present invention describes a recombinant agfA gene (1) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SERI7/TAF) nucleation depended are: CC enterobacteriaceae for the production of fimbriae comprising recombinant GC AgfA, CSgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene; and (4) eliciting a minumure response in an animal, CC comprising separating an amino acid polymer comprising a recombinant accombinate segment of the foreign are combinant AgfA contents of sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
AAB36341
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                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                  Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                        WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                                                    White AP,
                                                                                                                                                                                                                                                                                                                                                                          (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella; agfa; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36341 standard, protein, 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137;
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                                                                                                                                                                                                                                                                                                                                                Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLĹKVÁÁPÁÁÍVVSGSÁLÁGVVÞÓWGGGGNHNGGGNSSGÞDSTLSTYQYGSANAÁLÁLÓ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDVDQLVTRVVTHEMAHALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127888P.
                                                                                                                                                                                                                                                                                                                                             Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.6%;
                                                                                                                                                                                                                                                                                                                                             SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 691;
Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                          Kay
                                                                                                                                                                                                                                                                                                                                           W
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.8e-59;
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RESULT 4
AAW23570
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Best Local S
Matches 137
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29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW23570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                   03-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis 27655-3b agfA.
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Example 2; Fig 7; 85pp; English
                                                                                                  N-PSDB; AAT74142
                                                                                                                                                         Collinson
                                                                                                                                                                                                                                       26-APR-1993;
                                                                                                                                                                                                                                                                            26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                          US5635617-A
                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enteropathogenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW23570 standard;
                                      enteropathogenic
                                                                                                                                                                                                (TVYI-)
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                                                                                                                  1997-309886/28
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                                                                                                                                                                                              UNIV VICTORIA
                                                         Salmonella gene
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                                                                                                                                                         Kay WW,
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                                                                                                                                                                                                                                                                            94US-00233788
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                        bacteria
                                                                                                                                                                                                                                                                                                                                                                                               note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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                                                                                                                                                                                                INNOVATION
                                    agfA - u
                                                                                                                                                         Doran JL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enterobacteria; S.enteritidis; antibody.
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Pred. No. 6.8e
3; Mismatches
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                                      used for diagnosis of Salmonella e Enterobacteria family.
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No. 6.8e-59;
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The present sequence represents agfA encoded derived from Salmonella enteritidis 27655-3b.

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Best Local S
Matches 136
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant and AndA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from tirtually all other microbial organisms. (Updated on
                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                           Disclosure; Page 138; 139pp;
                                                                                                                                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AgfA::PT3#8 amino
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                                                                                                                                                                                                                                                                 White
                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine;
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                                                                                                                                                                                                                     2000-672631/65.
DB; AAC64629.
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                                                                                                                                                                                                                                                              Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid sequence SEQ ID NO:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
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90.1%;
                                                                                                                                                                                                                                                                 Collison
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No. 2.1e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 136;
   Recombinant agfA gene which encodes foreign
                                                                                                                                                                      White AP, Doran JL,
                                                                                               N-PSDB; AAC64626.
                                                                                                                        WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                    (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                 05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNAKNSDITVGQYGGNNAALVNQTASDSSVNVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                        99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        response;
having a segment replaced by a foreign DNA sequence epitope or antigen, expresses recombinant acts
                                                                                                                                                                         Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 675; DB 3;
Pred. No. 2.4e-57;
0; Mismatches 0
                                                                                                                                                                         SK,
                                                                                                                                                                   Kay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
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antigen, expresses recombinant

AgfA

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RESULT 7
AAB36348
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CC directing recombination of a recombinant gene into the chromosome of the CC back into the chromosome of the homologous species, (3) directing recombination of a recombinant gene into the chromosome of the CC back into the chromosome of the homologous species, replacing the native CC comprising separating an amino acid polymer comprising a recombinant Agfa CC protein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (1) is CC eliciting an immune response in an animal for CC system the heterologous antigens are presented in high numbers (up to 100,000 copies/cell), the hybrid fimbrin protein bossesses both the CC vaccine, the carrier fimbrial subunit proteins are usually strong CC against the inserted epitope, and hybrid fimbriae are usually strong CC inexpensive to purify in large amount. The present sequence is given in txx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
               05-APR-2000; 2000WO-CA000356.
                                                                                                                               12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                          WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AgfA::PT3#3 amino acid sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36348 standard; protein; 151
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(1) use of thin aggregative fimbriae (SEF1)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 137; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDARKYDQLVTRVVTHEMAHA-----
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28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----YDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNNATIDOWNÁKNSDITVGQYGGNNAALVNOTASDSSVMVROVGFGNNATANOV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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73.6%;
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Pred. No. 3.3e-52;
0; Mismatches 0
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05-APR-1999;

99US-0127888P

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RESULT 8
AAB36346
ID AAB3
XX
AC AAB3
XX
DT 26-F
XX
DE AgfA
XX
KW Salm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and the accomplished to purify in large amount. The present sequence is given in the accomplished to the present incompliance are cased and the present sequence is given in the accomplished to the present incompliance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                              AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                          26-FEB-2001
                                                                                                                                                                                          AAB36346 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 136; 139pp; English
vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White AP,
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                                                                                                                                                                                                                                                                                                                        ATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAH---
                                                                                                                                                                                                                                                                                                                                                                                                            -----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN
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                                                                                                                                                                                                                                                                                                                                                                                    PDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 618; DB 3
Pred. No. 8e-52;
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                                                                                                                                                                                                                                                                                                  151
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein passesses both the
                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombination of a recombination of a recombinant gene bomologous species; (3) directing recombination of a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                          immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene segment of the gene has been replaced by a segment of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 135; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-672631/65.
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121
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                                                                             61
                                     NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  NNAALVNYDOLVTRVVTHEMAHANNATANOY
                                                                                                                                                           MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doran JL,
                                                                                                                                                                                                                                           Conservative
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                                                                           ITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI
                                                                                                                                                                                                                                                            78.6%;
80.8%;
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                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                          Score 613; DB 3; Length 151
Pred. No. 2.4e-51;
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RESULT

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                                                                                                                                                                                                  CC assembly system of strains of Salmonella, Bscherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC Agfa, CsgA and Agfa-homologue fimbriae tombinis, respectively; (2) CC directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombinative CC back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, cC comprising separating an amino acid polymer comprising a recombinant Agfa CC protein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant Agfa protein which is useful for CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant Agfa protein which is useful for CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant Agfa protein which is useful for CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant Agfa protein which is useful for CC indunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are easy and convergence in the present invention of the present invention
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                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001
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      μ
                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                     151 AA;
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                     Conservative
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                                                                                                      78.3%;
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                                                                                Score 611; DB 3;
Pred. No. 3.8e-51;
6; Mismatches 22;
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                                                                                                                     Length 151;
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inexpensive to purify

large amount.

The present sequence is given

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RESULT 10
AAB36352
                                             directing recombination of a recombinant gene into the chromosome of the Chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or anterobacteriaceae host cell, from the host cell and introducing the Colymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for gystem the heterologous antigens are presented in high numbers (up to 500,000 coppies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, their high must be important for directing an immune response
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                   immunogens,
against the
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               which may be important for directing an immune inserted epitope, and hybrid fimbriae are easy
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                                    response
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RESULT 11
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ID AAB36
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Best Local Similarity 82.1
Matches 124; Conservative
          The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
                                                                                                                                                                                                                                                                                                                                                           Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                       for eliciting
                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0127888P
sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.9%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                              Collison
grown on a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ა</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 608;
Pred. No. 7.
                                                                                                                                                                                                                                                      immune response
                                                                                                                                                                                                                                                                                                                                                              SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                             Кау
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
.4e-51;
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                                                                                                                                                                                                                                                       in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT 12
AAB36351
ID AAB36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful, for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                   WPI; 2000-672631/65.
N-PSDB; AAC64627.
                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
                                                                                                                                                                                                                               05-APR-1999;
                                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                               WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                               vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36351 standard;
                                                                                                                                                                                                                                                                                    12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#6 amino acid sequence SEQ ID
                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                       Sscherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                         Doran JL,
                                                                                                                                                                                                                                                                                                                                                         coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                               99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.1%;
80.8%;
                                                                                                                                                                           Collison
                                                                                                                                                                                                                                                                                                                                                                                               ımmunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 601;
Pred. No. 3.
                                                                                                                                                                           SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                           Kay ww;
                                                                                                                                                                                                                                                                                                                                                                                                                                          NO:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign DI sequence which encodes a foreign epitope or antigen. Also describe

Disclosure; Page 137; 139pp; English.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

N-PSDB; AAC64631.

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RESULT 13
AAB36355
ID AAB36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copy of that gene; and (4) eliciting an immune response in an animal, and comprising separating an amino acid polymer comprising a recombinant AgfA Copyrotein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (1) is CC useful for the expression of recombinant AgfA protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CO you copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live concoine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC immunogens which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are easy and consequence to purify in large amount. The present sequence is given in the examplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
WPI; 2000-672631/65
                                          White AP,
                                                                                                                              05-APR-1999;
                                                                                                                                                                      05-APR-2000; 2000WO-CA000356
                                                                                  (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                       12-OCT-2000
                                                                                                                                                                                                                                                                    WO200060102-A2
                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36355 standard; protein; 151
                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNQGGNSSGPDYDQLVTRVVTHEMAHALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                     Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                   immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQCADNYDQLVTRVVTHEMAHADQMNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                              99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                              response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.9%;
81.5%;
                                       Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 600;
Pred. No. 4.
                                     SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                   Kay
                                     W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
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В Ś Ś

RESULT 14
AAB36343
ID AAB36

AAB36343 standard; protein; 151 AA

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> 61 61

SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG

SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG

120 120

121

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

NNAALVNOTASDSSVMVROVGFGNNATANOY 151

vaccine;

immune

response;

chromosomal gene replacement; fimbrin; epitope;

Salmonella; agfA;

26~FEB-2001 AAB36343;

(first entry)

Escherichia coli CsgA amino acid sequence SEQ ID NO:7

Escherichia coli

WO200060102-A2

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                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the cuseful for the expression of recombinant AgfA protein which is useful for celliciting an immune response in an animal. In a fimbrial presentation conjunction with a carrier or diluent. (I) is cuseful for the expression of recombinant AgfA protein which is useful for celliciting an immune response in an animal. In a fimbrial presentation conjunction properties relevant for an efficient live immunogenicity and adhesion properties relevant for an efficient live conjunctine, the carrier fimbrial subunit protein are usually strong conjunction of the present invention in the expressive to purify in large amount. The present sequence is given in the examplification of the present invention
                                                                                                     Matches
                                                                                                                           Query Match
Best Local
                                                                                                                                                                                          Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 139; 139pp; English
                                                                                                                      Local
                                                                                                   123;
            ы
                                                                                                                      Similarity
MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                 Conservative
                                                                                                                    76.8%;
81.5%;
                                                                                                 <u>υ</u>
                                                                                         Score 599; DB 3;
Pred. No. 5.5e-50;
5; Mismatches 23
                                                                                                                                     Length 151
                                                                                            Indels
                                                                                            0
                                                                                         Gaps
60
                                              60
                                                                                         0
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05-APR-2000;

2000WO-CA000356

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RESULT 15
ABR82651
ID ABR82
XX
AC ABR82
XX
DT 04-DE
XX
DE E CO
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
                         E, coli CsgA subunit 15 kDa protein.
                                                                                          04-DEC-2003
                                                                                                                                                       ABR82651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             segment of the gene has been replaced by a beginning. Also described a sequence which encodes a foreign epitope or antigen. Also described a sequence which encodes a foreign epitope or antigen. Also described a sequence which encodes a foreign expension of salmonella. Escherichia coli and
                                                                                                                                                                                                                 ABR82651 standard; protein; 151
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                                                                                          (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated peptide capable of binding a mammalian plasma prouseful in the manufacture of a medicament for the prevention treatment of a bacterial infection, such as Escherichia coli, or Shigella infections.
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N-PSDB; ACF36153.
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Query Match 87.9%; Score 686; DB 1; Length Best Local Similarity 90.1%; Pred. No. 2.2e-62; Matches 136; Conservative 3; Mismatches 12; Inde	US-08-233-788A-59 US-08-233-788A-59 US-08-233-788A-59  Sequence 59, Application US/08233788A  Patent No. 5635617  GENERAL INFORMATION: APPLICANT: DOYAN, James L. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Manuella Sharon C. TITLE OF INVENTION: OF SALMONELLA NUMBER OF SEQUENCES: 61 CORRESPONDENCE ADDRESS: ADDRESSEE: Seed and Berry STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle CITY: Seattle COMPUTER: Washington COUNTRY: U.S.A. ZIP: 98104-792: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOUTHARE: Patentln Release #1.0, Version #1.25 CURRENT APPLICATION DATA: OPERATION NUMBER: US/08/233,788A FILLING DATE: 26-APR-1994 CLASSIFICATION NUMBER: US/08/233,788A FILLING DATE: 26-APR-1994 TELEFAX: (206) 622-4900 TELEFAX: (206) 622-4900 TELEFAX: (206) 622-4900 TELEFAX: (206) 622-4900 TELEFAX: (206) 622-4900 TELEFAX: (206) 622-4900 TELEFAX: (206) 622-4900 TELEFAX: (206) 622-4900 TELEFAX: (206) 622-4900 TELEFAX: (206) 623-6031 TELEFAX: (206) 623-6031 TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: parotein US-08-233-788A-59	28 83 10.6 2354 4 US-09-268-347-47 29 83 10.6 2411 4 US-09-268-347-36 30 82 10.5 878 4 US-09-540-236-3401 31 81.5 10.4 211 1 US-08-276-852-34 32 81.5 10.4 211 1 US-08-322-730A-16 33 81.5 10.4 211 1 US-08-397-874-16 35 81.5 10.4 211 1 US-08-899-575-34 36 81.5 10.4 211 1 US-08-899-575-34 37 81.5 10.4 211 1 US-08-899-575-34 38 81.5 10.4 211 1 US-08-899-575-34 39 81.5 10.4 211 2 US-08-899-575-34 40 81.5 10.4 211 2 US-08-383-619-16 41 81.5 10.4 211 3 US-08-999-7739-16 42 81.5 10.4 211 3 US-08-997-739-16 43 81.5 10.4 211 5 PCT US93-08364-16 44 81.5 10.4 238 4 US-09-495-880A-24 42 81.5 10.4 266 4 US-09-495-880A-26 43 81.5 10.4 266 4 US-09-495-880A-26 44 81.5 10.4 293 3 US-08-438-745-6 45 81.5 10.4 293 3 US-08-438-745-6
ngth 151; Indels 0; Gaps 0	DETECTION	Sequence 47, Appl Sequence 36, Appl Sequence 34, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 21, Appl Sequence 22, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 43, Appl Sequence 44, Appl Sequence 46, Appli Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 47, Appl Sequence 48, Appl Sequence 49, Appl Sequence 49, Appl Sequence 49, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 40, Appl Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 44

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                                                       US-09-328-352-4764
                                                                          RESULT 3
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US-08-233-788A-57
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Sequence 4764, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
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Best Local
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APPLICANT: Doran,
APPLICANT: Kay, Will
APPLICANT: Collins
APPLICANT: Clouthic
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-603
TELEX: 3723836 SEEDANE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: li
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,78
FILING DATE: 26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                   y Match 64.9%;
Local Similarity 87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                               GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                      VVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADV
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                                                                                                                       GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
                                                                                                                                                                                             VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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                                                                                                                                                                                                                                                                                                                                                                                                          120 amino acids
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                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: KAMBOJ,
APPLICANT: ELIOTT,
APPLICANT: NUTT, S
                                                                                                                                                        APPLICATION UNMER: US/08/254,573
APPLICATION UNMER: US/08/254,573
FILING DATE: 06-JUN-1994
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 07/896,611
FILING DATE: 10-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/179;
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
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                                                                                   INFORMATION FOR SEQ ID NO: 2:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TYPE: PRT
                                                                     SEQUENCE CHARACTERISTICS:
OLECULE TYPE:
         TYPE: ami
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                                                                                                             TELEPHONE: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Alexandria
                                                 LENGTH:
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5. 5610032
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                               amino acid
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                                               906 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAMBOJ, Rajender
ELIOTT, Candace
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                                                                                                                                            (703)836-9300
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                                                                                                                                                                                    16777/179 ALLE
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Pred. No. 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suite 500
                                                                                                                                                                                                                                                                                                                                                                                            Version #1
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Patent No. 5756697

Patent No. 5756697

GENERAL INFORMATION:
APPLICANT: Hoeger, Thomas
APPLICANT: Ultsch, Andreas
APPLICANT: Bach, Alfred
APPLICANT: Sterrer, Sylvia
APPLICANT: Lemaire. Hann
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                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-687-379-2
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Best Local S
Matches 45
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 906 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 720 Kb storage
COMPUTER: IBM AT-compatible, 80286 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1101 Conr
CITY: Washington
                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/687,379 FILING DATE: 05-AUG-1996
                                                                                                                                                                                                                            Local Similarity
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                                         301 AEAFQSLRRQ---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNE
                                                                                                                           250 VTGFQLVNYTDTIPAKIMQQW------KNSDARDHTRVDWKRPKYTSALTYDGVKVM 300
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                                                                               56 AHALQSDARKSETTITQSGYGNGADV------GQGAD------NSTIELTQ
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NGFRNNAT-----IDQWNAKNSDI---TVGQYGGNNAALVNQT-----ASD
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NVENTION: Subunits of Glutamate Receptors, Their
NVENTION: Preparation and Their Use
SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                         11.5%; Score 90; DB 1; Length 906; 22.6%; Pred. No. 1.1;
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                                                                                                                                                                                                        26; Mismatches
                                                                                                                                                                                                        56; Indels
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US-08-687-379-4
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                                                                                                      RESULT 7
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Sequence 1, Application US/08172332
Patent No. 6313279
GENERAL INFORMATION:
APPLICANT: Burnett, J. Paul
APPLICANT: Mayne, Nancy G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08687379 Patent No. 5756697
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INFORMATION FOR SEQ ID NO: 4:
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APPLICANT:
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MEDIUM TYPE: Disette-3.5 inch, 720 Kb storag
COMPUTER: IBM AT-compatible, 80286 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,379
APPLICATION NUMBER: US/08/687,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bach, Alfred
APPLICANT: Sterrer, Sylvia
APPLICANT: Lemaire, Hans-Georg
TITLE OF INVENTION: Subunits of Glutamate Receptors, Their
TITLE OF INVENTION: Preparation and Their Use
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20036
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                                                                                                                                                                                                                                                                                           AEAFOSLRRO---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNE
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1101 Connecticut Avenue
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26; Mismatches
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Pred. No.
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US-08-216-326-2
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                                                                                                                                                  Sequence 2, Application US/08216326
Patent No. 6406868
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 906 amino acid
                                                                              APPLICANT: ELIOTT, Candace
APPLICANT: NUTT, Stephen
TITLE OF INVENTION: AMPA-BINDING
                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 07/879,688
FILING DATE: May 1, 1992
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CURRENT APPLICATION DATA:
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APPLICANT: Sharp, Robert I
TITLE OF INVENTION: HUMAN
TITLE OF INVENTION: COMPOU
ADDRESSEE: Foley & Lardner STREET: 3000 K Street N.W., CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Polocial
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                                                                                                               KAMBOJ, Rajender
ELIOTT, Candace
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Lilly Corporate Center
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SEQ ID NO: 1:
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Pred. No. 1.1;
26; Mismatches
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               Suite 500
                                                                              HUMAN Glur1 RECEPTORS
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RESULT 9
US-08-864-038A-3
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                                                                                                                                                                                                                                Sequence 3, Application US/08864038A

Patent No. 6001592

GENERAL INFORMATION:
APPLICANT: Kunio NAKASHIMA et al.
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
TITLE OF INVENTION: TO SAID POLYPEPTIDE
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Best Local (
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PLOS/MS-DOS
MEDIUM TYPE: PC-DOS/MS-DOS
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                                                                                     STREET: 1000
CITY: Tsu-city
CTATE: Mie-prefecture
TAPAN
                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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APPLICATION NUMBER: US/08/216,326
FILING DATE: 23-MAR-1994
PRIOR APPLICATION UTUBERIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
    COMPUTER: IBM CO
OPERATING SYSTEM:
                                                                               COUNTRY: JAPAN
ZIP: 514-01
                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AHALQSDARKSETTITQSGYGNGADV-------GQGAD-----NSTIELTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQL-----VTRVVTHE----M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 22.6
45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEAFQSLRRQ---RIDISRRGNAGDCLANFAVFWGQGIDIQRALQQVRFEGLTGNVQFNE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGRRTNYTLHVIEMKHDGIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTTILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGFRNNAT - - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIGFOLVNYTDTIPAKIMOOW------KNSDARDHTRVDWKRPKYTSALTYDGVKVM 300
IBM Compatible
WSTEM: Microsoft Windows 95
                                                                                                                                                                              812-5 Hirano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.5%;
                                      3.50 inch, 1.44 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----IDQWNAKNSDI---TVGQYGGNNAALVNQT-----ASD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 906;
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                                      storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:

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                                                                    / TYPE: PRT
/ ORGANISM: Moraxella catarrhalis
US-09-336-447A-5
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US-09-336-447A-5
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Best Local Similarity 25.6
Conservative
                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION:
                                                                                                                                      SOFTWARE: Patentin Ver. SEQ ID NO 5
Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                              APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                    FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                    APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
APPLICANT: WENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
                                                                                                                     LENGTH: 892
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LENGTH: 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: peptide LOCATION: from 1 to 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08 FILING DATE: May 28, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL TYPE: mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGGGSAAAAAAAAAASGGGGRALRRALRRQMRGGGSAAA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGGNNAALVNQTASDSS-----VMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARKSETTITQSGYGNGADVGQGADNSTIELTQ-----NGFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 986-2340
 Conservative
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25.6%; Pred. No. 1.5;
tive 11; Mismatches
10.8%; Score 84; DB 26.8%; Pred. No. 4.3; tive 17; Mismatches
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                                  DB 4;
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                                Length 892
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   Indels
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US-07-718-575-2
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                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-07-718-575-2
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Patent No. !
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 9103330318
INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Reiter Ph.D., Stephen E. REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19910813
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/718,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jensen Ph.D., Jan
TITLE OF INVENTION: GLUTAMA:
TITLE OF INVENTION: METHODS
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                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                     103
                                                                      310 Q---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNEKGRRTNYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 NNSTVAGGSHNQATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 IGGGYYSRAIGDSSTIGGGYYNQATGEKSTVAGGRNN----QATGNNSTVAGGSYNQATG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
                                                                                                          65 KSETTITQSGYGNGADV-----
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                                                                                                                                                                                                                  43;
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                                                                                                                                                                           6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGG-NSSGPDYDQLVTRVVTHEMAHALQSDAR
HVIEMKHDGIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTTILEDPYVMLKK---
                                                                                                                                                                                                                                                                                                                                       AMINO ACID
                                   -----IDQWNAKNSDI---TVGQYGGNNAALVNQT-----ASDSSVMVRQVG 141
                                                                                                                                           VTGFQLVNYTDTIPARIMQQWRTSDSRDHTRVDWKRPKYTSALTYDGVKVMAEAFQSLRR
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                                                                                                                                                                                                                                                                                                                                                        907 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  (619)535-8949
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VENTION: GLUTAMATE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boulter Ph.D., James R.
Hollmann Ph.D., Michael NMN
Bettler Ph.D., Bernhard NMN
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTASDSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                                 Score 84; DB Pred. No. 4.4;
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                                                                                                                                                                                                                  Mismatches
                                                                                                          GQGAD----
                                                                                                                                                                                                                                                 DB 1; Length 907;
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425 142

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Patent No.

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US-08-481-206-2
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US-08-481-206-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Reiter Ph.D., Stephen E. REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/481,206 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
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TITLE OF INVENTION: GLUTAMAT
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schr
STREET: 444 So. Flower
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 907 amino
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (619)535.
TELEX: 9103330318
                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                   142 FGNNATANOY 151
                                                                         367 HVIEMKHDGIRKİGYMNEDDKFVPAATDAQAĞDNSSVQNRTYIVTTILEDPYVNLKK--
                                                                                                                                         310 Q---RİDISRRÖNAGÖCLANPAVPWĞQĞIDIQRALQQVRFEGLTGNVQFNEKGRRTNYTL
                                                                                                                                                                            65 KSETTITQSGYGNGADV------GQGAD------NSTIELTQNGFRNNAT- 102
                                                                                                                                                                                                                                             6 VAAFAAIVVSGSALAGVVFQWGGGGNHNGGG-NSSGFDYDQLVTRVVTHEWAHALQSDAR 64
                         ----NANQF 429
                                                                                                                                                                                                             VTGFQLVNYTDTIPÁRIMQQMRTSDSRDHTRVDWKRFKÝTSALTYDGVKVMÁBÁFQSLRR 309
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                                                                                                          -----IDQWNAKNSDI---TVGQYGGNNAALVNQT----ASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                   907 amino acids
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                                                                                                                                                                                                                                                                                             10.8%; Score 84; DB 1; ilarity 22.6%; Pred. No. 4.4; Conservative 24; Mismatches 6
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Jensen Ph.D., Jan E.
VENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heinemann Ph.D., Stephen F.
Boulter Ph.D., James R.
Hollmann Ph.D., Michael NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (619)
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Suite 2000
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                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                                                                                                                         Length 907
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                    54;
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                                                                                                                                                                                                         Query Match
10.8%; Score 84; DB 2; Length 907;
Best Local Similarity 22.6%; Pred. No. 4.4;
Matches 43; Conservative 24; Mismatches 69; Indels
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US-08-486-269A-2
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 907 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/718,575
FILING DATE: 21-JUN-1991
APPLICATION NUMBER: PCT/US90/061.
FILING DATE: 25-OCT-1990
APPLICATION NUMBER: 07/428,116
FILING DATE: 27-OCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5945509
                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 941
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows DEMONSTRATION Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08/486,269A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/01
FILING DATE: 04-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GLUTAMATE R.
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Reiter, Stephen REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                 250 VTGFQLVNYTDT1PÅRIMQQWRTSDSRDHTRVDWKRPKYTSALTYDGVKVMÅBÅFQSLRR 309
                                                                                                                                                                  6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGG-NSSGPDYDQLVTRVVTHEMAHALQSDAR 64
HVIEMKHDGIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTTILEDPYVMLKK--
                                                                 Q---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNEKGRRTNYTL 366
                                                                                                            amino acid
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CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            619-677-1465
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4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Bettler, Bernhard
Jensen, Jan E.
VENTION: GLUTAMATE RECEPTOR COMPOSITIONS
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Boulter, James
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                               IDQWNAKNSDI---TVGQYGGNNAALVNQT----ASDSSVMVRQVG 141
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Matches Query Match

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Gaps

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                                                                                                   Sequence 199, Application US/09072596 Patent No. 6458366
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Reed, S
APPLICANT: Skeiky,
APPLICANT: Dillon,
          GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE; SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 943 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 25.2
Les 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 07-APF CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
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                                                                                                                                                                                                                                                                                                       YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY-----GGNNAA 124
                                                                                                                                                                                                                                                                                                                                            SGTGNVGI----
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Houghton, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                            10.8%;
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Search completed: March 11, 2004, 18:44:51
Job time : 13.4 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 (
CITY: Seattle
                                                                                                                                                                                                                                                                                                                  Local Similarity
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TOPOLOGY: li
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                                                                                                                                                                                                                        184 SGTGNVGI----GNSGTGNWGIGNSGNSYN------
                                                                                                                                                                                    75 YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY---
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Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                  Score 84; DB
Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                 41; Indels
                                                                                                                                                                                                                                                                                                                                     Length 943;
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                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                      -GGNNAA 124
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                          108
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85.5
84.5
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seq length: 2000000000
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110:
112:
123:
134:
145:
156:
177:
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1296.103 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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: /cgn2_6/ptcdata/1/pubpaa/USO6_NEW_PUB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO6_NEW_PUB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO6_NEW_PUB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO6_NEW_PUB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_PUBCOMB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*
: /cgn2_6/ptcdata/1/pubpaa/USO8_NEW_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                              14 US-10-251-661-2

US-09-810-264-28

15 US-10-369-493-1283

10 US-09-952-267-5

10 US-09-996-634-131

10 US-09-997-182-131

10 US-09-997-182-131

10 US-09-997-181-131

10 US-09-997-181-131

10 US-09-997-181-131

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US-09-793-306-146
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Sequence 20638, A
Sequence 146, App
Sequence 2, Appli
Sequence 28, Appli
Sequence 12833, A
Sequence 131, App
Sequence 131, App
Sequence 199, App
Sequence 199, App
Sequence 16, Appl
Sequence 16, Appl
Sequence 179, App
Sequence 179, App
Sequence 179, App
Sequence 179, App
Sequence 179, App
Sequence 179, App
Sequence 179, App
Sequence 179, App
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RESULT 1 US-10-369-493-206 SEQUENCE 20638, Publication No. GENERAL INFORMA APPLICANT: Ch APPLICANT: Hi APPLICANT: Ch APPLICANT: Ch TITLE OF INVEN FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILE REFERENCE CURRENT FILING FILENGTH: 445 TYPE: PRT ORGANISM: Rho		44	43	41	40	ა	37	3 6 5	34	332	ω,	30	28	26 27	25	) K	22	21	20	18	17	16	
SULT 1 -10-3638 -10-3638, Application US/1036949 Publication No. US20030233675A1 GENERAL INFORMATION: APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C. APPLICANT: Goldman, Barry S. APPLICANT: Goldman, Barry S. APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MIC TITLE OF INVENTION: PLANTS WITH IMPR FILE REFERENCE: 38-10 (52052) B CURRENT APPLICATION NUMBER: US/10/369 PRIOR APPLICATION NUMBER: US/10/369 PRIOR APPLICATION NUMBER: US/0360,0 PRIOR FILING DATE: 2003-02-28 PRIOR PILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 20638 LENGTH: 445 TYPE: PRT ORANISM: Rhodopseudomonas palustris ORGANISM: Rhodopseudomonas palustris		79.5 78.5	79.5	79.5	79.5	80 0	80	8 0 0	00	٥:	۳,		81.5	٠.		٠.	٠.	- !	٠.	ໍພ	83	83	
#493-20638 #ition No. US20030233675A1 #ITION NO. US20030233675A1 #ANT: Cao, Yongwei #ANT: Hinkle, Gregory J. #ANT: Slater, Steven C. #ANT: Goldman, Barry S. #ANT: Chen, Xianfeng OF INVENTION: EXPRESSION OF NOT INVENTION: EXPRESSION OF NOT INVENTION: PLANTS WITH IN ### REFERENCE: 38-10(52052) #### REPLICATION NUMBER: US/10/3 ####################################		10.2		•						10.4	•	10.4		10.4		10.4	10.4		10.6	•	10.6	•	
pplication US/10 20030233675A1 N: Congwei Congwei Le, Gregory J. Le, Gregory S. Lan, Barry S. Lan, Barry S. LANTS WITH B-10(52052)B CON UMBER: US/1 LTE: 2003-02-28 LTE: 2002-02-21 NOS: 47374 NOS: 47374		2834 274																			20	18	
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3 OVED PROPERTIES ,493	ALIGNMENTS	10-085-959- 10-156-761-	10-238-075-	US-10-121-032-63	10-156-761-	US-10-156-761-13173	US-10-369-493-20096	US-10-076-604-101 US-10-076-604-105	US-10-076-604-103	US-10-045-674-527 US-10-156-761-11286	US-09-896-095-272	US-09-809-517A-23 US-09-809-517A-26	US-09-809-517A-25	US-09-884-767A-213	US-09-884-767A-215	US-10-033-399B-12	US-09-809-517A-24	US-10-273-973-16	10-016-986-3	09-797-862-33	-09-801-368-1	-09-976-2	
IN PLANTS FOR PRODUCTION		252, 9107,	equence 1119	Sequence 63, Appl	equence 1197	12605	20096	101,	Sequence 103, App	Sequence 527, App Sequence 11286, A	עו	Sequence 26, Appl	25	Seguence 213, App	Sequence 215, App	Sequence 27, Appr	Sequence 24, Appl	Sequence 16, Appl	Sequence 34, Appl	Sequence 33, Appl	176	equence 2,	

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianteng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF INTEL CO. C. C.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF ITTLE OF INVENTION: WINDER: US/10/369,493

CURRENT FILING DATE: 2003-02-29

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

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PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NOS: 47374

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SEQ ID NOS: 47374

SEQ ID NOS: 47374

SEQ ID NOS: 47374

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SEQ ID NOS: 47374

SEQ ID NOS: 47374

SEQ ID NOS: 473

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RESULT 3
US-10-251-661-2
Sequence 2, Application US/10251661
Publication No. US20030166555A1
GENERAL INFORMATION:
APPLICANT: Alberini, Cristina M.
APPLICANT: Alberini, Mark F.
                          CURRENT APPLICATION NUMBER: US/10/251,661
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/193,614
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/US01/10661
PRIOR FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence:mTTC#3-His US-09-793-306-146
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US-09-7
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                      SEQ ID NO 2
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Best Local S
Matches 35
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                                                                                                                                                                              TITLE OF INVENTION: Methods and Compositions for TITLE OF INVENTION: Memory Consolidation FILE REFERENCE: 3499.1001-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-793-306-146
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Campos-Neto, Antonio APPLICANT: Skeiky, Yasir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 NNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 GNAGD--TNTGFGNAGFFNMGIGNAGNEDMGVGNGGSFNVGVGN--AGNQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 FGNSGNNNIGFFNSG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 WGGGGNHNGGGNSSGEDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 DPGVFNKITQDSSSNGSKVSVIQDGKNNVFSIKQGNTGNSTSVNQIG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 91; DB 9; Length 597; 27.8%; Pred. No. 0.8;
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              US-10-369-493-12833
; Sequence 12833, Application US/10369493
; Publication No. US20030233675A1
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 278
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                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Lingyu
TITLE OF INVENTION: WRKY Transcription Factors and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: 1183
CURRENT APPLICATION NUMBER: US/09/810,264
CURRENT FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/190,467
PRIOR FILING DATE: 2000-03-17
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Best Local
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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APPLICANT:
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APPLICANT: Crane, Virginia C.

Pamodii. Omolayo O.
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                              Local Similarity
les 35; Conserv
182 VGCPVRKHVERASHDNRÅVITTYEGRHSHDVPVGRGAGASRÅLPTSSSSDSSVVV 236
                                                                     122 DNEGSSGTGACVKPVREPRLVVQTLSDIDILDDGFRWRKYGQKVVKGNPNPRSYYKCTT
                                                                                                                                                                             15 SG$ALAGYVPQWGGGGNHNGGGNS$GPDYDQLVTRVVTHEMAHALQSDARKSETTITQSG 74
                                                                                                                 75 YGNGADVGQGA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 SSVMVROVGFGNNATANOY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 VTGPQLVNYTDTIFAKIMQQW-------KNSDARDHTRVDWKRPKYTSALTYDGVKVM 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQL----VTRVVTHE----M
                                                                                                                                             NSSGCAAVIAE----DHTNGSEHSGPTPENSSVTFGDDEADNGAEPETKRRK----EHG
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                              NNATIDQWNAKNS-DITVGQYGGNNAALVNQTASDSSVMV 137
                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                      Score 85.5; DI
Pred. No. 1.1;
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                            --DNSTIELTONGFR-----
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                                                                                                                                                                                                                                                         Length 278;
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SEQ ID NO 5
LENGTH: 892
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-952-267-5
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; LOCATION: (1)..(408)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12833
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                                                                                                                                                                       Query Match
Best Local Similarity
Matches 41; Conserv
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APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/952,267
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/336,447
PRIOR FILING DATE: 1999-06-21
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APPLICANT: Chen, Xianfeng

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052) B

FILE REFERENCE: 38-10 (52052) B
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CURRENT FILING DATE: 2003-02-28
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133 IGGGYYSRAIGDSSTIGGGYYNQATGEKSTVAGGRNN----QATGNNSTVAGGSYNQATG 188
                                       81 VGQG-----ADNSTI-----G 120
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                                                                                                                             28 GGGNHNGGGNSS----GPDYDQLVTRVVTHEMAHALQSDARKSETTI----TQSGYGNGAD
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                                                                                   GGKDNEAKGNYSTVGGGDYNEAKGNYST--VGGGSSNTAKGEKSTIGGGDTNDANGTYST 132
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No. US20030032772A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGFTNSSSFDPINIGGKDITITTTEGSVIDGNGQAYWDGLGSNGGV 117
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Goldman, Barry S.
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Slater, Steven C.
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28.3%; Pred. No. 2.3;
                                                                                                                                                                       10.8%; Score 84; DB 26.8%; Pred. No. 7; Live 17; Mismatches
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                                                                                                                                                                                                                   DB 10; Length 892;
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US-09-996-634-131
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US-09-996-634-131
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CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-01-03
PRIOR PRILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
                                                                        PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILLING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILLING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR PILLING DATE: 1996-06-14
PRIOR PILLING DATE: 1996-06-15
PRIOR FILLING DATE: 1995-66-15
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PRIOR FILLING DATE: 1995-66-15
SOFTWARE: Pat
SEQ ID NO 131
LENGTH: 943
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Patent No. US20020172684A1
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
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SEQ ID NO 131
LENGTH: 943
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APPLICANT: Namo, Fr
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CURRENT FILING DATE: 2001-11-28
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                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding TITLE OF INVENTION: immunostimulatory Peptides
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Local Similarity 25.2%;
les 31; Conservative (
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                                                       PatentIn
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o. US20030049263A1
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RESULT 10
US-10-193-002-199
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; Publication INFORMATION;
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APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
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PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR EILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
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PRIOR FILING DATE: 1995-06-15
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CURRENT APPLICATION NUMBER: US/09/997,181
CURRENT FILING DATE: 2001-11-28
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                       APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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                                                                                               Application US/10193002
o. US20030135026A1
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       Campos-Neto, Antonia
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Pred. No. 7.5;
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                                                                                                                                                                                                                                                                                                                                                           318
                                                                                           RESULT 11

US-10-084-843-204
; Sequence 204, Application US/10084843
; Publication No. US20030143243A1
; PENERAL INFORMATION:
; GENERAL INFORMATION:
; Skeiky, Yasir A.W.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 2101
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
mes 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/072,596 FILING DATE: 05-MAY-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                 272 LAN 274
                                                                                                                                                                                                                                                                                                                                                       212 FGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNSGNYNTG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                 184 SGTGNVGI---
                                                                                                                                                                                                                                                                                                                      125 LVN 127
                                                                                                                                                                                                                                                                                                                                                                                            75
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                                                                                                                                                                                                                                                                                                                                                                                          YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY------GGNNAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 943 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Washington
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
                                                    Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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Pred. No. 7.5;
9; Mismatches 41
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41;

42;

Gaps

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211

Length 943

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Best Local :
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         Sequence 16, Application US/09996194 Patent No. US20020151696A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
               APPLICANT: Bandaru, Rajasehkar
TITLE OF INVENTION: 84242, 8035, 55304, 52999, and 21999,
TITLE OF INVENTION: NO. US20020151696A1el Human Proteins and Methods of Use Thereof
FILE REPERENCE: 35800/240590
CURRENT APPLICATION NUMBER: US/09/996,194
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/250,348
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/250,073
PRIOR APPLICATION NUMBER: 60/253,878
PRIOR APPLICATION NUMBER: 60/253,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 204:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 LVN 127
                                                                                                                                                                                                                                                                                                                                                                                                           272 LAN 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 FGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNSGNYNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 SGTGNVGI----GNSGTGNWGIGNSGNSYN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 SGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 10.8%;
Similarity 25.2%;
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/084,843 FILING DATE: 25-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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NUMBER OF SEQ ID NOS: 98
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 873
TYPE: PRT
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; OTHER INFORMATION: Pfam consensus
US-09-996-194-16
                                                                                                                                                                                           RESULT 14
                                                                                                                                                                      US-10-238-075-1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Moraxella catarrhalis US-09-952-267-13
                  Sequence 1549, Application US/10238075
Publication No. US20030148324A1
GEMERAL INFORMATION:
APPLICANT: I.N.S.E.R.M.
TITLE OF INVENTION: Bolynucleotides which are of nature B2/D+ A- and which are isolar TITLE OF INVENTION: E.Coli, and biological uses of these polynucleotides and of the FILE REFERENCE: BLANDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/250,338
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 65
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Publication No. US20030032772A1
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Best Local Similarity
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APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USBA1 AND USBA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/952,267
CURRENT FILING DATE: 2001-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HANSEN, ERIC J. APPLICANT: AEBI, CHRISTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/336,447
PRIOR FILING DATE: 1999-06-21
CURRENT APPLICATION NUMBER: US/10/238,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                            120 SSTIG--GGDN
                                                                                                                                                                                                                                                                                                  112 DITVGQYGGNNAALVNQTASDSSVMVRQVGFG-NNATANQY 151
                                                                                                                                                                                                                                                                                                                                                86 -----AKGDSSTIGGGYYNEAN----GDSSTI----GGGFYN---
                                                                                                                                                                                                                                                                                                                                                                                      52 THEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                 34 LLIVGILGMATTASAQQTIARQ--GKGMHSIIGGGNDNEANGDYSTVSGGDYNE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LKVAAFAAIVVSGSALAGVVPQWGGGGNHN--GGGNS----SGPDYDQLVTRVV 51
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COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 83.5; DI 24.8%; Pred. No. 7.7; rative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 873;
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RESULT 15
US-09-820-843A-21
US-09-820-843A-21
Sequence 21, Application US/09820843A
Publication No. US20030039963A1
Publication No. US20030039963A1
PAPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION UNMEER: US/99/820,843A
CURRENT APPLICATION UNMEER: US/99/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTMARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 354
TYPE: PRT
ORGANISM: M. tuberculosis
Search completed: March 11, 2004, 19:18:37 Job time: 25.6 secs
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NAME/KBY: misc feature
OTHER INFORMATION: PPE
NAME/KBY: misc feature
OTHER INFORMATION: gi|1781260
US-09-820-843A-21
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PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1549
LENGTH: 182
TYPE: PRT
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US-10-238-075-1549
                                                                                                                                                                                                                                                                                                                                                        Query Match 10.6%;
Best Local Similarity 25.2%;
Matches 31; Conservative 1
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                                                                                                                                   147
                                                                                         132 TAN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 SDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 VQIQLLNSNGTSTILLGEADNGQDVQSETIGSDGSAT 153
                                                                                                                                                                               82 NIGIGLTGDG---QIGIGGLNSGSGNIGFGNSGTGNVGLFNSGTGN---
                                                                                                                                                                                                                       87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                      46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 LKDNAATSGLTPFAIRLTGCATGMNSAQNVKAYFEPSSNIDLATHNLKNTAT--PTKADN 116
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                                                                                                                                   TAN 149
                                                                                                                                                                                                                                                                        GNNGNFNFGSGNTG--
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                                                                                                                                                                                                                                                                                                                                                        ; Score 83; DB 10; Length 354; ; Pred. No. 2.7; 11; Mismatches 47; Indels
                                                                                                                                                                                                                                                                    ---SNNIGFGNTGSGNFGFGNTGNN
                                                                                                                                                                                                                                                                                                                                                          Indels 34;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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Perfect score:
pIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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780
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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11.2	11.3	11.3		11.5				11.5		11.7	11.7					12.2				13.8				64.3	64.3	67.1	88.6	88.6	Query Match
552	906	599	1655	599	906	906	968	602	590	2174	590	401	141	141	582	145	145	151	151	151	151	151	1748	152	152	151	151	151	Length
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probable PPE prote	glutamate receptor	leishmanolysin (EC	hypothetical prote	leishmanolysin (EC			glutamate receptor	leishmanolysin (EC	probable PPE prote	hypothetical glyci	leishmanolysin (EC	(n		hypothetical prote		hypothetical prote	conserved hypothet	nucleation compone	fimbrin protein ag	curlin minor chain	minor curlin subun	curlin nucleator p	-	hypothetical prote	curlin major subun	curlin protein csg	major curlin chain	fimbrin protein ag	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	. 30 .
84	84	84	84.5	85	85	85	85	85	85.5	86	86	87	87.5	87.5	87.5
10.8	10.8	10.8	10.8	10.9	10.9	10.9	10.9	10.9	11.0	11.0	11.0	11.2	11.2	11.2	11.2
646	633	586	639	5291	5188	3716	645	364	588	495	409	407	1567	1213	1028
۲	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
S19916	A25473	T26667	C42049	F90696	B85547	E70969	F70825	S43574	F70971	B71360	T20847	T21956	S11672	S16356	A56038
leishmanolysin (EC	chorion E2 protein	hypothetical prote	leishmanolysin (EC	hypothetical prote	probable RTX famil	probable PPE prote	probable PPE prote	C05B5.3 protein (c	hypothetical glyci	•	hypothetical prote	hypothetical prote	ice nucleation pro	ovo protein - frui	DNA-binding protei

### ALIGNMENTS

Qy  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNNNGGGNSSGPDXDQLVTRVVTHEMAHALQ 60	A;Gene: agfA C;Function: A;Description: major component of thin aggregative fimbriae A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C;Keywords: fimbria C;Keywords: fimbria E;1-20/Domain: signal sequence #status predicted <sig> F;1-20/Domain: signal sequence #status experimental <mat> F;21-151/Product: fimbrin protein agfA #status experimental <mat> Query Match B8.6%; Score 691; DB 2; Length 151; Best Local Similarity 90.7%; Pred. No. 9.7e-53; Matches 137; Conservative 3; Mismatches 11; Indels 0; Gaps 0;</mat></mat></sig>	A;Residues: 21-52 <co2> A;Experimental source: strain 27655-3b A;Experimental source: strain 27655-3b A;Note: the authors translated the codon ACG for residue 44 as Ile R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W. J. Bacteriol. 173, 4773-4781, 1991 A;Title: Purification and characterization of thin, aggregative fimbriae from Salmonell-A;Reference number: A44898; MUID:91310586; PMID:1677357 A;Contents: 27655 A;Accession: A44898 A;Stratus: preliminary A;Molecule type: protein A;Residues: 21-33 <co3> A;Note: sequence extracted from NCBI backbone (NCBIP:45936) C;Genetics:</co3></co2>	RESULT 1 JC6039 JC6039 JC6039 JC6039  fimbrin protein agfA precursor - Salmonella enteritidis C;Species: Salmonella enteritidis C;Species: Salmonella enteritidis C;Date: 31-Dec-1996 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999 C;Accession: JC6039; PC6015; A44898 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol: 178, 662-667, 1996 A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6039 A;Molecule type: DNA A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714 A;Accession: PC6015 A;Molecule type: protein

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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; E.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
A;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change C;Accession: S70788; G64846; S31202; S34560; S34559 C;Accession: A: A: Bian, Z: Olsen, A: Normark, S: Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production
     A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. Mol. Microbiol. 7, 523-536, 1993
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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: A10635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A;Residues: 1-151 <PAR>
                                                                                                   Residues: 1-151 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                             ;Residues: 1-151 <HAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title: Expression of two csg operons is required for production Reference number: S70783; MUID:96414468; PMID:8817489
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, Note: this species has also been called Salmonella typhi
, Date: 09 Nov-2001 #sequence_revision 09-Nov-2001 #text cha
                                                                                                                     Molecule type: DNA
                                                                                                                                                 Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: nucleic
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                           acid sequence not shown; translation not
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Pred. No. 9.7e-
3; Mismatches
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No. 9.7e-53;
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, L.; White,
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e, N.; Farrar,
                                                                         PID:g1787279
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QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHAL

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C;Accession: From R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurungur, T.; R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurungur, T.; R;Hattori, M.; Shinagawa, A. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, A. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, A. DNA Res. 8, 11-22, 2001

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence genome sequence of enterohemorrhagic Facherichia coli O157:H7 and A;Title: Complete genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence genome sequence gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Escherichia
C;Date: 18-Jul-2001 #se
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                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-152 < HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                curlin major subunit CsgA [imported] -
C;Species: Escherichia coli
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A; Residues: 1-133, 'RQRDSGWLW' <OLS3>
                                                                                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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A;Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S34559
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A;Cross-references: EMBL:L04979
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                                                                                                                                                       Genetics:
Gene: ECs1420
                                                                                                                                                                                                                                 Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
Experimental source: strain 0157:H7, substrain RIMD 0509952
    Matches
                                    Query Match
Best Local Similarity
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    102;
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                                64.3%;
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68.9%;
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Pred. No. 2.
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Pred. No. 3.1e-38;
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    Mismatches
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                                        .3e-36;
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    28;
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    Indels
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A;Molecule type: DNA
A;Residues: 1-1748 <TAY>
A;Residues: 1-1748 <TAY>
A;Residues: 1-1748 <TAY>
A;Cross-references: EMBL:L03710; NID:g161751; PID:g161752
A;Cross-references: EMBL:L03710; NID:g161751; PID:g161752
A;Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
Nucleic Acids Res. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and glycine-rich repeats
A;Reference number: S42135; MUID:94051569; PMID:8233798
A;Accession: S42135
    A;Moolecule type: DNA
A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-:
A;Residues: EMBL:L03710
A;Rcross-references: EMBL:L03710
R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A;Reference number: S03650; MUID:88189811; PMID:3357771
A;Accession: S03650
A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773 <MAR>
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H85665
hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain o157:H7, substrain hypothetical protein csgA [imported] - Escherichia coli (strain o157:H7, substrain o
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: H85665
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85665
A;Status: preliminary
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A;Reference number: S42136
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A; Residues: 1-152 <S7
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Nature 409, 529-533, 2001
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Molecule type: DNA;Residues: 236-250,'I',252-255,'N',257-773
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Pred. No. 2.3e-36;
1; Mismatches 28
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A;Cross-references: EMBL:
C;Genetics:
A;Genetics:
A;Genetic code: SGC5
A;Introns: 85/3; 136/1; 1
C;Keywords: zinc finger
F;1164-1450/Region: zinc
F;1451-1464/Region: zinc
F;14578-1491/Region: zinc
F;1530-1514/Region: zinc
F;1530-1543/Region: zinc
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F;1530-1543/Region: zinc
F;1530-1543/Region: zinc
F;1602-1615/Region: zinc
F;1602-1615/Region: zinc
F;1602-1615/Region: zinc
A;Description: minor component of wild-type curli; interaction between CsgA and CsgB A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli th and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <SIG> F;2-151/Product: minor curlin chain #status predicted <MAT>
                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-151 <BLAT>
A;Residues: 1-151 <BLAT>
A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278,
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62281.1; PID:g1147563
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augus
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; R.
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
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A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70787
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               curlin nucleator protein csgB precursor - Escherichia coli (strain K-12)
N;Alternate names: csgB protein; curlin nucleation component; minor curlin
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70787; F64846
                                                                                                                                  A; Gene: csgB
A; Map position: 23.15
C; Function:
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A;Status: nucleic ac
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A; Residues: 1-151 < HAM>
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A; Midleuule type: DNA
A; Molecule type: DNA
A; Residues: 1-151 < STO>
A; Cross-references: GB: AE005174; NID: g12514573; PIDN: AAG55787.1;
A; Cross-references: GB: AE005174; NID: g12514573; PIDN: AAG55787.1;
A; Cross-references: GB: AE005174; NID: g12514573; PIDN: AAG55787.1;
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                                                                                                                                                                                                                                                                                                                                                                    R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glassiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta,
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A;Molecule type: DNA
A;Residues: 1-151 <HAY>
A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Cross-references: Strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Hasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90806
                                                                                                                                                                                                                                                                                                                                                      iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                   curlin minor chain precursor, CsgA homolog [imported] - Escherichia coli (strain C_iSpecies: Escherichia coli
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Best Local :
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;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
;Accession: G85665
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                                                                                                                 Similarity
                     IGQAGTNNSAQLRQGGSKLLAVVAQEGSSNRAKIDQTGDYNL-AYIDQAGSANDASISQG
                                                       ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
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                                                                                            Score 107.5; DB Pred. No. 0.024; 9; Mismatches
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Pred. No. 0.024;
9; Mismatches
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9; Mismatches
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lanta, E.;
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A; Residues: 1-151 < PAR>
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C;Function:
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A;Cross-references: GB:U43280; NID:g1184712;
A;Experimental source: strain 276755-3b
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JC6040
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R;Collinson, S.K.; Clouthier, S.C
J. Bacteriol. 178, 662-667, 1996
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C;Species: Salmonella enteritidis
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NNATIDQWNAKUSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                         Score 106.5; DB Pred. No. 0.029; 7; Mismatches
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Pred. No. 0.0
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, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T.; Connecton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
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                                                                                                                                                                                                                                                                                         Cross-references: GB:AL513382; PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
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IATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQEGEN
                                                       MAHALQSDARKSE-----TTITQSGYGNGADVGQ-GADNST-----IELTQNGFR
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A;Residues: 1-145 <KUR>
A;Crose-references: GB.AE008689; PIDN:AAL45562.1;
A;Experimental source: strain C58 (Dupont)
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Science 294, 2317-2323, 2001
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A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                         R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                              hypothetical protein AGR_L_228 [imported] - Agrobacterium tumefaciens (strain c;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 22-Oct_2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C;Accession: H98144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Authors: Yoo, H.; ster, E.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 39
                                                                                                                                                                                                          Molecule type: DNA
Residues: 1-145 <K
                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                         Accession: H98144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: The Genome of the Natural Genetic Engineer Agrobacterium Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: AD3143
                                                                                                 Query Match
                                                                                                                                                                                        Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: Atu4768
                                                                                                                                   e: AGR L 22 position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 VVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAK 109
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                                                                                                                                                                                                          1-145 <KUR>
                                                                                   Similarity
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                                                                                                                   _228
n: linear chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIRKS FIASALVALVGLSAAAPAMANDVRIEQYGWSNSAGGAQEGYGNRIRTYQNGGYNR
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                                LLKVAAFAAI VVSGSALAGVVP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GQFGSNHTTILTQDGNGNIAAGVQVGRGCSANVSQ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tao,
                                                                                                                                                                                      GB:AE007870; PIDN:AAK88682.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y.; Biddle, P.; Jung, M.; Krespan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.2%;
                                                                                 12.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 95.5; D
Pred. No. 0.25
22; Mismatches
                                                                                 Score 95.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OYGRHNLSAVGQEGHDNYGSTTQNGNRNVAGI-----
                                                                  Mismatches
                                QWG----GGGNHNGGGNSSGPDYDQLVTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID:g17743277; GSPDB:GN00187
                                                                  57;
                                                                                                                                                                                      PID:g15158413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 145;
                                                                                                   Length 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                         GSPDB:GN00170
                                                                Gaps
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                                                                                                                                                                                                                                                                                                                          , B.; Goldman,
; Markelz, B.;
 60
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              A; Gene: Atu4766
A; Map position:
                                                                                                                                                                                                          A; Authors: Yoo, ster, E.W.
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                                                                                                                                     A;Status:
                                                                                                                                                     A;Accession: AB3143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
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A; Diatus, F----
A; Molecule type: DNA
A; Residues: 1-141 < KUR>
A; Cross-references: GB: AE008689; PIDN: AAL45560.1;
A; Cross-references: Strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jull-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: F70675
                                                                                             A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                             R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks erage, G.; Gillet, W.; Grant, C.; Guenthner, ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, ; Connor, R.; Davies, R.; Devlin, K.; Feltwell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                               A;Title: The Genome of the Natural Genetic Engineer Agrobacterium A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Atu4766 [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-582 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GB:Z82098;
Experimental source: strain |
                                                                                                                                                                                                                  preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SSVMVRQVGFGNNATAN
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                                                                                                                                                                                                                                                                                                                                        H.; Tao,
                                                linear chromosome
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                                                                                                                                                                                                                                                                                                                                           Y.; Biddle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.0%;
27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AL123456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93.5;
Pred. No. 1.
  Score
                                                                                                                                                                                                                                                                                                                                                                                                               R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence not
                                                                                                                                                                                                                                                                                                                                      P.;
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  93;
                                                                                                                                                                                                                                                                                                                                      Jung, M.; Krespan, W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium tumefaciens (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID: g3261664;
  DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shown;
                                                                                                                                             PID:g17743275; GSPDB:GN00187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71;
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Length
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     141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.; Harris, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                           Perry,
                                                                                                                                                                                                                                                                                             tumefaciens C58
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                                                                                                                                                                                                                                                                                                                                                                                                                    ; Woo, T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dupont)
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Search dobtim	DЬ	γQ	DЬ	γ	Дb	Q V	Best Lo Matches
Search completed: March 11, 2004, 18:42:09 Job time : 11.3 secs	112 YGIFQYERNTGTNVVQDGDNGSCLTFSYGW 141	113 ITVGQYGGNNAALVNQTASDSSVMVRQVGF 142	57RAYSLYRNFKDANIKQLGRGNAAGIAQNGGGNLGFIRQRGNGHSATLQQ-NGNNNA 111	53 HEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112	10 LKLLTVTLLVGGLTPLGFAAPAHAGGRISFDLAPGNNADGDLLSTGL 56	PQWGGGGNHNGG	Best Local Similarity 26.0%; Pred. No. 0.39; Matches 39; Conservative 22; Mismatches 63; Indels 26; Gaps 6;

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OM protein - protein search, using sw model

March 11, 2004, 18:14:48; Search time 6.3 Seconds (without alignments) 1248.031 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-543-407-18
780
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151

Searched: Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

3331088 331088	22222222222222222222222222222222222222	Result No.
81 81 81 81 80.5 80.5	691 501:5 107:5 106:5 106:5 91:6 91:9 91:9 91:9 92:9 91:8 88:9 88:9 87:5 87:5 87:5 88:8 81:5	Score
10.4 10.4 10.4 10.3		Query
365 576 678 1034 1185	151 151 151 151 151 151 151 151 151 151	Length 1
		B
ROAL DROME DEAF_DROME YF48 MYCTU ICEN_PANAN IMD_ARTGO MAPX_DROME	CSGA SALTY CSGA ECOLI CSGA ECOLI CSGA ECOS7 CSGB ECOLI CSGB ECOLI CSGB SALTY YKO3 CAEEL OMPB RICJA GP63 LEIDO PER DROME GP63 LEIMA GLR1 HUMAN OMPB RICCH GP63 LEICH OVO DROME ICEN GP63 LEICH OVO GROME ICEN GP63 LEICH GP63 LEIME GP63 LEIME GP63 LEIME GP63 LEIME GP63 LEIME GP63 LEIME GP63 LEIME GRATA RHIME GRATA RHIME GRATA RHIME GRATA RHIME GRATA RHIME GRATA RHAQ COAA BPM13 GATA AGRT5 COAA BPM13 GATA AGRT5	ID
p07909 drosophila Q24180 drosophila Q10778 mycobacteri Q47879 pantoea ana Q44052 arthrobacte P23226 drosophila	•	Description

## ALIGNMENTS

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SEQUENCE FROM N.A. SPECIES=S.Typhi; STRAIN=Ty2 / ATCC 700931; MEDLINE=25531367, PubMed=12644504; Deng W., Liou SR., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;	"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Nature 413:848-852(2001). [4]		Baker S., Basham D., Brooks K., Chlilingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,	K.L., Bentley S.D., Holden M.T.	SQUENCE FROM N.A.  SPECIES=S.typhi; STRAIN=CT18; MEDITINE-21524647. BubMed-11577508.	3:852-856(2001).	"Complete genome sequence of Salmonella enterica serovar Typhimurium	a L., Miller W., Stoneking T., Nhan M., .K.;	N., Mulvaney E.,	eth J., Clifton S.W., Latreille P.		SEQUENCE FROM N.A. SPECTES=S typhimurium: STRAIN=LT2 / SGSC1412 / ATCC 700720:		Escherichia coli with respect to operon structure and regulation.";		Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;	SPECIES=S.typhimurium; STRAIN=SR-11;	SEQUENCE FROM N.A.		bbacteriaceae; Salmonella.	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	Salmonella enteritidis.	Salmonella typhimurium,	CSGA OR AGPA OR STM1144 OR STY1181 OR T1776.	10-OCT-2003 (Rel. 42, Last annotation update)	(Rel. 34, Last		SGA_SALTY STANDARD; PRT; 151 AA.	

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SPECIES=S.enteritidis; STRALN=2....
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Mori H., Mori Y.,
Sampei G., Seki Y.,
Sampei M., Horiuchi J
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MEDIANE-7061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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"A 718-kb DNA sequence of the E corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
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Blattner F.R., Plunkett G. III, Bloch C.A
Riley M., Collado-Vides J., Glasner J.D.,
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MEDLINE=96414468; PubMed=8817489;
Hammar M., Arngyist A., Bian Z., Olsen
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Escherichia coli.";
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J. Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamous Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.G Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O15"
                                                                                                                                                                                                       App1.
                                                                                                                                                                                                                STRAIN-0157:H7 / ATCC 43895;
MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7."
Appl. Environ. Microbiol. 67:2367-2370(2001).
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Escherichia coli O157:H7.
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28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Major curlin subunit precursor.
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01-FEB-1995 (Rel. 34, Last sequence up

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Minor curlin subunit precursor.

CSGB OR B1041 OR 21675 OR ECS1419.
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLIED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GRITCHING THE STRUCTURES CELSIUS. CURLI CAN BIND TO
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STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Hammar M., Arnqvist A., Bian Z., Olsen A., "Expression of two csg operons is required fibronectin- and congo red-binding curli po
                                                                                                   STRAIN=K12 / MC4100;
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Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
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-i- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFER
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI C
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATI
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Mocomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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Science 277:1453-1474(1997).
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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EMBL; AE002554; BAB34842.1;
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT
-!- COILED SURFACE STRUCTURES THAT ASSEMBLE PRE
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURL
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLE
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MEBLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi st
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28-FEB-2003 (Rel. 41, Created,
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Minor curlin subunit precursor.
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                                                    CURLIN MONOMERS.
SIMILARITY: BELONGS
 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - suropean Bioinformatics Institute. There are no restrictions on its
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POTENTIAL.
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Pred. No. 0.
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CURLI CAN BIND TO
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RESULT 6
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Best Local S
Matches 35
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P55226;
01-OCT-1996
01-OCT-1996
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SPECIES=S. typhimurium; STRAIN=SR-11;

MEDLINE=98117058; PubMed=9457880;

ROmling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;

"Curli fibers are highly conserved between Salmonella typhimurium

Escherichia coli with respect to operon structure and regulation."

J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; ABUTESTY, FORDJETE PROTEOME.
PIMBIA; Signal; Complete proteome.
SIGNAL 1 21 POTENTIAL.
CHAIN 22 151 MINOR CURLIN SUBUNIT.
CHAIN 151 AA: 16254 MW; 161C54326E573495 CRC64;
                                                                                                                                                                                                                                                       McClelland M., Sanderson K.E., Spieth J., Clifton S.W. Courtney L., Porwollik S., Ali J., Dante M., Du F., Ho Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Ryan E., Sun H., Florea L., Miller W., Stoneking T., N Waterston R., Wilson R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minor curlin subunit precurs
CSGB OR AGFB OR STM1143.
Salmonella typhimurium, and
Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                    MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P
"Salmonella enteritidis agfBAC operon encoding thin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                         J. Bacteriol. 178:662-667(1996).
                                                                                                                                                                                                                                                                                                                                      SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae; Salmonella
                                                                                                                                                                      SPECIES=S.
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                               Nature 413:852-856(2001).
                                                                                                                                                                                                                                            'Complete
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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            FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI, CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.
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                                                                                                                                                                   enteritidis; STRAIN=27655-3B;
                                                                                                                                                                                                                                              genome
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
subunit precursor (Fimbrin SEF17
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30.7%;
                                                                                                                                                                                                                                              of Salmonella
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Pred. No. 0.
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                                                                                                                                                                                                                                              enterica
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M., Du F., Hou S., Layman D.
., Grewal N., Mulvaney E.,
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BELONGS

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CSGA/CSGB FAMILY

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Conservative

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Indels

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Gaps

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Query Match
Best Local S
Matches 46
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01-FEB-1994
30-MAY-2000
30-MAY-2000
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between
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Fimbria; Signal; Complete proteome
                                                                                         PIR;
                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                            Durbin R.; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239
                                                                                                                                                                                                                                                                                                                                                          Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
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                                                   Hypothetical
SEQUENCE 4
                                                                       NormPep;
                                                                                                                                                                                                                                                        REVISIONS.
                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKO3
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101 AA; 4
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protein C05B5.3 in chromosome
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                                                   MW;
                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis.
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 Score 92; DB Pred. No. 0.8; Pred. No. 0.8;
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MINOR CURLIN SUBUNIT
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                                                                                           SEQUENCE
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16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rCmpB)
(rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein
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Rickettsiaceae; Rickettsieae; Rickettsia.
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30-MAY-2000
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1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY. PLAY A ROLE AS A RICKETISIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         layer with hexagonal symmetry.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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                                                                                                                                                                                                                      PF03797; Autotransporter;
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                                                                                                                                                                                                                                 EMBL; M60048; AAA29244.1; HSSP; P08148; 1LML.
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InterPro; IPR001577; Peptidase.
Pfam; PF01457; Peptidase_M8; 1
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COPACTOR: Binds I zinc ion per subunit (By similarity).
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
SIMILARITY: Belongs to peptidase family MB.
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FUNCTION: Has an integral
in the mammalian host
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ignal; Cell adhesion; GPI-anchor; Lipoprotein.
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- outstation
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Matches 43
     period length of circadian and ultradian rhythms; an increase in PER dosage leads to shortened circadian rhythms and a decrease leads to lengthened circadian rhythms. Essential for the circadian rhythms is to lengthened circadian rhythms. Essential for the circadian rhythmic component of the male courtship song that originates in the thoracic nervous system. The biological cycle depends on the rhythmic formation and nuclear localization of the TIM-PER complex. Light induces the degradation of TIM, which promotes elimination of PER. Nuclear scityity of the heterodimer coordinatively regulates PER and TIM transcription through a negative feedback loop. Behaves as a negative element in circadian transcriptional loop. Does not appear to bind DNA, suggesting indirect transcriptional inhibition (By similarity); the complex then the nuclear with timeless (TIM); the complex then
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PER_DROWI STANDARD; PRT; 1093 AA. Q03297; O18421; O18422; P91721; P91722; O1-OCT-1993 (Rel. 27, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE=93196482; PubMed=8450754;
Peixoto A.A., Campesan S., Costa R.H., Kyriacou C.P.;
"Molecular evolution of a repetitive region within the
                                                                                                                                                                                                                                                                                           Gleason J.M., Powell J.R.; "Interspecific and intraspecific comparisons of the period locus the Drosophila willistoni sibling species."; Mol. Biol. Evol. 14:741-753(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila willistoni (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
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                                                                                                                                                                                                                          Drosophila."
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MEDLINE=97357421; PubMed=9214747;
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NCBI_TaxID=7260;
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                                                                                                                                                                                                              . Evol. 10:127-139(1993).
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Pred. No. 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Nuclear at specific periods of the day.
First accumulates in the perinuclear region about one hour before
translocation into the nucleus. Interaction with Tim is required
for nuclear localization (By similarity)
-i- prom: phosphorylated with a CIRCADIAN RHYTHMICITY, PROBABLY BY THE
DOUBLE-TIME ROCTEIN (DET). PHOSPHORYLATION COULD BE IMPLICATED IN
THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN ATLIXCO. SIMILARITY: Contains 2 PAS (PER-ARNY-SIM) dimerization domains SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
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or send an email to license@isb-sib.ch).

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EMBL; U51055; EMBL; U51056; EMBL; U51057; EMBL; U51069; EMBL; U51060; EMBL; U51061; EMBL; U51063; EMBL; U51064; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51066; EMBL; U51067; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EMBL; U51070; EM
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FlyBase; FBgn0013161; Dwii
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AAB41364.1;
AAB41365.1;
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AAB41361.1;
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G -> A (II
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F (IN STRAIN 0811.4).
V (IN STRAIN GUANA).
A (IN STRAIN SAWTA MARIA).
S (IN STRAIN SAWTA MARIA).
ING (IN STRAIN PORTO ALEGRE 3).
ING (IN STRAIN PORTO ALEGRE 4).
ING (IN STRAIN MANAUS 1 AND MANAUS
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VARIANT VARIANT

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(IN STRAIN PORTO ALEGRE 4)

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AINS GUADELOUPE, MAI PORTO ALEGRE 1 AND

MANAUS

ALEGRE 2,

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collaboration

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Query Match
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Matches 24
                                                                          MEDLINE=98416698; PubMed=9739
Schlagenhauf E., Etges R., Met
"The crystal structure of the
                                                       leishmanolysin.";
Structure 6:1035-1046(1998).
                                                                                                                                                                                                         Schneider P., Ferguson M.A.J., McConville M.J., Mehlert A., Homans S.W., Bordier C.; "Structure of the glycosyl-phosphatidylinositol membrane anchor the Leishmania major promastigote surface protease."; J. Biol. Chem. 265:16955-16964(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                          GP63_LEIMA STANDAKU; FALL, P08148; P15906; P08148; P15906; O1-AUG-1988 (Rel. 08, Created) O1-APR-1990 (Rel. 14, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) Leishmanolysin precursor (EC 3.4.24.36) (Cell (Major surface glycoprotein) (P63 protein) (P63 protein) (P63 protein)
                                                                                               X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS).
MEDLINE=98416698; PubMed=9739094;
                                                                                                                                                                                                                                                                                                 Button L.L.,
J. Exp. Med.
                                                                                                                                                          Schlagenhauf E., Etges R., Metcaif P., "Crystallization and preliminary X-ray diffraction studies of
                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                Proteins 22:58-66(1995).
                                                                                                                                                                                 MEDLINE=95406217;
                                                                                                                                                                                                                                                                  MEDLINE=91009116; PubMed=2145267;
                                                                                                                                                                                                                                                                               GPI-ANCHOR
                                                                                                                                                     eishmanolysin,
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE MEDLINE=88154764; PubMed=3346625;
                                                                                                                                                                                                                                                                                                                                                                                                   Leishmania major.
Eukaryota; Euglenozoa; Kinetophastida;
NCBI_TaxID=5664;
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NON TER
SEQUENCE
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Molecular cloning of the major surface
J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P1' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGGGGGGGGGGLPLFL-----DVTHTSSSSONKGPTGVAAGGAGGGVGGGGG-- 770
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1093
1093
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171:589-589(1990).
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                                                                                                                                                 surface metalloproteinase
                                                                        Metcalf P.;
the Leishmania major
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 91; DB
Pred. No. 3.1
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ALEGRE 1 AND PORTO ALEGRE 2).
S -> A (IN STRAINS GUADELOUPE
MISSING (IN STRAIN MANAUS 3).
A -> T (IN STRAIN 0811.4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR: Binds 1 zinc ion per subunit.
SUBCELULIAR LOCATION: Attached to the membrane by a GPI-anchor.
PTM: THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS
FULLY SATURATED, UNBRANCHED 1-O-ALKYL CHAIN (MAINLY C24:0) AND J.
MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0, C14:0, C16:0, AND C18:0).
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an email to license@isb-sib.ch).
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EMBL; K58633; CAA41491.1; -.
EMBL; M64752; AAA58613.1; -.
PIR; AA0222; A40222.
PIR; S25852; S25852.
HSSP; P19491; IGR2.
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P42261;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Glutamate receptor 1 precursor (GluR-1) (GluR-A) (GluR-K1) (Glutamate receptor 1 precursor (GluR-1) (GluR-A) (GluR-K1) (GluTamate receptor 1 precursor (GluR-1) (GluR-A) (GluR-K1) (GluTamate receptor 1 precursor (GluR-1) (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluR-A) (GluTamate receptor 1 precursor (GluR-A) (GluR-C) (GluTamate receptor 1 precursor (GluR-A) (GluR-C) (GluTamate receptor 1 precursor (GluR-A) (GluR-C) (GluTamate receptor 1 precursor (GluR-A) (GluR-C) (GluTamate receptor 1 precursor (GluR-A) (GluR-C) (GluTamate receptor 1 precursor (GluR-A) (GluR-C) (GluTamate receptor 1 precursor (GluR-A) (GluR-C) (GluTamate receptor 1 precursor (GluR-A) (GluR-C) (GluTamate receptor 1 precursor (GluR-A) (GluR-C) (GluTamate receptor 1 precursor (GluR-C) (GluR-C) (GluTamate receptor 1 precursor (GluR-C) (GluR-C) (GluTamate receptor 1 precursor (GluR-C) (GluR-C) (GluTamate receptor 1 precursor (GluR-C) (GluR-C) (GluTamate receptor 1 precursor (GluR-C) (GluR-C) (GluTamate receptor 1 precursor (GluR-C) (GluR-C) (GluTamate receptor 1 precursor (GluR-C) (GluR-C) (GluTamate receptor 1 precursor (GluR-C) (GluR-C) (GluTamate receptor 1 precursor (GluR-C) (GluTamate receptor 1 precursor (GluR-C) (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate receptor 1 precursor (GluTamate
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"Molecular cloning and chromosomal localization of one of the human glutamate receptor genes.",
Proc. Natl. Acad. Sci. U.S.A. 88:7557-7561(1991).
Proc. Natl. Acad. Sci. U.S.A. 88:7557-7561(1991).
Proc. Natl. Acad. Sci. U.S.A. 88:7557-7561(1991).
TOWNCTION: L-glutamate acts as an excitatory neurotransmitter at many synapses in the central nervous system. The postsynaptic actions of Glu are mediated by a variety of receptors that are named according to their selective agonists.

-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. I
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-|- SIMILARITY: Belongs to the ligand-gated ionic channel family.
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"The human glutamate receptor cDNA GluR1: cloning,
expression and localization to chromosome 5.";
DNA Seq. 2:211-218(1992).
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MEDLINE=92329975; PubMed=1320959;
Caillantini M.G., Ca
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Sun W., Ferrer-Montiel A.V., Schinder A.F., McPherson J.P.,
Evans G.A., Montal M.;
"Molecular cloning, chromosomal mapping, and functional exp.
"human brain glutamate receptors.";
Proc. Natl. Acad. Sci. U.S.A. 89:1443-1447(1992).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MISCELLANEOUS: This receptor binds AMPA(quisqualate) > glutama
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GO:0008066; F:glutamate receptor activity; TAS.
GO:0015277; F:kainate selective glutamate receptor activity; TAS.
GO:0007165; P:signal transduction; TAS.
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Raoult D.;
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CHAIN
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EMBL; AF123721; AAF34124.1;
EMBL; AF123726; AAF34129.1;
EMBL; AF149110; AAD39533.1;
PIR; E97835; E97835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stenos J., Walker D.;
"The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH HAVE - EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH STRUCTURAL RECEIVED A ROLE AS A RICKETTSIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
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Bacteria, Proteobacteria, Alphaproteobacteria,
Rickettsieae, Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered layer with hexagonal symmetry (By similarity).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren
Samson D., Roux V., Cossart P., Weisse
                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Indian tick typhus, and Malish MEDLINE=20393643; PubMed=10939649;
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PF03797; Autotransporter; 1.
AMs; TIGR01414; autotrans_barl; 2.
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| Complete pro-
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Matches 41
          MEROPS; MOB.001; -.
InterPro; IPRO06025; P
InterPro; IPRO01577; P
Pfam; PF01457; Peptida
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P15706;
                                                                            EMBL; M80672; AAA29238.1;
EMBL; M28527; AAA29235.1;
PIR; A44951; A44951.
                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                          "Three distinct RNAs for the surface protease gp63 are expressed during development of Leishmania donovani cha promastigotes to an infectious form.";
J. Biol. Chem. 267:1888-1895(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90205976; PubMed=2320059;
Miller R.A., Reed S.G., Parsons M.;
"Leishmania gp63 molecule implicated
Arg-Gly-Asp sequence.";
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10-OCT-2003
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NCBI_TaxID=44271;
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                                                                                                                                                                                                                                                        P1' and basic residues at P2 and P3' cleaved at -Ala-Tyr-|-Leu-Lys-Lys-COPACTOR: Binds 1 zinc ion per subunit SUBCELLULAR LOCATION: Attached to the
                                                                                                                                                                                                                                              SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                  P08148;
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(Rel. 14, Last sequence update)
(Rel. 42, Last annotation update)
sin precursor (EC 3.4.24.36) (Cell surface protease)
sin precursor) (GP63 protein) (Promastigote surface)
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01577; Peptidase M8
Peptidase M8; 1.
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LSHMANOLYSIN
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onelson J.E., Paetz
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Matches 21
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STRAIN=0regon-R;

MEDLINE=91293102; PubMed=1712294;

MEVEL-Ninio M.T.M., Terracol R., Kafat
"The ovo gene of Drosophila encodes a
for female germ line development.";

EMBO J. 10:2259-2266(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ULT 15
_DROME
                                                                                                                                                                                                    varrinkel M.D., Wang J., Liang Y., Mahowald A.P.;
"Multiple products from the shavenbaby-ovo gene region of Drosophila
melanogaster: relationship to genetic complexity.":
Mol. Cell. Biol. 14:6809-6819/1997.
                                                                                                                                                                                                                                                                                                                                                                                                     OVO_DROME STANDARD; PRT; 1028 AA
P51521; Q9XZU4;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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            -I- FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF I
LINE CELLS. PLAYS A ROLE INGERM LINE SEX DETERMINATION.
-I- SUBCELLULAR LOCATION: Nuclear (Potential).
-I- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND
ACCUMULATES IN NURSE CELLS DURING OGGENERIS. STORED IN T
BUT IS RAPIDLY LOST IN THE EMERSYOS EXCEPT FOR ITS CONTIL
PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Zymogen; Signal; Cell adhesion; GPI
                                                                                                                                                                                                                                                            TISSUE=Ovary;
MEDLINE=95021209;
                                                                                                                                                                                                                                                                                                            Ephydroidea; Drosophilidae;
NCBI_TaxID=7227;
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Tiang Y., Mahowald A.P.;
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EMBL; X59772; CABB5921.1; ALT_SEQ.
PIR; A56038; A56038.
HSSP; P07248; 2ADR.
TRANSFAC; T00669; -.
PlyBase; FBgn0003028; ovo.
InterPro; IPR007087; Znf C2H2.
Pfam; PF00096; zf-C2H2; 3.
SMART; SM00335; Znf C2H2; 4.
PROSITE; PS00028; ZNC_FINGER_C2H2_1; 3.
PROSITE; PS00028; ZNC_FINGER_C2H2_2; 3.
Zinc-finger; Metal-binding; DNA-binding; Re
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                                                                                                                                                                           ARKSETTITOSGYGNGADVGOGADN----STIELTONGFRNNATIDOWNAKNSDI---
                                                                                                                                                                                                                                                   LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSD 62
                                                                                                                                            ---GGGPSANSGGGGGGGGGYINCGGVGGPNNSLDGNNLLNFASVSNYNESNSKFHNH 146
                                                                                                                                                                                                                LQNAAAAAYIMSAGSG-----GGGCTGNGGGGASGP-
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                   11.2%;
                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                    Score 87.5; DB Pred. No. 5.7; 11; Mismatches
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POLY-GLN.
POLY-GLN.
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POLY-GLY.
POLY-HIS.
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                                                                                                                                                                                                                                                                                                                     DB 1;
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•
                                                                                                                                                                                                                                                                                                                     Length 1028;
                                                                                                                                                                                                                                                                                    Indels 47;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 11, 2004, 18:23:54; Search time 30.5 Seconds (without alignments)

Title: US-09-543-407-18
Perfect score: 780
Sequence: 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041
Minimum DB seq length: 0
```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: SPTREMBL\_25:\*

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\*
7: sp\_mhc:\*
9: sp\_phage:\*
10: sp\_plant:\*
11: sp\_vodent:\*
12: sp\_virus:\*
13: sp\_vertebrate:\*
14: sp\_unclassified:\*
15: sp\_bacteriap:\*
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

10 9 8 8 7 6 6 5 4 4 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
593.5 593.5 498.5 428.5 303.1 110.1 101.1 107.5 1107.5 1107.5 1107.5 1107.5	Score
87.4 76.1 138.8 14.5 13.8 13.8 13.8 13.8	Query Match
152 150 149 150 150 76 29 1748 502 1748 151 151 151 160 160 120 91	Query Match Length
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	DB
O33802 O7X243 O7X240 O8CW63 O7X237 O7X237 O9S3U5 O94821 O94821 O9EIH4 O7X24 O7X24 O7X	ID
O33802 salmonella O7x243 citrobacter O7x240 citrobacter O8xw63 escherichia O7x237 enterobacte O54069 salmonella O98359 escherichia O98481 tetrahymena O98481 tetrahymena O98614 shewanella O7x244 citrobacter O89ji3 bradyrhicob O7uc21 shigella fl O8cw64 escherichia O83ru7 shigella fl O80x65 bradyrhizob O983j8 escherichia	Description

			11.8	92	5
-				93	44
Q9kka8 rickettsia	2 Q9KKA8	1615 ;	12.0	93.5	43
Q7tw98 mycobacteri	16 Q7TW98		12.0	93.5	42
P71868 mycobacteri	Φ		12.0	93.5	41
Q9vix6 drosophila	o		12.0	93.5	40
Q8eih3 shewanella	16 Q8EIH3	139 :	12.0	93.5	39
		480	12.1	94	38
				94.5	37
Q89ji6 bradyrhizob	16 Q89JI6		12.1	94.5	36
		3552	12.2	95.5	5
			12.2	95.5	34
Q9kkb2 israeli tic	2 Q9KKB2			95.5	ũ
		145 :	12.2	95.5	ถ
	16 Q8EYY9	490 :		96	Ħ
Q7v8s5 prochloroco		1765	12.4	96.5	30
	16 Q8ZN57	2039 :	12.4	97	29
8	o		12.4	97	8
		1422	12.4	97	7
Q8ewd6 mycoplasma	16 Q8EWD6	368 1	12.4	97	9
Q7x241 citrobacter	2 Q7X241			97.5	ິທ
Q7x238 enterobacte	2 Q7X238	151 :	12.5	97.5	4
Q98ln6 rhizobium				98	ιŭ
				98	iš
	16 Q88HG0	157 :	12.6	98	21
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O33801 salmonella	o	179 :	12.8	100	19
Q.	o	N	12.9	101	œ
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## ALIGNMENTS

SULT 1 3033802 PRELIMINARY; PRT; 152 AA. 033802; Ol.JAN.1998 (TrembLrel. 05, Created) 01-JAN.1998 (TrembLrel. 05, Last sequence update) 01-JAN.1998 (TrembLrel. 05, Last sequence update) 01-JAN.1998 (TrembLrel. 19, Last annotation update) 01-DEC-2001 (TrembLrel. 19, Last annotation update) 01-DEC-2001 (TrembLrel. 19, Last annotation update) AgfA protein (Fragment). AgfA	Ş	B 성	B &		S	FT	R P.	RT	RT	R R	א ק	RX	RP	R.	ဋ	8	88	S S	2 E	Ţ	TO	DT	Ã	Ħ	0	<b>2</b> 0
preliminary; prt; 152 AA.  13802; preliminary; prt; 152 AA.  13902; preliminary; prt; 152 AA.  13902; present of trembirel of Last sequence update)  1-JAN-1998 (Trembirel 05, Last sequence update)  1-DEC-2001 (Trembirel 19, Last sequence update)  1-DEC-2001 (Trembirel 19, Last sequence update)  1-DEC-2001 (Trembirel 19, Last annotation update)  1-DEC-2001 (Trem	~	σ <	σ <	Que: Best	, ,																			0	3380	ESUL
· .	NNAALVNQTASDSSVMVRQVGFGNNATANQY	SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 	MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ	atch 87.4%; Score 682; DB 2; Length 152; Cal Similarity 89.4%; Pred. No. 1.7e-46; 135; Conservative 4; Mismatches 12; Indels 0;	152 AA; 15401 MW; 9DA7DADC2364B006	152 152	Infect. Immun. 65:5320-5325(1997).		typhimurium SR-11 with mouse small	ggregative fimbriae promotes	z R.G., Gordon J.I., Bian Z., Pfeifer		SEQUENCE FROM N.A.	[L] T	VCBI TaxID=602;		ia; Gammaproteobacteria;	Salmonella tyohimurium.	protein	(TrEMBLrel. 19, Last	(TrEMBLrel. 05, Last sequence	1998 (TrEMBLrel. 05,	333802;	33802 PRELIMINARY; PRT; 152		7 1

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RESULT 3
Q7X240
ID Q7X24
AC Q7X2
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DT 01-Q
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Matches 118
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01-OCT-2003
01-OCT-2003
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=546;
                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                 Citrobacter freundii.
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01-OCT-2003
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EMBL; AJ515700; CAD56672.1; -. SEQUENCE 150.3.
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Q7X243;
                                                                                                                                                                                                                                      Zogaj X., Bokranz W., Nimtz N
"Production of Cellulose and
                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae; Citrobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                          CSGA
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Bacteria; Proteobacteria;
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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                                                                                                                                                        149 AA;
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15016 MW; 1D7141B8D6973DC6 CRC64;
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72.2%;
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                                                                 Score 550; DB
Pred. No. 4.5e-
20; Mismatches
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Last annotation updat
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Last sequence update)
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Pred. No. 1.7e-39;
4; Mismatches 18
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.5e-36;
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                                                                                                       Length
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                                                                   Indels
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Q8CW63;
01-MAR-2003
  STRAIN=Fec39;
Zogaj X., Bok
                                                    Bacteria; Proteobacteria;
Enterobacteriaceae; Enter
                                                                                                        01-OCT-2003
01-OCT-2003
                                                                                                                              Q7X237;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                           Welch R.A., Burland V., Plunkett G. III, Redford P., Ro
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete ge
of uropathogenic Escherichia coli.";
proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                       SEQUENCE
                                         NCBI_TaxID=28141;
                                                                          Enterobacter sakazakii
                                                                                     CSGA.
                                                                                              Curlin-csgA
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STRAIN=06:H1 / C
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MEDLINE=22388234; PubMed=12471157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae;
NCBI_TaxID=217992;
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                                                                                                                                                                                                     GGNGAAVDQTASNSSVNVTQVGFGNNATAHQY
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67.1%;
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Pred. No. 5.
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Q54069;
01-NOV-1996
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Q9S3J5;
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01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
Curlin subunit monomer
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Enterobacteriaceae;
                                            Escherichia coli.
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Bacteria; Proteobacteria;
                      Bacteria;
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                      Proteobacteria;
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76 AA;
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                      Gammaproteobacteria;
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Pred. No. 6.6e-
3; Mismatches
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Pred. No. 1.8e
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EMBL; X06462; CAB37323 1; -.

EMBL; L03710; AAC37171.1; -.

PIR; S42136; S42136.
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Q94821; P92146; P92145; I
01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
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SMART; SM00343; ZnF C2HC; 7.
PROSITE; PSS0158; ZF CCHC; 7.
CONFLICT 251 251 M
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MEDLINE=88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.;
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Eukaryota; Alveolata; Ciliophora;
Tetrahymenina; Tetrahymena.
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MEDLINE-99314153; PubMed-10386375;
La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli 078:K80 isol
IS1 inserti on in csgB and reduced persistence i
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1; -.
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GO; GO:0003676; F:nucleic
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MEDLINE=94051569; PubMed=8233798;
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Enterobacteriaceae; Citrol
MCBI_TaxID=213763;
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                          SEQUENCE FROM N.A.
                                                                                                                      Citrobacter
                                                                                                                                                      Nucleation component
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete SEQUENCE 502 AA; 52441 MW;
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EMBL; AE015532; AAN53941.1;
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Alteromonadaceae; Shewanella.
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01-MAR-2003
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Bacteria; Proteobacteria;
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Gammaproteobacteria;

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Q89JI3;
01-JUN-2003
                                                                                                                                                                                                              "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                      MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchium
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kaw
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada
Tabata S.;
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Bacteria; Proteobacteria;
Bradyrhizobiaceae; Bradyrh
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CSGA OR BLL5300.
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"Production of Cellulose and Curli Fimbriae by Members
Enterobacteriaceae Isolated from the Human Gastrointest
Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515700; CAD56671.1;
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                                                         ALSSAAQAANTSTTVQVGLVNGSSVTQNGLTNDSSSTTQIGILNGASTMQGTSSPS----
                                                                                   ALQSDARKSETTIT-QSGYGNGADVGQ-GADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
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Bradyrhizobium.
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STRAIN-66:H1 / CFT073 / ATCC 700928;

WEDLINE-22388234; PubMed112471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., 19 and the complete G. Thou S., Schwartz D.C., Perna N.T., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

EMBL; AE016759; AAN79778.1; -.
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Enterobacteriaceae; Escherichia.
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RESULT 15
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DT B1177
GN Brady
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RN [1] -
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                                                                                                                                                                           MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchium Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kaw Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada Tabata S.;
                                                                                                            EMBL; AP005963; BAC53057.1; Complete proteome.
                                                                                                                                    Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                         Bradyrhizobium japonicum.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J
Jin Q., Yang F., Zhang X., Zhang J., Yang G., Wu H., Q
Yang J., Yang F., Zhao A., Gao Y., Zhu J., Kan B., Ding K
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen
                                                                                                   SEQUENCE
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                                                                                                                                                                "Complete genomic sequence of nitrogen-fixing
                                                                                                                                                                                                                                                                             NCBI_TaxID=375;
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                     FAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDYDOLVTRVVTHEMAH----ALQSDAR
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Bradyrhizobium.
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Shigella.
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-GNGNDTIDASG--YGNVITLGNGNDIVHPGDGASQTTAG
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Search completed: March 11, 2004, 18:40:33 Job time : 49.5 secs	1106 FGNQAIN 1113	142 FGNNATAN 149	1046 AIIAGSGSDNVVAGAGHDTIMLGGAANHVVLNGSQANVTNQIGQDVVTVNGGSDQFNFVG 1105	108AKNSDITVGQYGTASDSSVMVRQVG 141	988 NGNDLYTLSGYGNTVMLGNGNDVVAGRDGANSVTLGDGNNTVNLGGMGNQITVGSGTN 1045	3AD

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3: geneseqp2000s:*
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7: geneseqp2003bs:*
8: geneseqp2004s:*
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first 45 summaries
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σ	662		151	w	AAB36354	Aab36354	AgfA::PT3
7	622	•	151	w	AAB36349	Aab36349	AgfA:
8	619	•	151	w	AAB36351	Aab36351	
9	611		151	w	AAB36346	Aab36346	
10	609	78.7	151	w	AAB36347	Aab36347	
11	606	78.3	151	w	AAB36352	Aab36352	
12	597	•	151	ω	AAB36355	Aab36355	-
13	574		151	w	AAB36348	Aab36348	-
14	528	68.2	151	w	AAB36343	Aab36343	
15	523	67.6	151	7	ABR82651	Abr82651	
16	504	65.1	120	N	AAR62761	Aar62761	. AgfA sequ
17	504	65.1	120	N	AAW23569	Aaw23569	Salmo
18	450	٠	142	N	AAR52664	Aar52664	Fibronect
19	378		122	N	AAR52663	Aar52663	FNB curli
20	153	19.8	45	w	AAB36316	Aab36316	Salmonell
21	132		22	w	AAB36318	Aab36318	Salmonel
22	123		23	w	AAB36321	Aab36321	. Salmonell
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriacese for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinantion of a recombinant gene back into the chromosome of the homologous species, replacing the native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

45	44	43	42	41	40	39	38	37	36	ω 5	34	<b>ω</b>	32	31	30	29	28	27	26
89.5	89.5	89.5	90	90.5	91	91	92	95	96	96	96	96.5	102	109	109	109	111	111	111
11.6	11.6	11.6	11.6	11.7	11.8	11.8	11.9	12.3	12.4	12.4	12.4	12.5	13.2	14.1	14.1	14.1	14.3	14.3	14.3
468	447	423	24	677	502	186	23	24	19	19	19	151	26	23	23	23	22	22	22
ω	w	4	7	4	N	δ	w	7	w	w	w	w	7	ω	w	w	ω	w	ω
AAG29727	AAG29728	ABG07164	ABR82642	ABG04318	AAW32312	ABU21488	AAB36331	ABR82647	AAB36328	AAB36336	AAB36323	AAB36344	ABR82649	AAB36319	AAB36324	AAB36340	AAB36337	AAB36327	AAB36322
Aag29727	Aag29728	Abg07164	Abr82642	Abg04318	Aaw32312	Abu21488	Aab36331	Abr82647	Aab36328	Aab36336	Aab36323	Aab36344	Abr82649	Aab36319	Aab36324	Aab36340	Aab36337	Aab36327	Aab36322
Arabidops	Arabidops	Novel hum	E. coli	Novel hum	Leishmani	Protein e	Escherich	E. coli	Salmonel	Salmonell	Salmonell	Escherich	E. coli	Salmonel	Salmonel	_	Salmonel	Salmonel	Salmonel

## ALIGNMENTS

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RESULT 1
AAB36350
ID AAB3
WPI; 2000-672631/65.
N-PSDB; AAC64626.
                                                                                                                                                                 05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                   Salmonella enteritidis.
                                                                                                                                                                                                                                vaccine; immune response; immunogen.
                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                               26-FEB-2001
                                                                                                                                                                                                                                                                            AAB36350;
                                                                                                                                                                                                                                                                                        AAB36350 standard;
                                                                                                                                                    05-APR-1999;
                                                                                                                                                                             12-OCT-2000.
                                                                                                                                                                                          WO200060102-A2
                                                                                                                                                                                                                                                  AgfA::PT3#5 amino acid sequence SEQ ID NO:20
                                                                                                                                        (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                              Escherichia coli.
                                                                                                                           Doran JL,
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                     99US-0127888P
                                                                                                                                                                                                                                                                                       protein;
                                                                                                                            Collison
                                                                                                                                                                                                                                                                                        151
                                                                                                                            SK,
                                                                                                                                                                                                                                                                                        B
                                                                                                                            Kay WW;
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RESULT 2
AAB36353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                       WPI; 2000-672631/65.
N-PSDB; AAC64629.
                                                                                                                                                                                                            White AP,
                                                                                                                                                                                                                                                                                                                                 05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB36353 standard; protein; 151
                                                                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                         Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                            Collison SK,
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Pred. No. 8.8e-71;
; Mismatches 0;
                                                                                                                                                                                                            Kay WW
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Disclosure; Page 138; 139pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC The present invention describes a recombinant agfA gene (I) where a CC sequence which encodes a foreign placed by a segment of a foreign DNA CC sequence which encodes a foreign pitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended are: CR assembly system of strains of Salmonella, Escherichia coli and CR Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbria gene into the chromosome of the homologous species, (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native CC copy of that gene, and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC useful for the expression of recombinant AgfA protein which is useful for CC useful for the expression of recombinant AgfA protein which is useful for CC useful contained a natigens are presented in high numbers (up to Sou,000 copies/cell), the hybrid fimbria protein seems both the communogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response cagainst the inserted epitope, and hybrid fimbriae are easy and cCC inexpensive to purify in large amount. The present sequence is given in tx
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Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
26-JUN-1995
                                                                                                                                   26-APR-1993;
                                                                                                                                                                                                  26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                              Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR74625 standard; protein; 151 AA
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                                    (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP (KING/) KING J.
                                                                                                                                                                                                                                                                  10-NOV-1994
                                                                                                                                                                                                                                                                                                                               WO9425598-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AgfA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                   93US-00054452
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Pred. No. 3.7e-64;
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RESULT 4
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Best Local Similarity 90.7
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36341 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                        WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                                                                                                                                                                                                                              05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB36341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 7B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ87467.
                                                                                                                                                                                                                                   05-APR-1999;
                                                                                                                                                                                                                                                                                         12-OCT-2000
                                                                                                                                                                                                                                                                                                                    WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kay ww,
                                                       Disclosure; Page 135; 139pp; English
                                                                                                                                                                                                         (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                         vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1994-358275/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                   99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                       response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95pp; English
                                                                                                                                                                                Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                         1mmunogen.
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Pred. No. 4.1e-62;
                                                                                                                                                                                SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                Kay
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RESULT 5
AAW23570
ID AAW2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for the immune response in an animal. In a fimbrial presentation eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
Collinson SK,
                                                                                                                                           03-JUN-1997
                                                                                                                                                                                                                                                                                    Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                     Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                           Salmonella
                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW23570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
                                                                                                         26-APR-1994;
                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW23570 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the exemplification of the present invention
                                   (UYVI-) UNIV VICTORIA INNOVATION &
                                                                      26-APR-1993;
                                                                                                                                                                              US5635617-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                           enteritidis 27655-3b agfA
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                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
Kay
                                                                      93US-00054452
                                                                                                         94US-00233788
                                                                                                                                                                                                                                  Location/Qualifiers 123
                                                                                                                                                                                                              /note= "Encoded by GCC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 151 AA.
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   Doran JL;
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Pred. No. 4.1e-62;
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                                      DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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RESULT 6
AAB36354
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Best Local Similarity
Matches 136; Conserv
Recombinant agfA gene which encodes foreign
                                            N-PSDB; AAC64630.
                                                         WPI; 2000-672631/65.
                                                                                     White AP,
                                                                                                                (UYVI-) UNIV VICTORIA
                                                                                                                                           05-APR-1999;
                                                                                                                                                                   05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                  12-OCT-2000
                                                                                                                                                                                                                              WO200060102-A2
                                                                                                                                                                                                                                                                       Escherichia
                                                                                                                                                                                                                                                                                   Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#9
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36354 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
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N-PSDB; AAT74142.
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                                                                                                                                                                                                                                                                                                                 immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKYDQLVTRVVTHEMAHAGQGADNSTIBLTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                  Doran JL,
                                                                                                                                                                                                                                                                                                                             agfA;
                                                                                                                                                                                                                                                                                                                                                         amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                           99US-0127888P
                                                                                                                                                                                                                                                                                                                 response;
                                                                                                                                                                                                                                                                                                                           chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.4%;
90.1%;
having a segment replaced by a foreign DNA sequence epitope or antigen, expresses recombinant AgfA
                                                                                    Collison
                                                                                                                                                                                                                                                                                                               immunogen.
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                                                                                    SK,
                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:28.
                                                                                 Kay WW
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RESULT 7
AAB36349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) Cd directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species, replacing the native Cd copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino Cd acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is Cd useful for the expression of recombinant AgfA protein which is useful for celliciting an immune response in an animal. In a fimbrial presentation Cd system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong cimmunogens, which may be important for directing an immune response constitution of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 136
               05-APR-2000; 2000WO-CA000356
                                                                                                                           Synthetic
                                                                                                                                                              Salmonella enteritidis
                                                                                                                                                                                                                Salmonella; agfA; chromosomal gene replacement; fimbrin;
                                                                                                                                                                                                                                                                                                                                                                   AAB36349 standard; protein; 151
                                                    12-OCT-2000
                                                                                      WO200060102-A2
                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                       AgfA::PT3#4 amino acid sequence SEQ ID NO:18.
                                                                                                                                                                                                                                                                                             26-FEB-2001
                                                                                                                                                                                                                                                                                                                                  AAB36349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein useful for eliciting immune response in animal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARK-----
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milarity 81.9%;
Conservative
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                                                                                                                                                                                                 response; ımmunogen
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1es 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                  epitope;
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99US-0127888P

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RESULT 8
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AC AAB3
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for system immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA, CsgA and Agra-nomotogue the transfer of the directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, commortaing separating an amino acid polymer comprising a recombinant AgfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriacee for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 151 AA;
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                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                            AgfA::PT3#6 amino acid sequence SEQ ID NO:22
                                                                                                         26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising separating an amino acid polymer comprising a recombinant protein containing a replacement segment or segments of foreign amino
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vaccine; immune response; immunogen
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                                                                                                         (first entry)
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Pred. No. 2.8e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Escherobacteriaceae for the production of fimbriae comprising recombinant actions are supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of supposed to the production of
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N-PSDB; AAC64627.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nomologous species; (3) directing recombination of a recombinant gene
104
                                                                                                                                                                                                                                                                                                                                                                                    129;
                                                                                                                                                                                        13
                                                     99 NNATIDOWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                        13
                                                                                                                                                                                                                                                                                                                    \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                             MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                            SDARKSETTI TQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA
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                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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74.6%;
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Pred. No. 5.6e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    44;
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RESULT 9

98 60 60

103

26-FEB-2001

(first entry)

AgfA::PT3#1 amino acid sequence SEQ ID

NO:12

AAB36346 standard; protein; 151

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AAB36346

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                                                                                                                             Query Match
Best Local Similarity
Matches 122; Conser
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       The present invention describes a recombinant agfA gene (I) where a composition of the gene has been replaced by a segment of a foreign DNA composition of thin aggregative finbriae (SEF17/TAF) nucleation depended are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended composition of strains of Salmonella, Escherichia coli and composition of strains of Salmonella, Escherichia coli and composition of strains of salmonella, Escherichia coli and composition of strains of salmonella, Escherichia coli and composition of a recombinant specification of a recombinant gene into the chromosome of the homologous specifies; (3) directing recombinant gene into the chromosome of the homologous specifies, replacing the native composition of that gene; and (4) eliciting an immune response in an animal. Composition of the homologous specifies, replacing the native composition gene; and (4) eliciting an immune response in an animal of compositing a recombinant AgfA protein containing a replacement segment or segments of foreign amino coli greater containing a replacement segment or segments of foreign amino coli greater containing a replacement segment or segments of foreign amino coli greater containing a replacement segment and introducing the greater containing a replacement segment or segments of foreign amino coli greater contains and introducing the considerable contains and introducing the seguing the network of the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation conjunction the host cell and introducing the system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrian protein possesses both the immune greater fimbrial subunit proteins are usually strong cimmunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Escherichia coli.
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Best Local
AgfA, C8gA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant on 6 a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                 The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriacese for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign DI sequence which encodes a foreign epitope or antigen. Also describe

foreign DNA so described

Recombinant agfA gene having a segment replaced by a foreign which encodes foreign epitope or antigen, expresses recombina protein useful for eliciting immune response in animal.

- ~y « roreign DNA sequence expresses recombinant AgfA nse in animal.

Disclosure; Page 139; 139pp; English

WPI; 2000-672631/65. N-PSDB; AAC64631.

05-APR-2000; 2000WO-CA000356

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99US-0127888P

(UYVI-) UNIV VICTORIA

Doran JL,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#10 amino acid sequence SEQ ID NO:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36355 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEMAHANQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.3%;
82.1%;
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Pred. No. 1.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
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RESULT 13
AAB36348
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Best Local Similarity
WPI; 2000-672631/65
                                                           White AP,
                                                                                                                                                                                   05-APR-1999;
                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                        12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA; chromos vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36348 standard; protein; 151
                                                                                                                       (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino
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                                                                                                                                                                             99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid sequence SEQ ID NO:16.
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81.5%;
                                                           Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 597; DB Pred. No. 9.8e-5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                        SK,
                                                        Kay WW
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.8e-53;
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Escherichia coli

12-OCT-2000 WO200060102-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively (2)

Cd directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 100 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit for proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 122
                                                                                                                                                                                               Escherichia coli CsgA amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                       Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                         26-FEB-2001
                                                                                                                                                                                                                                                                                                                     AAB36343 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 151
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                                                                                                                                      vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC64624
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                                                                                                                                      immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                    response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.2%;
80.8%;
                                                                                                                                    immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 574; DB
Pred. No. 2.2e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3,
2.2e-50;
23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
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05-APR-2000;

2000WO-CA000356

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RESULT 15
ABR82651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cc segment of the gene has been replaced by a segment of a foreign DNA
cc sequence which encodes a foreign epitope or antigen. Also described are:
(1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
cc assembly system of strains of Salmonella, Escherichia coli and
cc Enterobacteriaceae for the production of fimbriae comprising recombinant
cc AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2)
cdirecting recombination of a recombinant gene into the chromosome of the
homologous species; (3) directing recombination of a recombinant
cc back into the chromosome of the homologous species, replacing the native
cc copy of that gene; and (4) eliciting an immune response in an animal,
cc comprising separating a maino acid polymer comprising a recombinant AgfA
protein containing a replacement segments of foreign amino
cc acid sequence or sequences grown on a Salmonella, E. coli or
cacid sequence or sequences grown on a Salmonella, E. coli or
conjymer into the animal in conjunction with a carrier or diluent. (I) is
custing an immune response in an animal. In a fimbrial precentation
cs system the heterologous antigens are presented in high numbers (up to
conjourned to the carrier fimbrial subunit proteins are usually strong
c immunogenicity and adhesion properties relevant for an efficient live
vaccine, the carrier fimbrial subunit proteins are usually strong
c immunogens, which may be important for directing an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 104
             E. coli CsgA subunit 15 kDa protein
                                                   04-DEC-2003
                                                                                        ABR82651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                         ABR82651 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                           104;
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                                                                                                                                                                                                                   GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                    SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                           TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention describes a recombinant agfA gene he dene has been replaced by a segment of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 135; 139pp; English.
                                                (first entry)
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Pred. No. 1.1e-45;
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Best Local S
Matches 103
                                                                                                                                                                                                                                                                              The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR02642, ABR026449. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli 15 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmor or Shigella infections.
                                                                                                                                                                                                                                                    Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2002; 2002GB-00002275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasma protein; immune response; antibacterial; vaccine; gene therapy.
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                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                          NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                          TDARNSDITITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEWTVKQFGG
                                                                                      SDARKYDQLVTRVVTHEMAHAGQGADNSTIBLTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                          MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
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Pred. No. 3.4e-45;
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US-09-498-520A-18
US-09-328-352-4764
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US-09-072-596-199
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US-09-477-135A-131
US-09-072-596-199
US-09-471-135A-131
US-09-471-135A-131
US-09-540-236-3739
US-09-431-887-32
US-09-316-447A-5
US-09-318-352-6167
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Sequence 59, Appl Sequence 27661, A Appl Sequence 27661, A Appli Sequence 4764, Appli Sequence 4764, Appli Sequence 2, Appli Sequence 2, Appli Sequence 26, Appli Sequence 26, Appli Sequence 214, Appl Sequence 204, Appl Sequence 213, Appl Sequence 213, Appl Sequence 3739, Appl Sequence 3739, Appl Sequence 6167, Appl Sequence 6167, Appl Sequence 6167, Appl Sequence 10, Appl Sequence 11, Appl Sequence 10, Appl Sequence 23, Appl Sequence 10, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 24, Appl Sequence 26, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 28, Appl Sequence 28, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Ap
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

60

Query Match 88.4%; Score 684; DB 1; Len Best Local Similarity 90.1%; Pred. No. 5.5e-66; Matches 136; Conservative 3; Mismatches 12; I	US-08-233-788A-59  Sequence 59, Application US/08233788A  Patent No. 5635617  GENERAL INFORMATION: APPLICANT: Doran, James L. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. ANDRESSE: Seed and Berry STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE Washington COUNTRY: U.S.A. COMPUTER: EADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LEADABLE FORM: COMPUTER: LEADABLE FORM: APPLICATION NUMBER: US/08/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,788A FILING DATE: 26-APR-1994 CLASSIFICATION HUMBER: US/08/233,788A FILING DATE: 26-APR-1994 CLASSIFICATION NUMBER: US/08/233,788A FILING SYSTEM: US/08/233,788A FILING DATE: 26-APR-1994 CLASSIFICATION NUMBER: US/08/233,788A FILEFAN: (206) 622-4900 TELEFAN: (206) 622-4900 TELEFAN: (206) 682-6031 TELEGOMMINICATION INFORMATION: MAME: King, JOSHNATION: MAME: KING, MAME:	28 74.5 9.6 304 1 US-07-851-976B-8 29 74.5 9.6 304 1 US-08-291-609-8 30 74.5 9.6 304 1 US-08-401-136-8 31 74.5 9.6 304 1 US-08-401-136-8 32 73.5 9.5 211 1 US-08-276-852-34 33 73.5 9.5 211 1 US-08-273-2730A-16 34 73.5 9.5 211 1 US-08-322-730A-16 35 73.5 9.5 211 1 US-08-399-575-34 37 73.5 9.5 211 1 US-08-399-575-34 38 73.5 9.5 211 1 US-08-399-575-34 39 73.5 9.5 211 1 US-08-393-619-16 39 73.5 9.5 211 2 US-08-393-619-16 40 73.5 9.5 211 3 US-08-393-619-16 41 73.5 9.5 211 4 US-09-729-97-16 42 73.5 9.5 211 5 PCT-US93-0874-16 42 73.5 9.5 211 5 PCT-US93-0874-3-34 43 73.5 9.5 238 4 US-09-495-880A-42 44 73.5 9.5 238 4 US-09-495-880A-26 45 73.5 9.5 293 3 US-08-438-745-4
ength 151; Indels 0; Gaps 0	DETECTION	Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 34, Appli Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 34, Appl Sequence 34, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 26, Appl Sequence 27, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl

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RESULT 3
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Sequence 27661, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Seed and Berry
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APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: King, Joshua REGISTRATION NUMBER: 35,570 REFERENCE/DOCKET NUMBER: 92
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amino acid
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                                                                                                                                    GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                   VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHA
                                                                                                                                                                   VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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87.5%;
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Pred. No. 9.2e-47;
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Sequence 3, Application US/08864038A

Patent No. 6001592

GENERAL INFORMATION:

APPLICANT: Kunio NAKASHIMA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: VCCTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SEQ ID NO 27661
LENGTH: 208
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                 TELEPHONE: (212)986-2340
TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 1
FILING DATE: May 28,
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 150-city
                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 8-
FILING DATE: 15-July-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: JAPAN
ZIP: 514-01
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TOPOLOGY:
                    TYPE:
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                                      LENGTH:
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               amino acid
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IBM Compatible
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3, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.50 inch, 1.44 MB storage
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                                                                                                                                                                       F-5610
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RESULT 5
US-09-498-520A-18
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                                                                                                   RESULT 6
                                                                                 US-09-328-352-4764
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                             Sequence 4764, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 18
LENGTH: 321
TYPE: PRT
ORGANISM: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/498,520A CURRENT FILING DATE: 2000-02-04 NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. 6613553el Enoyl Reductases and Methods of Use Thereof FILE REFERENCE: SJ-0022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rock, Charles O APPLICANT: Heath, Richard
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Pin
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LOCATION:
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                                                                                                                                                     276
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                                                                                                                                                                                                                                                                                                                                                       109 LKAAGLKVMVVCGAVKHAVKAEQAGCDAVICQGGEGGGHTGLVGTLPLVAQAVEAVKIPV 168
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                                                                                                                                                                                                                                                   84 GADNSTIEL-TONG----FRNNATIDOWNAKNSDITV----
                                                                                                                                                                                                                                                                                                                      35 ---GGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAG-----Q 83
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                                                                                                                                                                                   QTASDSSVMVRQVGFG 143
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                                                                                                                                                                                                                      AADEDTVRTRCYSGKPMRVKKNPYVDDWEARPGDIQPFPQQAMVSIRNGAMGGIGGQIEG
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from 1 to 738
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Pred. No. 1.7;
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Pred. No. 2;
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US-08-458-023B-6
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                                                                    US-08-458-023B-6
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Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08458023B Patent No. 5667990
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                              TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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APPLICANT:
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,02
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                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Takagi, Shinobu
APPLICANT: Boominathan, Karuppan
TITLE OF INVENTION: ASPERGILLUS E
NUMBER OF SEQUENCES: 16
                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                               TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
ZIP: 101
                                                                                                                                                                                                                                                   NAME: Lowney Dr., Karen A. REGISTRATION NUMBER: 31,27
                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                   LENGTH:
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                                                                                                                                     363 amino acids
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                  Score 78;
Pred. No.
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Pred. No. 8;
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EXPRESSION SYSTEM
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                                   DB 1;
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Conservative

13;

Mismatches

38;

Gaps

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RESULT 9
US-09-168-406A-2
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US-08-331-515A-2
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US-08-331-515A-2
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Sequence 2, Application US/09168406A
Patent No. 6258769
GENERAL INFORMATION:
APPLICANT: Welinder, Karen G.
APPLICANT: Andersen, Morten B.
TITLE OF INVENTION: Peroxidase Variants With Improved
TITLE OF INVENTION: Hydrogen Peroxidase Stability
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 212-867-0123
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Andersen, Morten B
TITLE OF INVENTION: PEROXIDASE VARIANTS WITH IMPROVED
TITLE OF INVENTION: HYDROGEN PEROXIDE STABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Harrington, James J. REGISTRATION NUMBER: 38,711 REFERENCE/DOCKET NUMBER: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/331,515A
FILING DATE: 01-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                             48 YQYGSANAALALQSDARKYDQLVTRVVTHE-----MAHAGQ-----GADNSTI 90
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5: 5851811
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                                                                                                                                                                                                           YQ-GS-----KCESPVRK----ILRIVFHDAIGFSPALTAAGQFGGGADGSII 101
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US-09-128-450-26
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; NAME/KEY: VARIANT
; LOCATION: (1)...(435)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-168-406A-2
                                                                                                                                                                                Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/16
CURRENT FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 08/331,51
PRIOR FILLING DATE: 1994-11-01
PRIOR APPLICATION NUMBER: PCT/DK93/
PRIOR FILLING DATE: 1993-06-01
PRIOR FILLING DATE: 1993-06-01
PRIOR FILLING DATE: 1992-06-01
NUMBER: 0F SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 50121
CURRENT APPLICATION NUMBER: US/09/128,450
CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
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Best Local &
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LENGTH: 435
TYPE: PRI
ORGANISM: Coprinus cinereus
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chesebro,
                                                                                                                                                                                                                                                       LENGTH: 254
TYPE: PRT
ORGANISM: Hamster sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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 205
                           135 VMVRQV 140
                                                      145 WEDRYYRENMIRYPNOVYYRPVDOYNNONNFVHDCVNITIKOHTVTTTTKGENFTETDIK 204
                                                                                 85 ADNSTIELTQNGFRNNA----TIDQWNAKNS-----DITVGQYGGNNAAL-VNQTASDSS 134
                                                                                                                     89
                                                                                                                                            26 WG-GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQG 84
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                                                                                                                                                                                             Similarity
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IMERVV 210
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Chabry, Joelle
Priola
                                                                                                                 WGQGGGTHNQWNKPSKPKTNMK--HMAGAAAAGAVVGGLGGY--MLGSAMSRPMMHFGND 144
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Pred. No. 2;
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Pred. No. 3.8;
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER PACE
SOFTWARE: PACE
SEQ ID NO 26
FIGTH: 254
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Best Local :
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Patent No. 6355610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/128,450
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
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CURRENT APPLICATION NUMBER: US/09/823,494
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Caughey, Byron APPLICANT: Chabry, Joelle
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                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. STREET, N.W.
                                                                                                                                                                                                                                                                                                                                APPLICANT: SUMIDA, MOTOO
TITLE OF INVENTION: PEROXIDE GENE OF MICROBIAL ORIGIN
NUMBER OF SEQUENCES: 17
ATTORNEY/AGENT INFORMATION: NAME: SCOTT, WATSON T.
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                  APPLICATION NUMBER: FILING DATE: 199111 CLASSIFICATION: 43
                                                                                                                                                                                                                                                        CITY: WASHINGTON
                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                    ASHIKARI, TOSHIHIKO
HATANAKA, HARUYO
SHIBANO, YUJI
AMACHI, TERUO
NAKAYAMA, TORU
                                                                                                                                                                                                                     USA
                                                       19911115
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Pred. No. 2;
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Query Match 9.9
Best Local Similarity 26.3
Matches 37; Conservative
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
LENGTH: 943 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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STREET: Seattle
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TOPOLOGY: 15
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9.9%; Score 77; DB
26.2%; Pred. No. 14;
htive 14; Mismatches
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                                                                    DB 4;
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US-09-072-596-199
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Matches 37; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                      NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFO
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LENGTH: 943 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: li
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129 TASDSSVMVRQVGFGNNATAN 149
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o. 6458366
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                                                          RVVTHEMAHAGQGADNSTIELT---QNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
                             NTGNNNIGFANTGNNNIGIGLSGDNQQGFN---IASGWNSGTGNSGLFNSGTNNVGIFNA 573
                                                                                           ĠŚGNIĠVFNVGSĠSLĠNYNIĠSĠN-----LGIYNIGFGNVGDYNVGFGNAGDFNQGFA 516
                                                                                                                            GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAA--LALQSDARKYDQLVT
                                                                                                                                                                                                                                                                                  amino acid
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6300 Columbia Center,
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Vedvick, Thomas S.
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Dillon, Davin C.
Campos-Neto, Antonia
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Hendrickson, Ronald C.
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                                                                                                                                                                                9.9%; Score 77; DB 26.2%; Pred. No. 14;
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Search completed: March 11, Job time: 12.4 secs

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US-09-477-135A-131
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Best Local Similarity
Matches 37; Conserv
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PRIOR FILING DATE: 1997-12:
PRIOR APPLICATION NUMBER: 1
PRIOR FILING DATE: 1996-06
PRIOR APPLICATION NUMBER: 6
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CURRENT FILING DATE: 2000-01-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding TITLE OF INVENTION: immunostimulatory Peptides
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 681 GTGN---
                               129 TASDSSVMVRQVGFGNNATAN 149
                                                             624 NTGNNNIGFANTGNNNIGIGLSGDNQQGFN---IASGWNSGTGNSGLFNSGTNNVGIFNA 680
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26.2%; Pred. No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                     101.5
94.5
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83.5
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      82
82
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774
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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Gapop 10.0 , Gapext 0.5
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: //Ggn2_6/ptcdate/1/pubpaa/USO7_PUBCOMB.pep:*

: //Ggn2_6/ptcdate/1/pubpaa/PCT_NEW_PUB.pep:*

: //Cgn2_6/ptcdate/1/pubpaa/USO6_NEW_PUB.pep:*
      13.1
12.2
10.9
10.9
10.7
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110.3
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Copyright (c) 1993 - 2004 Compugen Ltd
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/ cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
      445
438
1778
278
597
515
2732
2834
486
688
9 US-09-810-264-28

9 US-09-793-306-146

14 US-10-128-714-8213

14 US-10-128-714-8213

14 US-10-238-075-1119

14 US-10-238-075-1119

15 US-09-996-194-16

10 US-09-820-643A-21

15 US-10-369-493-20619

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US-10-156-761-9343
US-10-238-075-749
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Sequence 20638, A
Sequence 9343, App
Sequence 749, App1
Sequence 28, App1
Sequence 3213, Ap
Sequence 8213, Ap
Sequence 8213, Ap
Sequence 16, App1
Sequence 16, App1
Sequence 21, App1
Sequence 21, App1
Sequence 20619, A
Sequence 30619, A
Sequence 3641, Ap
Sequence 37876, Ap
Sequence 37876, Ap
                                                                                                                                                                                                                                                                                                                         Description
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GENERAL INFORMATION:

Sequence 20638, Application US/10369493 Publication No. US20030233675A1

## ALIGNMENTS

S 밁 Ś US-10-369-493-20638 NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 20638

LENGTH: 445

TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations Query Match
Best Local Similarity
Matches 45; Conserv APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21 APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng 51 GSANAALALQSDARKYDQLVTRVVTHEMAHAGQGA-----DNSTIELTQNGFRNNATID 104 19 AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS 45; 7 AAFAA-----IVVSGSALAGVVPQWGGGG-----WHNGG-----GNSSGPDSTLSIYQY Conservative 13.1%; Score 101.5; DB 15; Length 445; 26.0%; Pred. No. 0.046; ive 20; Mismatches 55; Indels 53; 20; IN PLANTS FOR PRODUCTION OF 53; 77

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; ORGANISM: Escherichia coli
US-10-238-075-749
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                    Query Match
                                                                                        NUMBER OF SEQ ID NOS: 1576
SOFTWARE: PatentIn version 3.1
SEQ ID NO 749
LENGTH: 1778
TYPE: PRT
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US-10-156-761-9343
                                                                                                                                                                                                                                                                                                                                Sequence 749, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR PRILING DATE: 2001-05-30
PRIOR BILLING DATE: 2001-05-30
                                                                                                                                                                      FILE REFERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
                                                                                                                                                                                                                                        APPLICANT: I.N.S.E.R.M.
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ś
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9443
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APPLICANT: IKEDA,
APPLICANT: ISHIRZ,
APPLICANT: HORIKI
APPLICANT: SAKAK
APPLICANT: SAKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9343, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 TGALLPWDAKNFD----KIGGKD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 NATIDOWNAKNSDITVGOYGGNN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LOSDARKYDQ------LVTRVVTHEMAHAGQGADNSTIELTQN-GFRN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKVĹÓPELDKFEEQTGIKVKLEVVPWSDĽLNŘILŤ--ATTSĠÓĠPĎVLNÍGNŤWSASLQA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRSIRAAAVGAVTMSLALAASAC----GGGSSTGGGSNDSD-KTLT-YWASNQGASIAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNSNS-----VGRDIQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPS 123
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                10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.2%; Score 94.5; DB 25.9%; Pred. No. 0.24; tive 27; Mismatches
          Score 84.5;
DB 14; Length 1778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14;
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US-09-793-306-146
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APPLICANT: Famodu, Omolayo O.
APPLICANT: Hu, Xu
APPLICANT: Hu, Xu
APPLICANT: Lu, Guihua
APPLICANT: Lu, Guihua
TITLE OF INVENTION: WRKY Transcription Factors and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: 1183
CURRENT APPLICATION NUMBER: US/09/810,264
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2000-03-17
NUMBER OF CEO TO NOR. A
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                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                       GENERAL
                                                                                                                                                                              Sequence 146, Application US/09793306
Patent No. US20020098200A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 20.8.
37; Conservative
   APPLICANT: Jen, Shyian
APPLICANT: Lodes, Shyian
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: of Tuberculosis
FILE REFERENCE: 014058-008740US
FILE REFERENCE: 014058-008740US
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APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 278
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                                                                                                                                                                    INFORMATION
                                                                                                                                                                                                                                                            179 CTTVGCPVRKHVERASHDNRAVÍTTYEGRHSHDVÞVGRGAGASRÁLÞTSSSSDSSVVV 236
                                                                                                                                                                                                                                                                                                                        120 -HGDNĖGSSGGTGACVKPVREPRLVVQTLSDIDILDDGFRWRKYGQKVVKGNPNPRSYYK 178
                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                            75 TH---EMAHAGQGA------DNSTIELTQNGFR---
                                                                                                                                                                                                                                                                                                                                                                                                                      15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVV 74
                                                                                                                                                                                                                                                                                                                                                                                      71 NSŚGCAAVIAE-----DHTNGSEHŚGPTPENŚSVTFGDDEADNGAEPETKRRKE----- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1020 LYGVSDYIADALGGN--AVVN---TDGSI 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            966 NTSFSTSLGDÁLLWD-----ATAGKFSÁKHGINNAPSVITDVANGAVSSTSSDAINGSQ 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        906 KISSNSTDAINĠŚQĹYĠVADSFTSYLĠĠĠADISDTĠVLŚĠĖTYŤIGGTDÝTNVGDÁĹÁAI 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 -----QSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQ--NGFRNNATIDQWNAKN 110
                                                                                                                                                                                                                                                                                         Skeiky, Yasir
Ovendale, Pamela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 KVAAFAAIVVSGSALAGVVPQW----GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL- 59
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1; Mismatches
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RESULT 6
US-10-128-714-3213
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                                                                                                                                                     ; ORGANISM: Aspergillus fumigatus US-10-128-714-3213
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                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version
SEQ ID NO 3213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 146
LENGTH: 597
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 34;
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Best Local Similarity
                                                                            Matches
                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
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PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,821
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                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/316,362
                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-06-05
                                                                                                                                                                                            LENGTH: 435
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 NNATAN 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 FGNSGNNNIGFFNSG-NNNVGFFNSGNNNFGFGNAGD----
    274
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                                    13 VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGA 85
                                                                                               Similarity
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  VLTGHKGSVTCVRWGGTGKI----YTSSHDRTIKIWNAQNGSLLQTLSAHAHRVNHLALS
                                                                            Conservative
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                                                                        30; Mismatches
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                                                                                             Score 82.5;
Pred. No. 4;
                                                                                                               DB 14;
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APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemisux, Sebastien M
ITITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
ITITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/316,362
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                                                                                                                                                                                                                                       RESULT 8
US-10-238-075-1119
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US-10-128-714-8213
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                                                                                                                                         Sequence 1119, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
APPLICANT: I.N.S.B.R.M.
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LENGTH: 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Publication No. US20030119013A1
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TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolal TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of the: FILE REFERENCE: BLANDING CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
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SOFTWARE: PatentIn ver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                    388
                                                                                                                                                                                                                                                                                                                                                                              108 AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 VLTGHKGSVTCVRWGGTGKI----YTSSHDRTIKIWNAQNGSLLQTLSAHAHRVNHLALS 329
                                                                                                                                                                                                                                                                                                                                                                                                                               330 TDFALRTAYHD--HTGKVPGSDTEKVAVAKKRFEQAAMVNNKIVEKLVSASDDFTMYLWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNN 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 --- VTRVVTHEMAHAGQ--GADNSTIELTQNGFR-----NNATIDQ------WN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQL---
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                                                                                                                                                                                                                                                                                                                                    PENSTKPIARLLGHOKEVNHVTFSPDMAYIASAGFDNH
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Tishkoff, Daniel
Zamudio, Carlos
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Pred. No. 5;
30; Mismatches
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                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1158)..(1158)
OTHER INFORMATION: The 'Xaa' at location 1158 stands for NAME/KEY: misc feature
LOCATION: (1159)..(1159)
OTHER INFORMATION: The 'Xaa' at location 1159 stands for NAME/KEY: misc_feature
LOCATION: (1168)..(1168)
OTHER INFORMATION: The 'Xaa' at location 1168 stands for NAME/KEY: misc_feature
LOCATION: (1270)..(1270)
OTHER INFORMATION: The 'Xaa' at location 1270 stands for NAME/KEY: misc_feature
LOCATION: (13480)..(1340)
OTHER INFORMATION: Unsure
NAME/KEY: misc_feature
LOCATION: (1378) '21018)
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APPLICANT: Welch, Rodney A.
APPLICANT: Burland, Valerie D.
TITLE OF INVENTION: No. US20030165870A1el Ser
FILE REFERENCE: 960296.97648
CURRENT APPLICATION NUMBER: US/10/085,959
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: 60/242,412
PRIOR FILING DATE: 2000-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Escherichia coli
US-10-238-075-1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1
SEQ ID NO 252
LENGTH: 2834
TYPE: PRT
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1119
LENGTH: 2732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 252, Appropriate Publication No.
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                                                                                     NAME/KEY: misc_feature
LOCATION: (31038)..(31038)
OTHER INFORMATION: Unsure
NAME/KEY: misc_fe
LOCATION: (31770)
                                 OTHER INFORMATION: Unsure
                                                      NAME/KEY: misc_feat
LOCATION: (31042)..
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature LOCATION: (493) . (493) OTHER INFORMATION: The 'Xaa' at location 493 stands for Asn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 ASGRLTVNNSLATGAVTAKGOGVTLTGDHKAGGNLSVSSRRDIVLS---NGTLNSDKDLS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTAGGRITQQ-----NEKLTAGRDVTLAAKNITQD-----TASQINAARDIVTV--- 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10085959
o. US20030165870A1
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                                                      feature
(2)..(31042)
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27.8%; Pred.
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                                                                                                                                                                                                           location 1270 stands for
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RESULT 11 US-09-820-843A-21

Sequence 21, Application US/09820843A
Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTE
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915

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                                                                                                                                         ; OTHER INFORMATION: US-09-996-194-16
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US-09-996-194-16
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                                                              Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 16
LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, App
Patent No. US20
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                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/250, 348
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/250,073
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/253,878
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 35800/240590
CURRENT APPLICATION NUMBER: US/09/996,194
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 201
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/250,338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bandaru, Rajasehkar
TITLE OF INVENTION: 84242, 8035, 55304, 52999, au
TITLE OF INVENTION: No. US20020151696A1el Human
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (44972)..(44922)
OTHER INFORMATION: Unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Unsure NAME/KEY: misc feature LOCATION: (31799)..(31799) OTHER INFORMATION: Unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 GGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                               51 GSANAALALQSDARKYDQLVTRVVTHEMAHA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AFAAIVVSGSALAGVVPQWGGG----GNHNGGGN---SSGPDSTLSIYQYGSANA--ALA 58
GVINIPAANITSRNHYDOLVTRVVTHEIAHA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTAGGRITOO-----NEKLTAGRDVTLAAKNITOD-----TASQINAARDIVTV---
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                                                                 10.6%;
ilarity 58.1%;
Conservative
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                                                                                  Score 82; I
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Pred. No. 45,
                                                                   Mismatches
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                                                                                                                                                       sequence
                                                                                                      DB
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                                                                                                Length 65;
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Best Local (
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SEQ ID NO 20619
LENGTH: 486
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Best Local Similarity
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                               .10-369-493-20619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21
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OTHER INFORMATION: PPE
NAME/KBY: misc_feature
OTHER INFORMATION: gi|1781260
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ORGANISM: M. tuberculosis
                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure
LOCATION: (1)..(486)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                           145
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                                                                                                                                                                   11 AIVVSGS----ALAGVVPQWGGGGNHNGGGNSSGP-----DSTLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 GNNGNFNFGSGNTG-SNNIGFGNTGSGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGAD
                                                                                                                                                                                                                              Similarity
                                                                                  ALQSDARKYDQLVTRVVTHEMAHAG--QGADNSTIELTQNG---FRNNATIDQWNAKNSD 112
                                                                                                                            SVVVAGTDYRDIVAGVLÞSLGGVKKAYAIGDGSGÞFAPFKDLASDTPFSAPEFGAADGF- 144
                                                                                                                                                                                                            Conservative
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    -QYGGNNAALVNQTASDSSVM 136
                                                                                                                                                                                                                              10.4%;
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                                           -VIIHTAAVGGRPRGA-----LISQGNLLIAQSSLVDAWRLTEAD 183
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                                                                                                                                                                                                        ; Score 80.5; DB 15; ; Pred. No. 7.5; 22; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 82; DB 10;
Pred. No. 3.5;
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                                                                                                                                                                                                                                                    Length 486;
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US-10-156-761-13039
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Best Local Sim
Matches 53;
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LENGTH: 562
TYPE: PRT
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APPLICANT: IKEDA,
APPLICANT: ISHIKA
APPLICANT: HORIKA
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SEQ ID NO 3641
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                   Sequence 3641, Application US/10369493 Publication No. US20030233675A1
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                                                                                                        APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                    APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory
APPLICANT: Slater, Steven C
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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                                               NUMBER OF SEQ ID NOS:
                                                                    PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21
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PPLICANT: SAKAKI, YOSHIYUKI
PPLICANT: HATTORI, MASAHIRA
ITTLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 VNIGMLPLFHVTGLGLMLTLQQAGGASVI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 NITSGDYAGONTALRIGGNNTVNKDVLLSISSDMONSGRRWGFRAN 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 VHCHWELEVADATGALQGRLEIPFIDQSKLSNAVDTTTIGIAWTNIRTN--LADFSIRAQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 IRHFMMRSDAKTMQAFYIPVQTSNKKGGYDATTRDPLSTGVSWKPVVWQGAHYEANDHGS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 SGSPSYASLPKGIAGRSENAGLIIGSSYIGGDDDGTGTDSTGRLNLYSYQRANVGSFGEN 202
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Similarity 23.5%; Pred. No. 11;
53; Conservative 20; Mismatches
                                                                                                                                                                                                                            Goldman, Barry S. Chen, Xianfan
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HORIKAWA, HIROSHI
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APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Howard, Bussey
ITILE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILLING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 7876
LENGTH: 688
TYPE: PRT
ORGANISM: Candida albicans
US-10-032-585-7876
Search completed: March 11, 2004, 19:18:38 Job time: 25.6 secs
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US-10-032-585-7876
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Best Local Similarity 23.5

Matches 42; Conservative
                                                                                                                                                                                                                                                                                      Query Match 10.2%; Score 79; DB 14; Length 688; Best Local Similarity 22.7%; Pred. No. 17; Matches 27; Conservative 24; Mismatches 60; Indels
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                                                                                               544 AKSKKKSNFDNNSNSALNNLDKSKLKINT---NEITNISETTSNSSSPVINLNHGGRSS 599
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Database

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A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasmin G;Keywords: fimbria F;1-20/Domain: signal sequence #status predicted <SIG> F;21-151/Product: fimbrin protein agfA #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 21-52 <CO2>
A;Experimental source: strain 27655-3b
A;Note: the authors translated the codon ACG for residue 44 as Ile
R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W.
J. Bacteriol. 173, 4773-4781, 1991
A;Title: Purification and characterization of thin, aggregative fimbriae from Salmonell-A;Reference number: A44898; MUID:91310586; PMID:1677357
A;Contents: 27655
A;Accession: A44898
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C;Date: 31-Dec-1996 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999
C;Accession: JC6039; DC6015; A44898
R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996
A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fi
A;Reference number: JC6039; MUID:96146512; PMID:8550497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: agfA
C;Function:
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A;Molecule type: DNA
A;Residues: 1-151 <COL>
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A; Accession: PC6015
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A,Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Rile A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. Mol. Microbiol. 7, 523-536, 1993
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MOI. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70788
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                                                                                                                                                                      A; Accession: G64846
                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-151 < HAM>
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Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

A;Title: Complete genome sequence of a multiple drug resistant

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AI0635
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A; Residues: 1-151 < PAR>
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R;Parkhill, J.; Dougan, G.; Jam
Connerton, P.; Cronin,
                                                                                               Residues: 1-151 <BLAT>
                                                                                                                                          Status: nucleic acid sequence
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Best Local S
Matches 137
                                                                                                                         Molecule type: DNA
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secies has also been called Salmonella typhi
2001 #sequence_revision 09-Nov-2001 #text_c
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Pred. No. 3.1e~51;
3; Mismatches 11
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ies, R.M.; Dowd, L.;
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curlin major subunit CsgA [imported] - Escherichia coli (C;Species: Escherichia coli (C;Species: Escherichia coli (C;Date: 18-Jul-2001 #text_C;Accession: D90806 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ish gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattor DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Eschiperation (Complete Genome Sequence of Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence (Complete Genome Sequence 
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A;Molecule type: DNA
A;Residues: 1-152 <HAY>
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D90806
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A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424;
A;Experimental source: strain K-12, substrain
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A; Residues: 21-42; 44-50 <OLS2>
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Tasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
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llarity 67.1%;
Conservative 2
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                                                                                                                 ; Score 506.5; DB 2;
; Pred. No. 7.7e-36;
21; Mismatches 28;
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Pred. No. 1.2e-37;
0; Mismatches 27
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W3110
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QSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG

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conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AD3143
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AD3143
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: H85665
C;Accession: H85665
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mailer, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apo Nature 409, 529-533, 2001
                                                                           A;Residues: 1-145 <KUR>
A;Crose-references: GB:AE008689; PIDN:AAL45562.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4768
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                   R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
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A;Cross-references: GB:AB005174; NID:g12514574; PIDN:AAG55788.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                  A; Reference number: A; Accession: AD3143
                                                                                                                                                                                                                                                                                                            A; Authors: Yoo, H.; ster, E.W.
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Matches 102
Query Match
Best Local S
Matches 36
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                                                                                                                                                                                                                                                                                                                                Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.4%;
                   13.6%;
                                                                                                                                                                                                                                                                     Natural Genetic Engineer Agrobacterium tumefaciens C58 MUID:21608550; PMID:11743193
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Score 105.5; DB Pred. No. 0.049; 7; Mismatches 6
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Guenthner, D.; Kutyavin, T
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  61;
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    Indels
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                                         145;
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Potamousis, K.; Apodaca
                                                                                                                                                                  GSPDB:GN00187
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F3FF9.21 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Cste: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C;Accession: C86266
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conm, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, X.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Status: preliminary
A;Molecule type: DNA
A;Molecule: 1-573 <STO>
A;Residues: 1-573 <STO>
A;Cross-references: GB:AE005172; NID:g4850402; PIDN:AAD31072.1;
C;Genetics:
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A;Accession: H98144
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein AGR L_228 [imported] - Agrobac C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 C;Accession: H98144
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A; Residues: 1-145 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.; Miller, N.; Blanchard, M.; Qurollo, M.; Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GGNHNGGGNSSGPDSTLSIYQYGSANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
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                                 GSPDB: GN00141
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Markelz, B.
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RESULT 9
S70797
Curlin nucleator protein csgB precursor - Escherichia coli (strain K-12)
N;Alternate names: csgB protein; curlin nucleation component; minor curl
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2
C;Accession: S70787; F64846
C;Accession: S70787; F64846
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
C90806
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                                                                                                                                                                                                                                                                                                                    A;Description: minor component of wild-type curli; A;Note: curli are thin, coiled fibers expressed on and H-kininogén; in the absence of CsgA, CsgB can F;1-21/Domain: signal sequence #status predicted <S F;22-151/Product: minor curlin chain #status predic
                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X90754; NID:gl147558; PIDN:CAA62281.1; PID:gl147563 A;Experimental source: strain K12, substrain W3110 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augu. R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOL. Microbiol. 18, 661-670, 1995

A;Title: Expression of two csg operons is required for production of A;Reference number: S70783; MUID:96414468; PMID:8817489

A;Accession: S70787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F64846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              ;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: csgB
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                                                                                                                                                                                                                                                             Similarity
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                                                                        SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                RNNATIDOWNAKNSDITVGQYGGNNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                             SSGPDSTLSIYOYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGF
                                                                                                                                                         AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVTHEMAHAGQGADNSTIELTQNGFRNNA-TIDQWNAKNS-----DITVGQYGGNN 122
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                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                             12.5%;
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                                                                                                                                                                                                                                                             Score 96.5;
Pred. No. 0.
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                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                          interaction between CsgA and the surface of Escherichia self-assemble into polymers
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V.; Riley, M.;
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C;Accession: E95965
R;Finan, T.M.; Weidner, S.; Wong,
Proc. Natl. Acad. Sci. U.S.A. 98,
Proc. Natl. Acad. Sci. U.S.A. 98,

K.; Buhrmester, J.; Chain, P.; Vorholter, 9889-9894, 2001
the 1,683-kb pSymB megaplasmid from the N.

N2-fixing

Hernar Ig endo C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change C;Accession: E95965

hypothetical glycine-rich protein C; Species: Sinorhizobium meliloti

[imported] -

Sinorhizobium meliloti (strain

1021)

maga

30-Sep-2001

E95965

β δ

77

129

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A; Notecus - Francis - A; Notecus - Lype: DNA - A; Residues: 1-151 <STO> A; Residues: 1-151 <STO> A; Residues: 1-151 <STO> A; Residues: 1-251 <STO> A; Cross-references: GB: AB: O157: H7, Substrain EDL933
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G85665
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                                                                                                                                                                                                                                                                                     iller, L.; Grotbeck, E.J.
Nature 409, 529-533, 2001
A; Title: Genome sequence
                                                                                                                                                                                                                                                                                                                       R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; D
                                                                                                                                                                                                                                                                                                                                                             C;Date: 16-Feb-2001
C;Accession: G85665
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                                                                                                                                                                                                                                                         A; Accession: G85665
                                                                                                                                                                                                                                                                         A; Reference number: A85480;
                                                                                                                                                                                                                                                                                                                                                                                               C;Species:
                                                                                                                                                                                                                                                                                                                                                                                                         curlin minor chain precursor,
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A;Tille: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Hayashi, T.; Makino, K.; Ohnishi,
gasawara, N.; Yasunaga, T.; Kuhara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hayashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: C90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A99629;
A;Accession: C90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-151 <HAY>
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                                                                   Best Loc
Matches
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Matches
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32; Conserv
                                                                                 Similarity
 AAGYDLANSEYNF ---
                                SSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNNATIDOWNAKNSDITVGOYGGNNAALVNOTASDSSVMVROVGFGNNATANOY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.5%;
llarity 28.1%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                         #sequence_revision 16-Feb-2001
                                                                                                                                                                                                                                                                       of enterohemorrhagic
80; MUID:21074935; PMI
                                                                                12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                           CsgA homolog
-AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
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                                                                 Score 96.5; DB
Pred. No. 0.29;
5; Mismatches
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kurokawa, K
Shiba, T.;
                                                                                                                                                                                                                                                                         jic Escherichia
PMID:11206551
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                                                                                                                                                                                                                                                                                                                                         B.,
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                                                                                                                                                                                                                                                                                                                      ; Glasner,
lanta, E.;
                                                                                                 Length
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Potamousis,
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K.; Apodaca,
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RESULT 13
S11672
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A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lhebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Zhao, J.; Orser, C.S.

MO1. Gen. Genet. 223, 163-166, 1990

A; Title: Conserved repetition in the ice nucleation gene A; Reference number: S11672; MUID:91080859; PMID:2259339

A; Accession: S11672
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S07053
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A;Accession: E95965
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-1567 <ZHA>
A;Cross-references: EMBL:X52970; NID:g48531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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A;Cross_references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ce nucleation protein - Xanthomonas campestris
;Species: Xanthomonas campestris
;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
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Best Local S
Matches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIATAGAGAYGILAQSIGGGGGG---GGNATGGDAGFGSFQIGGGGGGGGGYANTANVGFK 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIVVSGSALAGVVPO--WGGGGNHNGGGNSSGPDSTLSIYQYGS-----ANAA----
                                                                                                                                                                                                                                          VYGSTLTGADQSRLVAGYGSTETAGDHSDLTAGYGSTGTAGSDSSI-LAGYGSTQTAAGR 263
                                                                              STQTARKGSDITAG-YGSTGTAGSDSALIAGYGSTQTAGSESSLT--AGYGSTQTARK 374
                                                                                                                                                              STLTAGYGSTQTAQEGSRLTSGYGSTATSGSDSAVI - - - - SGYGSTQTAGSESSLTAGYG
                                                                                                                                                                                                                                                                                  VSGSALAG----VVPQWGG---GGNHN-----GGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGGNGGAGGEVSVSLTDSAIRTGQGG
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                                                                                                                    -DQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
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                                                                                                                                                                                                                                                                                                                                                                                                      protein
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Pred. No. 8
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A;Molecule type: DNA
R;Bouvier, J; Bordier, C; Vogel, H; Reichelt,
R;Bouvier, J; Bordier, C,; Vogel, H; Reichelt,
Mol. Biochem. Parasitol. 37, 235-246, 1989
A;Title: Characterization of the promastigote sur
A;Reference number: A60648; MUID:90114330; PMID:3
A;Accession: A60648
A;Recsidues: 101,'E',103-118,'SV',121-123 <BOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: PL0221
A;Molecule type: DNA
A;Residues: 1-602 < ABUTY
A;Cross-references: GB:Y00647; NID:g9554; PIDN:CAA68673.1;
A;Cross-references: GB:Y00647; NID:g9554; PIDN:CAA68673.1;
A;Note: this is a revision to the sequence from reference A
A;Note: this is a revision to the sequence from reference A
B;Button, L.L.; McMaster; W.R.
J. Exp. Med. 167, 724-729, 1988
A;Title: Molecular cloning of the major surface antigen of A;Reference number: A27598; MUID:88154764; PMID:3346625
A;Accession: A27598
A;Status: significant sequence differences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Leishmania major
C;Date: 16-Sep-1992 #sequence_revision
C;Accession: PL0221; A27598; A60648
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PL0221
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A;Residues: 1-1322 <ABB>
A;Cross-references: GB:X17316; NID:g296095; PIDN:CAA35194.1;
C;Superfamily: ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ice nucleation protein inaA - Erwinia ananas C;Species: Erwinia ananas C;Species: Erwinia ananas C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change C;Accession: S07053 R;Abe, K.; Watabe, S.; Emori, Y.; Watanabe, M.; Arai, S. FEBS Lett. 258, 297-300, 1989
                                                                              C;Complex: homodimer
C;Function:
                                                                                                                           submitted to the Brookhaven Protein Data Bank, A;Reference number: A68135; PDB:LIML A;Contente: annotation; X-ray crystallography, A;Note: strain LRC-L119
                                                                                                                                                                                                                                 A;Experimental source: strain LEM513 R;Schlagenhauf, E.; Etges, R.; Metcalf, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N; Alternate
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A; Note: the activated form car
C; Superfamily: leishmanolysin
                     A_i, Description: catalyzes the hydrolysis of peptide bonds between two hydrophobic residue A_i, Note: the activated form can activate the proenzyme form
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N;Alternate names: promastigote surface proteinase; surface endopeptidase glycoprotein
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Best Local
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                                                                                                                                                      X-ray crystallography, 1.86 angstroms,
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Pred. No. 8
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C;Reywords: blocked carboxyl end; cell adhesion; glycoprotein; homodimer; hydrolase; lip F;1-39/Domain: signal sequence #status predicted <SITo>
F;40-100/Domain: activation peptide #status predicted <ATP>
F;101-577/Product: leishmanolysin #status experimental cMAT>
F;578-602/Domain: activation peptide #status predicted <CTP>
F;578-602/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;48,264,268,334/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status F;100-101/Cleavage site: val-val (autolytic) #status experimental
F;125-142,191-230,314-386,393-455,406-425,415-489,466-510,515-565,535-558/Disulfide bond
F;264,268,334/Binding site: zinc, catalytic (His) (active) #status experimental
F;265/Active site: Glu #status predicted
F;370/407/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Collinson S.K., Emoedy L., Mueller K.-M., Trainification and characterization of thin,
Salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991).
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REF. 6).
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RESULT 2
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01-DEC-1992
01-OCT-1996
28-FEB-2003
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SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAIN=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K.
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.
                                                                                                                                                                                                                                                                                                                                                                                                            Science [4]
         Salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                           Arnqvist A., Olsen A., Pfeifer J., "The Cr1 protein activates cryptic fibronectin binding in Escherichia Mol. Microbiol. 6:2443-2452(1992).
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                                                                                    SEQUENCE OF 21-31.
MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emoedy L., Trust
                                                                                                                                                                                                                                      DNA
[5]
                                                                                                                                                                                                                                                  "A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                         Sampei G., Seki Y.,
Yano M., Horiuchi T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olsen A., Arnqvist A.;
"The RpoS sigma factor relieves
repression of csgA, the subunit
Escherichia coli.";
                                                                          Collinson S.K., Emoedy L., Trust T. "Purification and characterization
                                                                                                                                                                                              STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1357528;
                                                                                                                                                                                                                         SEQUENCE OF 21-40.
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MEDLINE=96414468; PubMed=8817489;
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Enterobacteriaceae; Eschei
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RESULT 3
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Best Local S
Matches 104
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Q93UZ4;
28-FEB-2003
28-FEB-2003
      SEQUENCE FROM N.A.

STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
Escherichia coli O157:H7.
                                                                                                                                                                Appl.
                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-0157:H7 / ATCC 43895;

STRAIN-01218556;

MEDLINE-21218556; PubMed-11319125;

Whlich G.A., Keen J.E., Elder R.O.;

"Mutations in the csgD promoter associated with variations in expression in certain strains of Bscherichia coli 0157:H7.";

Appl. Environ. Microbiol. 67:2367-2370(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Fimbria; Signal; Complete
SIGNAL 20
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EMBL; X90754; CAA62282.1; -.
EMBL; AE000205; AAC74126.1;
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NCBI_TaxID=83334;
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01-OCT-1996 (Rel. 34, Last sequence updi
28-FEB-2003 (Rel. 41, Last annotation updi
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Escherichia.
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SEQUENCE FROM N.A.
STRÄÏN=0157:H7 / R:
STRÄÏN=0156231;
SEQUENCE FROM N.A.
STRAIN-KI2 / MC4100;
MEDLINE-96414468; PubMed-8817489;
Hammar M., Arngviet A., Bian Z., Olsen A.,
"Expression of two csg operons is required fibronectin- and congo red-binding curli po
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Topplete genome sequence of enterohemorrhagic Escherichia coli

0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

-IPONCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI

COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROW

TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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EMBL; AE005315; AAG55788.1; -.
EMBL; AP002554; BAB34843.1; -.
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-!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
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MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.U., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim M., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyi Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe I Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Kuhara S., Shiba T., Hattori M., Shinagawa H., "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.", DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita K., Kanai K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Mishimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., May
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Roman B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the 12.7 DNA Res. 3:137-155(1996).
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Yano M., Horiuchi T.;
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PROSITE; PS00314; ICE\_NUCLEATION;

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EMBL; X52970; HSSP; P06620;

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EMBL; AB005315; AAG55787.1;
EMBL; AP002554; BAB34842.1;
EMBL; C90806; C90806.
PIR; C90806; C90806.
PIR; S70787; S70787.
ECOGene; EG12621; C59B.
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                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-L-T; FUNTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
-!- MISCELLANBOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xanthomonas campestris pv. transluc Mol. Gen. Genet. 223:163-166(1990).
                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Conserved repetition in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91080859;
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1 21 PC

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E 151 AA; 15882 MW;
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ia; Gammaproteobacteria;
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Pred. No. 0
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Matches 37
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Best Local
                                                                               Ice nucleation; Repeat; Outer membrane.

DOMAIN 162 1281 OCTAPEFTIDE PERIODICITY
SEQUENCE 1322 AA; 131094 MW; 8980EE24AA837039 CR
                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                   InterPro; IPR000258; Ice nucleatn Pfam; PF00818; Ice nucleation; 69 PRINTS; PR00327; ICENUCLEATN.
                                                                                                                                                                           EMBL; X17316; CAA35194.1; -. PIR; S07053; S07053. HSSP; P06620; IINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleation activity."; FEBS Lett. 258:297-300(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abe K., Watabe S., Emori Y., Watanabe M., Arai S.; "An ice nucleation active gene of Erwinia ananas. Se to those of Pseudomonas species and regions required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pantoea ananas (Erwinia uredovora).
                                                                                                                        PROSITE; PS00314; ICE_NUCLEATION; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=553;
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                                                                                                                                                                                                                                                                                                                                                    CTYSTAILIZATION IN SUPERCOOLED WATER.
SUBCELULAR LOCATION: OUTER membrane (By similarity).
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
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  GGGNSSGPDSTLS1YQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNST1ELT
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(Rel. 17, Last sequence update)
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                            Conservative
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GP63_LEIMA S
P08148; P15906;
01-AUG-1988 (Rel
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                                                                                                                                                                                    Structure
                                                                                                                                                                                                         MEDLINE=98416698; PubMed=9739094;
Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase
                                                                                                                                                                                                                                                                                                                 Schlagenhauf E., Etges R., Metcalf P., "Crystallization and preliminary X-ray
                                                                                                                                                                                                                                                                                                                                                                                                          Schneider P., Ferguson M.A.J., McConville M.J., Homans S.W., Bordier C.; "Structure of the glycosyl-phosphatidylinositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Button L.L., McMaster W.R.;
"Molecular cloning of the major surface
J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE MEDLINE=88154764; PubMed=3346625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leishmania major.
Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ol-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
[Major surface glycoprotein) (GP63 protein) (
                                                                                                                                                                                                                                                                                                                                           MEDLINE=95406217; PubMed=7675788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPI-ANCHOR
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                                                                                                                                                                                                                                                                                                                                                         K-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                   the Leishmania major promastigote surface
J. Biol. Chem. 265:16955-16964(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91009116; PubMed=2145267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5664;
                                                                                                                                                                                                                                                  (-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS)
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                                                  cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.

COFACTOR: Binds 1 zinc ion per subunit.

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

PTM: THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS

FULLY SATURATED, UNBRANCHED 1-O-ALKYL CHAIN (MAINLY C24:0) AND F

MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0,
                                                                                                                             FUNCTION: Has an integral role during the infection the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic P1' and basic residues at P2 and P3'. A model n
                        SIMILARITY: Belongs to peptidase family
                                       MIXTURE OF FU
C14:0, C16:0,
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171:589-589(1990)
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PIR; PL0221; PL0221.
PDB; 1LML; 17-SEP-97.
MEROPS; MOB.001; -.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptidase M8.
Pfam; PF01457; Peptidase M8.
PRINTS; PR00782; LSHMANOLYSIN.
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Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Zymogen; Signal; Cell adhesion; GPI-anchor; 3D-structure; Lipoprotein.
SIGNAL 1 39 POTENTIAL.
PROPEP 40 100 ACTIVATION PEPTIDE.
CHAIN 101 577 LEISHMANDLYSIN
PROPEP 578 602 REMOVED IN MATURE FORM.
METAL 264 264 ZINC (CATALYTIC).
ACT_SITE 265 265 METAL 268 268 ZINC (CATALYTIC).
METAL 334 334 ZINC (CATALYTIC).
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P55276;

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01-OCT-1996

28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=1534947; PubMed=11677608;

Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain , Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hen T.T., Holroyd S., Jagels K., Krogh A., Largen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL,
                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatice Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and CT18.";

J. Bacteriol. 185:2330-2337 (2003).

J. Bacteriol. 185:2330-2337 (2003).

-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.

-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI AND TO TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367;
MEDLINE=22531367;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner
"Comparative genomics of Salmonella enterica serova
                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Ty2 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
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1 21 POTENT
22 151 MINOR
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                                                                                                                                            QSAYGNSAAI I QKGSGNKANI TQY
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                                                                                                                                                                                                                                                                                                                               22
151 AA;
   (Rel. 34, Created)
(Rel. 34, Last seq
(Rel. 41, Last ann
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 42, Last annotation
                                                                  STANDARD;
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OR T1777.
                                                                                                                                                                                                                                                                                                                               16254 MW;
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    sequence up
annotation
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Pred. No. 0.48
L3; Mismatches
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MINOR CURLIN SUBUNIT:
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                                                                                                                                                                                                                                                                                                DB 1; Length 151;
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StyGene; SG10609; cage.
Fimbria; Signal; Complete proteome
POTEN
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MINOR
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EMBL; AE008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96146512; PubMed=8550497; Collinson S.K., Clouthier S.C., Doran "Salmonella enteritidia agfBAC operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille E Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.; "Curli fibers are highly conserved between Salmonella typhimurium Escherichia coli with respect to operon structure and regulation."
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SPECIES=S.typhimurium; STRAIN=SR-
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., S
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.typhimurium; STRAIN=LT2 / MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium,
Salmonella enteritidis.
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=S.enteritidis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AU COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURLIN MONOMERS
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106
                                                         48
                                                                                    69
                                                                                                                              Similarity
                                                                                    LVTRVVTHEMAHAGOGADNSTIELTONGFRUNATIDOWNAKNSDIT-VGOYGGNNAALVN
                        QTASDSSVMVRQVGFGNNATANQY
                                                       IIGQVGTDNSARVRQEGSKLLSVISQEGGNNRAKVDQ--AGNYNFAYIEQTGNANDASIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome sequence of Salmonella enterica serovar Typhimurium
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151 /
                                                                                                                  Conservative
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Pred.
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                                                                                                                                                                                                                                                    PROSITE; PS00142; ZINC PROTEASE; 1. Hydrolase; Metalloprotease; Glycopr Zymogen; Signal; Cell adhesion; GPI
                                                                                                                                                                                                                                                                                                                                     EMBL; M60048; AAA29244.1; -. HSSP; P08148; 1LML.
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                                   InterPro; IPR006025; Pept M_Zn_Bs.
InterPro; IPR001577; Peptidase_M8.
Pfam; PF01457; Peptidase_M8; 1.
PRINTS; PR00782; LSHMANOLYSIN.
                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: Binds 1 zinc ion per subunit (By similar-!- SUBCELLULAR LOCATION: Attached to the membrane by -!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Heterogeneity of the genes encoding of Leishmania donovani.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leishmania donovani.
Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                             MEROPS; M08.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Biochem. Parasitol. 48:173-184(1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=LV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5661;
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10-OCT-2003
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(Major surface
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  Local Similarity
                                                                                                                                                                                           SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the mammalian host. CATALYTIC ACTIVITY: Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: Binds 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEIDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                 590 AA;
                                                              25044
                                                                                                                 (Rel.
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Rel. 20, Last sec
Rel. 42, Last an
n precursor (EC:
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L.L., McMaster R.W.;
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t annotation update)
(EC 3.4.24.36) (Cell :
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similarity).
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ХВ)
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(BY SIMILARITY).
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P15706;
01-APR-1990
                                                                               Interru,

Pfam; PF01457; Peptidase

PRINTS; PR01782; LSHMANOLYSIN

PROSITE; PS00142; ZINC_PROTEASE; 1

PROSITE; PS00142; ZINC_PROTEASE; 1

PROSITE; PS00142; ZINC_PROTEASE; 1

PROSITE; PS00142; ZINC_PROTEASE; 1

PROSITE; PS00142; ZINC_PROTEASE; 1

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PROSITE; PS00142; ZINC_PROTEASE; 1

PROSITE; PS00142; ZINC_PROTEASE; 1

PROSITE; PS00142; ZINC_PROTEASE; 1
                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed during development of Leishmania promastigotes to an infectious form."; J. Biol. Chem. 267:1888-1895(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Leishmania gp63 molecule implicated Arg-Gly-Asp sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GP63
                                                                                                                                          InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptidase M8.
Pfam; PF01457; Peptidase M8; 1.
                                                                                                                                                                                                                       EMBL; M80672;
EMBL; M28527;
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MEDLINE=92112918; PubMed=1370484;
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Eukaryota; Euglenozoa;
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10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (I
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COFACTOR: Binds 1 zinc ion per subunit (By simi
SUBCELIULAR LOCATION: Attached to the membrane
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AAA29235.1; -.
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STRAIN=MNYC/BZ/62/M379;

MEDLINE=93149206; PubMed=8426614;

Medina-Acosta E., Karess R.E., Russell D.G.;

Medina-Acosta E, Karess R.E., Russell D.G.;

Medina-Acosta E, Karess R.E., Russell D.G.;

Medina-Acosta E, Karess R.E., Russell D.G.;

"Structurally distinct genes for the surface mexicana are developmentally regulated.";

Mol. Biochem. Parasitol. 57:31-46(1993).

-!- FUNCTION: Has an integral role during the property of the mammalian host.
EMBL; X64394; CAN45733.1; -.
PIR; S19916; S19916.
HSSP; P08148; ILML.
MEROPS; MO8.001; -.
GlycoSuiteDB; P43150; -.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; PeptIdase M8.
Pfam; PF01457; Peptidase M8; 1.
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01-NOV-1995 (Rel. 32, Last septence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin C1 precursor (EC 3.4.24.36) (Cell surface [(Major surface glycoprotein) (GP63 protein) (Promastigote
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Eukaryota; Euglenozoa;
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                                                                                                                                                                                                                                                                                                                       amastigote forms.
SIMILARITY: Belongs to
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Zymogen; Si
SIGNAL
                                                                                                                                                                                 Carroll J.D., Wallace R.C., Keane J., Arbeit R.D.;
"Identification of Mycobacterium avium DNA sequences
exported proteins by using phoA gene fusions.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databa-
!- FUNCTION: Required for binding-protein-mediated
transport (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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           This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are nuse by non-profit institutions as long as its comodified and this statement is not removed. Usage entities requires a license agreement (See http://worsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                 SEQUENCE FROM STRAIN=969A45;
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                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria;
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28-FEB-2003 (Rel.
10-OCT-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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PROSITE; PS00142; ZINC PROTEASE;
Hydrolase; Metalloprotease; Glyco
Zymogen; Signal; Cell adhesion; I
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1764;
                                                                                                                                                                                                                                                                                                                                               Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
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SIMILARITY: Belongs to the
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no protein 3 precursor (
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STRAIN=Ob:H1 / ... PubMed=1247113/,

( MEDLINE=22388234, PubMed=1247113/,

A Welch R.A., Burland V., Plunkett G. III, Redford r., ......

A Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Strow M.S., Schwartz D.C., Perna N.T.,

A Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

AN Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
77-2 fimbrial protein precursor (F7-2 pilin).
F7-2 OR PAPA OR C3592.
Escherichia coli, and
                                                                                                                                                                                                                                                                                         van Die I., Bergmans H.;
"Nucleotide sequence of the gene encoding a
a uropathogenic Escherichia coli strain.";
Gene 32:83-90(1984).
                                                                                                                                                                                   "DNA sequences of three papA genes from uropathogenic Escherichia coli strains: evidence of structural and serological conservation Infect. Immun. 59:3849-3858(1991).
                                                                                                                                                                                                                            Denich K., Bly O'Hanley P.D.;
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InterPro; IPR006059; SBP_E
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HSSP; P06128; 1A54.
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16-OCT-2001
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                                                                                                                                                  uredovora.";
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EMBL; M68060; AAA24278.1; -.
EMBL; M68060; AAA24278.1; ALT_INIT.
EMBL; AE016766; AAN82040.1; ALT_INIT.
PIR; A03496; YOECF2.
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                                                                                                                                                                                                                                               NCBI_TaxID=553;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        micrometers and numbering 100-300 per cell, enable bacteria to colonize the epithelium of specific host organs.
-i- SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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       PERIODICITY IS SUPERIMPOSED.

MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED SIMILARITY: Belongs to the bactarial income.
                                                              sci. Biotechnol. Biochem. 58:762-764(1994)
FUNCTION: Ice nucleation proteins enable
crystallization in supercooled water.
SUBCELLULAR LOCATION: Outer membrane.
DOMAIN: CONTAINS IMPERFECT REPEATS OF A (A.G.-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE
                                                                                                                                                                                                                                                                                                                 nucleation protein
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IPR000259; Fimbrial.
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proteins enable
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000258; Ice_nucleatn.

Pfam; PF00818; Ice_nucleation; 51.

PRINTS; PR003127; ICENUCLEATUN.

PROSITE; PS00314; ICE_NUCLEATION; 34.

Ice_nucleation; Repeat; Outer_membrane.

DOMAIN 162 993 OCTAPEPTIDE PERIODICITY.

SEQUENCE 1034 AA; 103378 MW; FA222523D333EADD CRC64;
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                                                                                                                                                                                                            58 ALQSDARKYDQLVTRV----VTHEMAHAGQGADNSTIELTQNGFRNNATID------
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033802 salmonella

Q7x243 citrobacter

Q7x240 citrobacter

Q8cw63 escherichia

Q7x237 enterobacte

Q54069 salmonella

Q99315 escherichia

Q89114 bradyrhizob

Q8eih3 shewanella

Q8eih3 shewanella

Q8eih3 shewanella

Q8eih6 sarobacteri

Q89116 bradyrhizob

Q9esaf2 arabidopsis

Q89116 bradyrhizob

Q9v885 prochloroco

Q88hg0 pseudomonas
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11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6		11.6	11.6	11.7	11.8	11.8	11.8	11.8	11.9	11.9	12.0	12.0	12.0	12.2	12.2	12.2	12.3	12.4	12.5	12.5	12.5
333	297	151	3552	3501	3056	1460	714	644	639	152	329	2734	1410	646	645	1408	644	151	91	480	1209	598	438	1422	2174	160	160	151
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Q8t986 drosophila	Q9ziy5 borrelia bu		σ			Q8k6b1 streptococc	Q7u5x6 synechococc	۳		Q7x241 citrobacter	7	Q89c73 bradyrhizob			Q7u1c5 mycobacteri	Q8e833 shewanella	O43994 leishmania		Q9s3j8 escherichia	•	Q89ck5 bradyrhizob	$\vdash$	Q82m56 streptomyce	Q8efu3 shewanella	_	_	Q8cw64 escherichia	Q7uczl shigella fl

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Q7X243;
01-OCT-2003
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                                                                                                                                                                                                                                            STRAIN=Fec4;
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                               Enterobacteriaceae;
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Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
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Q7X237;
01-0CT-2003
01-0CT-2003
  STRAIN=Fec39;
Zogaj X., Bok
                                                                                                                                                                                                 CSGA.
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Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna I
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete ge
of uropathogenic Escherichia coli.",
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                  SEQUENCE FROM
                                                                                           NCBI_TaxID=28141;
                                                                                                                          Enterobacteriaceae;
                                                                                                                                              Bacteria;
                                                                                                                                                                          Enterobacter sakazakii.
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MEDLINE=22388234; PubMed=12471157;
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(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                              Gammaproteobacteria;
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Last
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Romling
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Best Local S
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                                                                                                 Q9S3J5;
Q9S3J5;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virulence of Salmonella enteritidis in chickens correlates colony morphology and expression of SEF17 fimbriae."; Submitted (ARR-1996) to the EMBL/GenBank/DDBJ databases.
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STRAIN-SE30;
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                      Bacteria; Proteobacteria;
                                         Escherichia
                                                                                 Curlin subunit monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=592;
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7704 MW;
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Salmonella.
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Pred. No. 1.3e-17;
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7; Mismatches
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Matches 26
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Q89JI4;
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01-JUN-2003
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STRAIN-USDA 110;
MEDLINE-22484998; PubMed=12597275;
MEDLINE-22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kaneko T., Watanabe A., Idesawa K., Iriguchi M., Kawashima
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima
Sasamoto S., Watanabe A., Shimpo S., Tsuruoka H., Wada T., Yar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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MEDLINE=99314153; PubMed=10386375;
La Ragione R.M., Collighan R.J., Woodward M.J.;
La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia Coll 078:K80 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia Coll 078:K90 isolates associated "Non-curliation of Escherichia" isolates associated "Non-curliation of Escherichia" isolates associated "Non-curliation of Escherichia" isolates associated "Non-curliation of Escherichia" isolates associated "Non-curliation of Escherichia" isolates associated "Non-curliation of Escherichia" isolates associated "Non-curliation of Escherichia" isolates associated "Non-curliation of Escherichia" isolates associated "Non-curliation of Escherichia" isolates associated "Non-curliation of Escherichia" isolates associated "Non-curliation" isolates associated "Non-curliation" isolates associated "Non-curliation" isolates associated "Non-curliation" isolated "Non-curliation" isolated "Non-curliation" isolated "Non-curliation" is
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EMBL; AJI31756; CAB45380.1; -.
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LT-GQVGGSNSSLIGQIGANNTAGVGQLGILNGSTILQ
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                                                                                                                                                                                                                                                                                       MRITYLVATAIALSALTTVDAQAGNSASVLQFGTTNSSFISQTGSTSNNATTL---QFGA
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89.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 115; DB
Pred. No. 0.04
27; Mismatches
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Pred. No. 0.00
1; Mismatches
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.0019;
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                           Hypothetical
                                                                                        Nat. Biotechnol.
                                                                                                                                                                                                                                                                                                                            MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shewanella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8EIH4;
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                                                               AE015532; AAN53941.1;
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139 AA;
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  ll protein; Complete proteome.
502 AA; 52441 MW; D08CA23D6C46B62D
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AA;
                                                                                    20:1118-1123(2002)
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Paulsen I.T., Nelson K.E., Galdos E.J., Nelson W.C.,
J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Shewanella
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18; Mismatches
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Matches 40
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01-JUN-2002
01-JUN-2003
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                                                                                                          Hypothetical SEQUENCE 14
                                                                                                                                       PIR;
                                                                                                                                                     PIR;
                                                                                                                                                                                         Cielo C., Slater S., "Genome sequence of the plant Agrobacterium tumefaciens C58. Science 294:2323-2328(2001).
                                                                                                                                                                                                                                             Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullir Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                                                              Chapman P., Clendenning J., Deatherage G., Gillet W., Grant Kutyavin T., Levy R., Li M.-J., McClelland B., Palmiereri A. Raymond C., Rouse G., Senaphimmachak C., Wu Z., Romero Y., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., I Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., I Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8U6N9;
                                                                                                                                                                EMBL; AE009405; AAL45562.1; -. EMBL; AE008209; AAK88682.1; -.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                        "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein Atu4768. ATU4768 OR AGR_L_228.
                                                                                                                                                                                                                                                                                                                                                           Science
                                                                                                                                                                                                                                                                                                                                                                                                  Chumley F.,
Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobiaceae; Rhiz
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21608550; PubMed=11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                     H98144; H98144.
                                                                                                                                                  AD3143; AD3143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. Sr., an P., Clendenning J., Deatherage G., Gillet W., Grant C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43
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27; Mismatches
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C Q9SAF2;
C Q9SAF2;
C Q9SAF2;
T 01-MAY-2000 (TrEMBLrel. 13, Created)
T 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
T 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E 33F19.21 protein (Hypothetical protein).
N P3F19.21 OR ATIG13190, F3F19.21 OR ATIG13190.
N P3F19.21 OR ATIG13190, F3F19.21 OR ATIG13190.
S Arabidopsis thaliana (Mouse-ear cress).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
S Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicersids Tr
C Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
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MEDLINE-22484998; PubMed=12597275;
MEDLINE-22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Wada T., Yamada
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Bacteria; Proteobacteria;
Baradyrhizobiaceae; Bradyrh
NCBI_TaxID=375;
                                                                                                      SEQUENCE FROM N.A.
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Q1-JUN-2003
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Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Scker J., Theologis A., Davis R.W.;
                                                          Bradyrhizobium japonicum.
Bacteria; Proteobacteria;
Bradyrhizobiaceae; Bradyrh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0003676; F:nucleic acid binding; InterPro; IPR000504; RNA_rec_mot. Pfam; PF00076; rrm; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC007357; AAD31072.1; -.
EMBL; AY062527; AAL32605.1; -.
EMBL; BT002575; AA000935.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nguyen M., Southwick A., Tripp M., Palm C.J., Jones T., Wu T., Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya Deng J.M., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai Satou M., Seki M., Shinn P., Tang C.C., Toroumi M., Wong C., Wu H.C Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,
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Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn I
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
"Arabidopsis thaliana chromosome, 1 BAC F3F19 sequence.";
                                                                                                                                        Bl15298 protein.
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Southwick A., Karlin-Neumann
                                  NCBI_TaxID=375;
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Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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573 AA; 6
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EMBL; AP005954; BAC50563.1; -.
COmplete proteome.
SEQUENCE 154 AA; 15420 MW; 9D698D711E2EED19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=USDA 110;
MEDLINB=22404998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kaneko T., Nakamura Y., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7V8S5;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hemolysin-type calcium-binding region:RTX N-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete
SEQUENCE
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MEDLINE=2282569; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
Nature 424:1042-1047(2003).
EMBL; BX572095; CAE20431.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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21; Mismatches
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Search completed: March 11, Job time: 39.5 secs

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11.7	11.7	11.9	11.9	12.2	12.2	12.3	12.4	12.4	12.4	12.4	12.6	12.6	13.1	14.0	14.0	14.0	14.3	14.3	14.3
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ABG91039	ADD42761	ABP45119	AAB36344	AAW56163	AAU08231	ADE83865	ABB66232	AAB36328	AAB36336	AAB36323	AAO16497	ABR82645	ABR82649	AAB36319	AAB36324	AAB36340	AAB36337	AAB36327	AAB36322
Abg91039	Add42761	Abp45119	Aab36344	Aaw56163	Aau08231	Ade83865	Abb66232	Aab36328	Aab36336	Aab36323	Aao16497	Abr82645	Abr82649	Aab36319	Aab36324	Aab36340	Aab36337	Aab36327	Aab36322
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## ALIGNMENTS

RESULT 1

AAB36351 WPI; 2000-672631/65. N-PSDB; AAC64627. Salmonella enteritidis. Escherichia coli. Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; White AP, 05-APR-1999; 05-APR-2000; 2000WO-CA000356 12-OCT-2000. WO200060102-A2 Synthetic. vaccine; immune response; immunogen 26-FEB-2001 AAB36351; AAB36351 standard; AgfA::PT3#6 amino acid sequence SEQ ID NO:22 (UYVI-) UNIV VICTORIA. Doran JL, (first entry) 99US-0127888P protein; Collison SK, 151 ₽ Kay WW;

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmontala, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of the homologous species; (3) directing recombination of a recombination of a recombination of the homologous species, replacing the native

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RESULT 2
AAB36354
ID AAB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the golymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for cell citing an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live carcine, the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the arms.
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                              WPI; 2000-672631/65.
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Escherichia coli.
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Pred. No. 9.5e-68;
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Disclosure;

Page 138; 139pp; English

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)

CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene combinant gene combination of the chromosome of the homologous species replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comparising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA compression containing a replacement segment or segments of foreign amino concept and containing a replacement segment or segments of foreign amino concept and containing a replacement segment or segments of foreign amino concept and containing an immune response in an animal. In a fimbrial presentation containing an immune response in an animal. In a fimbrial presentation conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for conjunction with a carrier or diluent. (1) is useful for conjunction with a carrier or diluent. (1) is useful for conjunction and immal. In a fimbrial presentation conjunction with a carrier or diluent (1) is useful for conjunction and infinal. In a fimbrial presentation conjunction with a carrier such conjunction with a carrier or diluent. (1) is useful for conjunction and infinal. In a fimbrial presentation conjunction with a carrier or diluent. (1) is useful for conjunction and introducing the conjunction of the hybrid fimbrian are usually strong conjunction, the hybrid fimbrian are usually strong conjunction, the carrier fimbrial subunit proteins are usually strong conjunction, the conjunction of the normal invention. The present sequence is given in the companies of the normal invention.
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Best Local
                                                                                                                                                                                                                                                                                               Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR74625 standard;
                                                                               26-APR-1993;
                                                                                                                        26-APR-1994;
                                                                                                                                                                                                           WO9425598-A2
                                                                                                                                                                                                                                                      Salmonella.
                                                                                                                                                                                                                                                                                                                                          AgfA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                  (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                   10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SDARKSETTITQSGYGNGAD-----YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDI
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(first entry)
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                                                                               93US-00054452
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91.1%;
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Pred. No. 1.7e-61;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                    WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36341 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune respond Salmonella in animals (e.g. food producing animals) and humans. (Upo on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
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N-PSDB; AAQ87467.
                                                                                                                                                                                                                                                                                                                                                                      White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001
                                                                                                              Disclosure; Page 135; 139pp; English
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                                                                                                                                                                                                                                                                                                                                                                      Doran JL,
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Pred. No. 1.4e-58;
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RESULT 5
AAW23570
ID AAW2
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Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in given in the present sequence is given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the present sequence in given in the pres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
Collinson SK,
                                                                                                                                                                                                            03-JUN-1997
                                                                                                                                                                                                                                                                US5635617-A
                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW23570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW23570 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                           26-APR-1994;
                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the exemplification of the present invention
                                                   (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                       26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enteritidis 27655-3b agfA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
Kay
                                                                                                       93US-00054452
                                                                                                                                                           94US-00233788
                                                                                                                                                                                                                                                                                                                 /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.9%;
90.7%;
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Pred. No. 1.4e-58;
2; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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RESULT 6
AAB36355
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Best Local Similarity
                                N-PSDB; AAC64631.
                                                                         White
                                                                                                                         05-APR-1999;
                                                                                                                                                   05-APR-2000; 2000WO-CA000356
                                                                                                                                                                           12-OCT-2000
                                                                                                                                                                                                     WO200060102-A2
                                                                                                                                                                                                                                           Escherichia
                                                                                                                                                                                                                                                      Salmonella enteritidis.
                                                                                                                                                                                                                                                                                             Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                  (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                                                                                                   AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                               AAB36355 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                              26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated Salmonella gene agfa - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 7; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-309886/28
N-PSDB; AAT74142.
                                               2000-672631/65
                                                                         ΑP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136;
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                                                                                                                                                                                                                                                                                la; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNPALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                      Doran JL,
                                                                                                                                                                                                                                          coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                         99US-0127888P
                                                                                                                                                                                                                                                                             response;
                                                                                                                                                                                                                                                                                         chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.2%;
                                                                       Collison
                                                                                                                                                                                                                                                                                immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 677; DB 2;
Pred. No. 4.4e-58;
2; Mismatches 13
                                                                      Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                            CC The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbria gene into the chromosome of the CC homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native CC comprising segarating an amino acid polymer comprising a recombinant AgfA grotein containing a replacement segment or segments of foreign amino CC comprising separating an amino acid polymer comprising a recombinant AgfA grotein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for extern the host cell and introducing the polymer the heaterologous sequences are presented in the combinant.
                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                                                 system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                            Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein useful for eliciting immune response
  119
                                106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                   136;
                                                                                             61
                                                                                                                                         61
                                                                                                                                                                                                                                    μ.
                                                                                                                                                                                                                                                                                 Similarity 81.
                                                                                                                           SDARKSETTITQSGYGNGADVGQGADN------
                                                                                                                                                                                   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 139; 139pp;
                                                                                                                                                                                                                                                                                                                                                                            A,
                                                                                                                                                                                                                                                                                                       84.7%;
-GGNNAALVNOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                            Score 657; DB
Pred. No. 4e-5
0; Mismatches
                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                    4e-56;
                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                        Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       animal.
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                    YDOLVTRVVTHEMAHADO 105
                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                   60
                                                                                                                                                                                                                                    60
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## Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope AgfA::PT3#5 26-FEB-2001 AAB36350; AAB36350 standard; protein; 151 amino acid sequence SEQ ID NO:20 (first entry) Ą

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA

05-APR-2000; 2000WO-CA000356

12-OCT-2000

WO200060102-A2

Escherichia coli. Synthetic. Salmonella enteritidis.

vaccine;

immune

response;

immunogen

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ARBSULT 8
AAB36352
ID AAB3
XX
AC AAB3
XX
DT 26-F
XX
XX
DE AgfA
XX
XX
XX
VACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directing recombination of a recombinant gene into the chromosome of the CC homologous species; (3) directing recombination of a recombinant gene coback into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA CC comprising a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live carcine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and consense to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella, Escharichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
                                                          AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                     26-FEB-2001
                                                                                                                                                                                      AAB36352 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 137; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                  104
                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                     -----DQWNAKNSDITVGQYGGNNAALVNQTASDSSYMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                              SDARK----
                                                                                                                                                                                                                                                                                                                                                                                                                SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA------
                                                                                                                                                                                                                                                                                           NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                   (first entry)
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                                                                                                                                                                                   protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 619; DB 3
Pred. No. 2e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 128; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 138; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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121
                                                             86
                                                                                                                                 61
                                                                                                                                                                                                     61
                                                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGAD------
                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                             HEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               78.5%;
73.6%;
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                                                                                                                                 /GNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
                                                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                              Score 609; DB 3;
Pred. No. 1.9e-51;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                         NYDQLVTRVVT
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                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                             The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA grotein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC interobacteriaceae host cell, from the host cell and introducing the CC useful for the expression of recombinant AgfA protein which is useful for CC useful for the expression of recombinant AgfA protein which is useful for CC system the heterologous antigens are presented in high numbers (up to colimonogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC inexpensive to purify in large amount. The present sequence is given in CC the exemplification of the present invention.
                                                                                         Best
                                                                                                           Query Match
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                          inexpensive to purify in large amount. The present sequence the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#1 amino acid sequence SEQ ID NO:12
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                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-672631/65.
                                                                                           Similarity
                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                           151 AA;
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosomal gene replacement; fimbrin; epitope;
                                                                                     77.8%;
80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collison
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                                                                         6
                                                                                       Score
Pred.
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                                                                       Mismatches
                                                                                       No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kay WW;
                                                                     DB 3; 1
5.9e-51;
1es 23;
                                                                                                      Length 151;
                                                                       Indels
                                                                    0
                                                                    Gaps
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CC copy of that gene; and (4) eliciting an immune response in an animal. CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for coliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response consist the inserted epitope, and hybrid fimbriae are easy and consequence is given in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
AAB36347
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                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 136; 139pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SK,
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RESULT 11
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Best Local Similarity 81.9
Matches 123; Conservative
The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinantion of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing an immune response in an animal, comprising separating an amino acid polymer comprising a replacement acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                 White AP,
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                                                                                                                                                                                                                           Disclosure; Page 138; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                               Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid sequence SEQ ID NO:26
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Pred. No. 9.3e-51;
5; Mismatches 23
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RESULT 12
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Matches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgfA::PT3#4 amino acid sequence SEQ ID NO:18
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                                                                                                                                                                                                                                                       2000-672631/65.
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                                                                                                                                                                                                                                                                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coli.
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                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127888P
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                                                                                                                                                                                                                                                                                                        Collison
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Pred. No. 1.2e-
4; Mismatches
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                                                                                                                                                                                                                                                                                                        SK,
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No. 1.2e-50;
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign DI sequence which encodes a foreign epitope or antigen. Also describe

Also described

DNA

Disclosure; Page 136; 139pp; English

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

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RESULT 13
AAB36348
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WPI; 2000-672631/65
                                                    White AP,
                                                                                                                                                              05-APR-1999;
                                                                                                                                                                                                           05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella;
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                                                                                                         (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKLLKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                  Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                     coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                              99US-0127888P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.3%;
81.5%;
                                                  Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 600; DB
Pred. No. 1.5e
5; Mismatches
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                                                    XS,
                                               Kay WW
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.5e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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WO200060102-A2

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RESULT 14
AAB36343
ID AAB3
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CC directing recombination of a recombinant gene into the chromosome of the
CC homologous species; (3) directing recombination of a recombinant gene
CC back into the chromosome of the homologous species, replacing the native
CC comprising separating an amino acid polymer comprising a recombinant
CC protein containing a replacement segment or segments of foreign amino
CC acid sequence or sequences grown on a Salmonella, E. coli or
CC Enterobacteriaceae host cell, from the host cell and introducing the
CC polymer into the animal in conjunction with a carrier or diluent (I) is
CC useful for the expression of recombinant AgfA protein which is useful for
CC eliciting an immune response in an animal. In a fimbrial presentation
CC system the heterologous antigens are presented in high numbers (up to
CC immunogenicity and adhesion properties relevant for an efficient live
CC vaccine, the carrier fimbrial subunit proteins are usually strong
CC immunogens, which may be important for directing an immune response
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Best Local S
Matches 122
                                                                                               Escherichia coli
                                                                                                                                          vaccine;
                                                                                                                                                         Salmonella; agfA;
                                                                                                                                                                                                 Escherichia coli CsgA amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                         26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                    AAB36343;
                                                                                                                                                                                                                                                                                                                        AAB36343 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SET17/MAF) nucleation depended assembly system of strains of Sahmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a recombinant agfA gene segment of the gene has been replaced by a segment of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAC64624
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                                                                                                                                          1mmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNOTASDSSVMVROVGFGNNATANOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVYDOLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                        response;
                                                                                                                                                         chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.1%;
80.8%;
                                                                                                                                          immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.
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Pred. No. 2.4e-47;
5; Mismatches 24
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n foreign DN
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05-APR-2000;

2000WO-CA000356

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RESULT 15
ABR82651
ID ABR82
XX
AC ABR82
XX
DT 04-DE
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DE E. CO
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC segment of the gene has been replaced by a segment of a foreign DNA C sequence which encodes a foreign epitope or antigen. Also described are: C(1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombinant gene comprising the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino card sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or coliverbacteriaceae host cell, from the host cell and introducing the polymer into the expression of recombinant AgfA protein which is useful for segments on a minal. In a fimbrial presentation conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to compression), the hybrial fimbrial protein possesses both the carrier fimbrial subunit proteins are usually strong communogenicity and adhesion properties relevant for an efficient live vaccine, the inserted sentence and hybrial fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                  E. coli CsgA subunit 15 kDa protein.
                                                         04-DEC-2003
                                                                                                                                    ABR82651 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                               ABR82651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-672631/65
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                                                                                                                                                                                                                                                                        NNAALVNOTASDSSVMVROVGFGNNATANOV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AA;
                                                                                                                                                                                                                                       GNGAAVDOTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                                  TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 135; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 521; DB
Pred. No. 7.5e-
17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
7.5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
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Best Local
                                                                                                                                                Matches
                                                                                                                                                                                                                                             The invention relates to an isolated peptide capable of binding a mammal manmalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                              or Shigella infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2002; 2002GB-00002275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasma protein; immune response; antibacterial; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                     15 kDa protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-646136/61.
   121
                                                                                                                                                104;
                              61
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                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACF36153.
                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQVGGGGNHNGGGNSSGPDSTLSIYQYGGSNAALALQ
                                                                                                                                                                                                         151
                                                SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
   NNAALVNQTASDSSVMVRQVGFGNNATANQY
                              TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olsen A,
                                                                                                                                                Conservative
                                                                                                                                                                                                         ₽,
                                                                                                                                                              66.5%;
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                                                                                                                                                17;
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Pred. No. 2.
                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herwald
                                                                                                                                                              DB 7;
                                                                                                                                                  30;
                                                                                                                                                                            Length 151;
                                                                                                                                                  Indels
                                                                                                                                                0;
                                                                                                                                                Gaps
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Search completed: March 11, Job time: 51.9 secs

121

GNGAAVDQTASNSSVNVTQVGFGNNATAHQY

151

THIS PACE BLANK (USPTO)

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                677
497
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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776
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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             GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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          US-08-233-788A-59
US-08-233-788A-57
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US-09-495-880A-42
US-09-59-8477-180
US-09-556-877-180
US-09-556-877-180
US-09-588-419-180
US-09-489-039A-7849
US-09-489-039A-7849
US-09-252-991A-24717
US-09-252-991A-2658
US-09-072-591A-2658
US-09-336-115C-6
US-09-336-115C-6
US-09-336-115C-6
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Sequence 337, App
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Sequence 180, App
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Sequence 180, App
Sequence 7849, Ap
Sequence 24717, A
Sequence 24717, A
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Sequence 191, App
Sequence 192, App
Sequence 204, App
Sequence 204, App
Sequence 214, App
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIXQXGSANAALALQ

Query Match 87.2%; Score 677; DB 1; Length Best Local Similarity 90.1%; Pred. No. 3.3e-59; Matches 136; Conservative 2; Mismatches 13; Inde	US-08-233-788A-59  iSequence 59, Application US/08233788A  Patent No. 5635617  iGENERAL INFORMATION: APPLICANT: Kay, William W. APPLICANT: LOINEON, Karen S. APPLICANT: COllinson, Karen S. APPLICANT: Clouthier, Sharon C. TITLE OF INVENTION: OF SALMONELLA NUMBER OF SEQUENCES: 61  CORRESPONDENCE ADDRESS: ADDRESSE: Seed and Berry STREET: 6300 Columbia Center, 701 Fifth Avenue STATE: Washington COUNTRY: U.S.A. ZIP: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,788A FILING DATE: 26-APR-1994 CLASSIFICATION NUMBER: 920043.403C2 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 682-6031 TELEPHONE: (206) 682-6031 TELEPHONE: 151 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: protein	28 78 10.1 878 4 US-09-540-236-3401 29 78 10.1 1216 4 US-09-134-000C-5130 30 77.5 10.0 212 4 US-09-125-619-32 31 77.5 10.0 437 2 US-08-737-716-2 32 77.5 10.0 673 4 US-09-196-387-8 33 77.5 10.0 702 4 US-09-252-991A-22119 35 77.5 10.0 941 4 US-09-36-447A-9 36 77.5 10.0 949 3 US-09-196-387-10 37 77.5 10.0 949 3 US-09-196-387-10 38 77.5 10.0 1327 4 US-09-841-835-10 39 77.5 10.0 1327 4 US-09-841-835-2 40 77.5 10.0 1327 4 US-09-841-835-2 40 77.5 10.0 1327 4 US-09-841-835-2 41 77.5 10.0 1327 4 US-09-972-115A-8 42 77 9.9 266 4 US-09-972-115A-8 43 77 9.9 339 4 US-09-495-880A-26 44 77 9.9 339 4 US-09-252-991A-32096 45 77 9.9 1139 1 US-08-537-210A-4
ngth 151; Indels 0; Gaps 0;	DETECTION	Sequence 3401, Ap Sequence 5130, Appl Sequence 32, Appl Sequence 2, Appli Sequence 8, Appli Sequence 8, Appli Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 36, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli

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US-08-864-038A-3
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US-08-233-788A-57
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Sequence 3, Application US/08864038A Patent No. 6001592 GENERAL INFORMATION:
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Best Local
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APPLICANT: Doran,
APPLICANT: Kay, W.
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APPLICANT: Clouthier
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
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ADDRESSEE: Seed and Berry
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                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92
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98104-7092
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5635617
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GY: linear
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                                                                                                                  GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
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Kay, William W.

Collinson, Karen S.

Clouthier, Sharon C.

NVENTION: METHODS AND CO.

NVENTION: OF SALMONELLA
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N: 435
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87.5%;
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Pred. No. 1.2e-41;
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US-09-336-447A-5

Sequence 5, Application US/09336447A Patent No. 6310190

GENERAL INFORMATION:

APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.

COPE, LESLIE D. MACIVER, ISOBEL

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: '22,389
REFERENCE/DOCKET NUMBER: F-56
TELECOMMUNICATION INFORMATION:
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ORIGINAL SOURCE:
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FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184459
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CURRENT APPLICATION DATA:
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TTTY: Tsu-city
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LOCATION:
                                                                                                                                                                                                                           Local Similarity 27.6
10s 43; Conservative
                                                                                                                                                                                                                                                                                                                      NAME/KEY: peptide LOCATION: from 1 to 738 IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Com
OPERATING SYSTEM:
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508 SAAAAAAAAAASGGGGRALRRALRROMRGGGSAAA 543
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                                 NAALVNQTASDSS-----VMVRQVGFGNNATA 148
                                                                                                          ARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDI-TVGQYGGN 121
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VERVION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

VERVION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

VERVION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
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CURRENT APPLICATION NUMBER: US/09/336,447A;
CURRENT FILING DATE: 1999-06-21;
NUMBER OF SEQ ID NOS: 98;
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 5;
LENGTH: 892
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-336-447A-5
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US-09-495-880A-42
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SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 42
LENGTH: 238
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                             Query Match
Best Local S
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Patent No. 6667150
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Best Local :
                                                                                                                                                                                                                                                                                                                -09-495-880A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/495,880A
CURRENT FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: PCT/EP98/04836
PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: EP 97 11 3319.4
PRIOR FILING DATE: 1997-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC TITLE OF INVENTION: (POLY) PEPTIDE COMPLEX FILE REFERENCE: MORPHO/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: RUDERT, FRITZ
APPLICANT: GE, LIMING
APPLICANT: ILAG, VIC
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APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                       PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-peptide3-
OTHER INFORMATION: gene IIIs encoded by phage vector fpep3_1B-IR3seq (circular)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: AMCY: 024
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGDYNEAKGNYSTVGGGSSNTAKGEKSTIGGGDTN-----DANGTYSTIGGGYYSRA 141
                                                                                      YQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWN 107
AKNSDI-----TVGQYG-----GNNAALVNQTA----SDSSVMVRQVGFGNNA 146
                                              ---GSGGGSEGGGSEGGGSEGG-GSGGGSGSGDFDYEKMANANKGAMTENADE-N 110
                                                                                                                                    KTAIAIAVALAGFATVAQADYKDVDCIVYHAHYLVAKCGGGGSEFNAGGGSGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG---GNNAALV----N
                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                             11.1%; Score 86.5; DB 4; Length 238; 24.3%; Pred. No. 0.69;
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US-09-598-419-337
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US-09-620-412C-337
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CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASESEQ for Windows Version 3.0/4.0
SEQ ID NO 337
LENGTH: 585
                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 357

SOFTWARE: FASTSEQ for Windows Version 3.0/4.0

SEQ ID NO 337

LENGTH: 585

TYPE: PRT
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Scholler, John
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APPLICANT: Steven P. Fling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.469C6
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/598,419
                                                                                                                                                                                                                                                                                           ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Chlamydia trachomatis
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                                        258 GLYTDKNLSITNITGIIEIANNKATDVGGGA-----YVKGTLTCENSHRLQFLKNSSDKQ 312
                                                                                                                  206 LKAQASAG---NADAWASSSPQSGSGATTVSDSGDSSSGSDSDTSETVPVTAKGG---- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 GLYTDKNLSITNITGIIEIANNKATDVGGGA----
                                                                           58 ALQSDARKSETTIT----QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 ALQSDARKSETTIT----QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
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                                                                                                                                                         4 LKVAAFAAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL 57
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Pred. No. 2.2;
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US-09-620-412C-180
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SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 180
                                                                                                                        Matches
                                                                                                                                                      Query Match
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SOFTWARE: FastSEQ for
SEQ ID NO 180
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                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/620,412C CURRENT FILING DATE: 2000-07-20
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL
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                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 210121.469C7
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CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Chlamydia
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
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ORGANISM: Chlamydia
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                                                                                                                                                                                                                                       LENGTH: 1752
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                                                                                                                                    Local Similarity
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58 ALQSDARKSETTIT---QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
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                                                                             LKVAAFAAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL
                                                  LKAQASAG----NADAWASSSPQSGSGATTVSDSGDSSSGSDSDTSETVPVTAKGG-----
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Fling, Steve
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                                                                                                                                   Score 86.5;
Pred. No. 9;
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                                                                                                                                                  DB 4;
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                                                                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-7849
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US-09-598-419-180
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SEQ ID NO 7849
LENGTH: 589
                                                                                                                      Query Match
Best Local Similarity
Matches 32; Conservat
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APPLICANT: Skeiky, Yang APPLICANT: Scholler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Gary Br
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SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 180
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
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CURRENT FILING DATE: 2000-06-20
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TYPE: PRT
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                                       259 GGLDRNGANANGQTDTFGIYAFDTLTLTERIEINGGLRLDNYHTKYDSATACGGSGRGAI 318
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o. 6610836
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VGQGADNYDQLVTRVVTHEMAHADQWNA-----KNSDITVGQYGGNNAALVNQTASDS 133
                                                                             GGNHNGGGNSSGPDSTLSIYQYGS------ANAALALQSDARKSETTITQSGYGNGAD 80
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                                                                                                                      11.0%; Score 85.5; Dilarity 23.2%; Pred. No. 2.8; Conservative 17; Mismatches
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31.6%; Pred. No. 9;
ative 12; Mismatches
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US-09-328-352-4764
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// ORGANISM: Acinetobacter baumannii
US-09-328-352-4764

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LENGTH: 461
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SEQ ID NO 4764
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APPLICANT: GATY L. Breton et al.

APPLICANT: GATY L. BYETON ET AL.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04
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                                                                        Matches
                                                                                         Query Match
Best Local
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Best Local Similarity
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Patent No. 6562958
                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-02-10
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR ETITING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE:
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                                                                                                                                                                                   TYPE: PRT
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                                 6 VAAFAAIVVSG-SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANA---ALALQS
                                                                        43;
                                                                                         Similarity
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VAALPEVARSGPGAPSGTAPAGGGAA---GGKSPAGLGRLARRSSFPSSSATPPAATTYF 356
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1998-02-18
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Pred. No. 12;
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30710
LENGTH: 812
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SEQ ID NO 26658
LENGTH: 1034
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GENERAL INFORMATION:
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                                                                                                  Best
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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                                       14 VSGSALAGVVPQWGGGGNHNG-----GGNSSGPDSTLSIYQYGS-ANAALALQSDAR-- 64
                                                                              47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 GSANAALALQSDARKSE-----TTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHAD 104
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                                                                                                Similarity
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  VSDSSASGQV-EAGGAGNTGGLVGLSSGGEIFRSQASGSVYSKGGLATGGLIGKAEGNGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                marc J. Rubenfield et al.
rention: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
rention: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                              Conservative
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                                                                                                10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.3%;
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                                                                            19;
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Pred. No.
                                                                                                Score 80;
Pred. No.
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                                                                                                                   DB 4;
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                                                                                62;
                                                                                                                     Length 1034;
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Search Job ti	皮	8	Дb	Ş
Search completed: March 11, 2004, 18:44:52 Job time : 13.4 secs	864 SVAHAISRGDVSGGFNS-LVGGLVGHNGGELVNVDASGRVSAAASASVGGLVGSNA 918	96 -VTHEMAHADQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNA 146	807 LGNLKASGSVTDQGGADLGGLVGNNSQSAIETAEATGKVSGGSNSRVGGLIGHNLGG 863	65KSETTITQSGYGNGADVGQGADNYDQLVTRV95

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Result
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                       Score
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1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

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15: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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10 US-09-880-748-1130

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10 US-09-880-748-1122-

10 US-09-880-748-1122-

10 US-09-952-267-5

9 US-09-841-132-180

10 US-09-841-132-180

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Sequence 20638, A
Sequence 145, App
Sequence 445, App
Sequence 594, App
Sequence 5122, Ap
Sequence 20619, A
Sequence 5, Appli
Sequence 180, App
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence 1153, Ap
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10.1	10.1	10.1	10.1	•	10.1	10.2	•				10.2	10.2	10.2	10.2	10.2	0	0	0	10.4	0	10.4	0	10.5		10.6	10.6	0	10.7	10.7
745	252	251	246	209	209	943	943	943	943	943	255	254	247	2834	2732	2338	688	251	252	251	255	65	253	252	470	256	254	254	254
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US-08-834-666A-6	US-09-880-748-1537	US-09-880-748-1554	US-09-880-748-1286	US-10-143-024-42	US-10-222-162-42	US-10-084-843-204	US-10-193-002-199	US-09-997-181-131	US-09-997-182-131	US-09-996-634-131	US-09-880-748-1539	US-09-880-748-1466	US-09-880-748-2127	-10-	US-10-238-075-1119	-10-029	US-10-032-585-7876	US-09-880-748-1216	US-10-151-882-14	US-09-880-748-1011	US-09-880-748-1281	US-09-996-194-16	US-09-880-748-1850	US-10-151-882-13	US-10-156-761-10459	880-748	US-09-880-748-1226	US-09-880-748-1165	US-09-880-748-1136
Sequence 6, Appli	1537,	1554,	1286	42,	42,	204,	199	131	e 131	131, Aç	153	1466,	2127	252, 1		31982,	7876,	1216	14, A	1011,	12	16, Apj	1850	Sequence 13, Appl	10459,	1209,	12	1165,	Sequence 1136, Ap

## ALIGNMENTS

US-10-369-493-20638

Sequence 20638, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory G.
APPLICANT: Glater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITITLE OF INVENTION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/60,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLING DATE: 2002-02-21
NUMBER OF SEG ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
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                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                               ORGANISM: Rhodopseudomonas palustris FEATURE: FEATURE: NAME/KEY: unsure LOCATION: (1)...(445)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
69 TITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQW-NAKNSDITVGQ---YGGN-NA 123
                                                                                                                          30 GNHNGGGNSS-----GPDSTLSIYQYGSANAA-----
                                                                           GKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTNDPGVFNKITQDSSSNGSKV 148
                                                                                                                                                                               Conservative
                                                                                                                                                                                                    12.2%; Score 95; DB 15; Length 445; 24.6%; Pred. No. 0.25;
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                               CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                           Sequence 1130, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.2%; Score 95; DB 9 Best Local Similarity 27.4%; Pred. No. 0.36;
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SEQ ID NO 146
LENGTH: 597
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Patent No. US20020098200A1
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                                                                                                                                                                                                                                                             APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: of Tuberculosis
TILE REFERENCE: 014058-008740US
CURRENT FILING DATE: 2001-02-26
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR APPLICATION NUMBER: US 60/23,828
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Campos-Neto, Antonio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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         APPLICATION NUMBER: 60/293,499
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; Sequence 594, Application US/09841132
; Patent NO. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INI
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
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US-09-880-748-1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 445
LENGTH: 1751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 445, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID. NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1130
LENGTH: 251
TYPE: PRT
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469CB
CURRENT FILLING DATE: 2001-04-23
CURRENT FILLING DATE: 2001-04-23
CURRENT FILLING DATE: 2001-04-23
CURRENT FILLING DATE: 2001-04-23
CURRENT FILLING DATE: 2001-04-23
CURRENT FILLING DATE: 2001-04-23
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TYPE: PRT
ORGANISM: Chlamydia trachomatis serovar
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tes 40; Conserv
                                                                                                                                                                                                                                                                                                                                                   508 T 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 NADAWASSSPQSGSGATTVSNSGDSSSGSDSDTSETVPATAKGG-GLYTDKNLSITNITG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 QRVTMSCSGSSSNIGSNTVNWYQQLPGAAPKLLIYRSDQRSSGVPDRFSGSKSGTSASL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 -- QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ-YGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 SGSALAGVVPQWGGGGN--HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TTITQSGYGNGADVGQGADN-YDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAAL 125
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27.7%;
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33.1%; Pred. No. 3.5;
ive 10; Mismatches 5
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Pred. No. 0.22;
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                                                                       FOR TREATMENT INFECTION
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507

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RESULT 7
US-10-369-493-20619
; Sequence 20619, Application US/10369493
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SEQ ID NO 1122
LENGTH: 251
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SOFTWARE: FRANCED for Windows Version 3.0/4.0
SEQ ID NO 594
LENGTH: 1751
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Best Local (
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
-09-880-748-1122
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
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NUMBER OF SEQ ID NOS: 3239
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PF523
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                                                                                                                                                                             156 QRVTISCS--GSASNVGNNAVNWYQQLPGKPPKLLIYYDDLLPSGVSDRFSGSKSGTSAS
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                                                                                                                                                                                                              66 SETTITQSGYGNGADVGQGADN-YDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAA 124
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Similarity 28.9%;
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                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 0.43;
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Pred. No. 3
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; NAME/KEY: unsure
; LOCATION: (1)..(486)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-20619
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                                                         Query Match
Best Local S
Matches 38
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20619
LENGTH: 486
                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 5
LENGTH: 892
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Publication No. US20030032772A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local:
                                                                                                                                                                                                                                                 APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/952,267
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/336,447
PRIOR FILING DATE: 1999-66-21
NUMBER: OF SEQ ID NOS: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXCRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
                                                                                                                                                         ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                TYPE: PRT
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28 GGGNHN-------
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                                                           38;
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                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- QYGGNNAALVNQTASDSSVM 136
                                                         11.2%; Score 87; DB ilarity 26.8%; Pred. No. 3.8; Conservative 15; Mismatches
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24;
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Pred. No. 1.6;
24; Mismatches
                                                                                                DB 10;
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                                                             Indels 32;
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                                                             Gaps
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RESULT 10
US-09-841-132-180
                                                                               ; ORGANISM: Chlamydia
US-09-841-132-180
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US-09-841-132-337
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Patent No. US20020061848A1
GENERAL INFORMATION:
     Matches
                                         Query Match
                                                                                                                                  SEQ ID NO 180
LENGTH: 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 337 LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 337, Applic Patent No. US2002006 GENERAL INFORMATION:
                                                                                                                                                                                                          APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL
FILE REFERENCE: 210121.46908
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                    NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yas
APPLICANT: Probst, Pet
                                                                                                                    TYPE: PRT
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   Local Similarity nes 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 VGQ-YGGNNAALVNOT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 GLYTDKNLSITNITGIIEIANNKATDVGGGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 LKAQASAG---NADAWASSSPQSGSGATTVSDSGDSSSGSDSDTSETVPVTAKGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 ALQSDARKSETTIT---QSGYGNGADYGQGADNYDQLYTRVVTHEMAHADQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LKVAAFAAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGIYGEDNITLSNLT 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probst, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGDSSTIGGG--YYNQATGEKSTVAGGRNNQATGNNSTVAGGSYNQATGNNSTVAGGSHN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG---GNNAALV----N 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.1%; Score 86.5; Di
ilarity 31.6%; Pred. No. 2.5;
Conservative 12; Mismatches
   Conservative
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                 11.1%;
   12;
                   Score 86.5; I
Pred. No. 10;
   Mismatches
                                     DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --YVKGTLTCENSHRLQFLKNSSDKQ 312
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                                     Length 1752;
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   Indels
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23;
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Gaps
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, NAME/KEY: misc_feature
; OTHER INFORMATION: PPE
; NAME/KEY: misc_feature
; OTHER INFORMATION: gi|1781260
US-09-820-843A-21
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                                                                            US-09-880-748-2098
                                                                                             RESULT 12
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US-09-820-843A-21
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Sequence 2098, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
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Publication No. US20030039933A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR T
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 354
TYPE: PRT
ORGANISM: M. tuberculosis
                                                                                                                                                  289 TSMFGGNSGVLNTGYGNSGFYNAAVNNTGIFVTGVMSSGFFNFGTGN
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                                                                                                                                                                                                                                                              55 AALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                    10 AAIVVSGSALAG-VVPQWGGGGNHNGGG-----NSSGPDSTLSIYQYGSAN
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                                                                                                                                                                                                                         SGFGHNDPAGSGNSGIQNSGFGNSGYVNTS---
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                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                           Score 85; DB
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             10; Length 354;
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523 CURRENT APPLICATION NUMBER: US/09/880,748 CURRENT FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: 60/212,210 PRIOR FILING DATE: 2000-06-15 PRIOR FILING DATE: 2000-06-15 PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21

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                                                     RESULT 14
US-09-880-748-1494
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US-09-880-748-2098
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Matches
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 2098
LENGTH: 253
              Sequence 1494, Application US/09880748 Publication No. US20030059937A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn
SEQ ID NO 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1153, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
GENERAL
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/240,816
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 255
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Local Similarity 26.2%;
les 34; Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/277,379 FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/293,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 PDRFSGSKSD 211
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                                                                                                                                  154
                                                                                                                                                                                                              104 ILTGYYMGSAFDQWGKGTMVTVSSGGGGSGGGGGGGGG
                                                                                                                                                                     64 RKSE-TTITOSGYGNGADVGOGADNY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 NAALALQSDARKSE-TTITQSGYGNGADVGQGADN--YDQL---VTRVVTHEMAH----- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 AVFYCVREGGGDAYDVAPYYFDYWGQGTLVTVSSGGGGGGGGGGGGG
                                                                                                                                                                                                                                                    13 VVSGSALAGVVPQWG-----GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AAFAAIVVSGSALAGVVP----QWG------GGGNHNGGGNSSGPDSTLSIYQYGSA 53
                                                                                                                                SGAPGQRVTISCTGSSSNIGAGYDVY 179
                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                              10.8%;
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                                                                                                                                                                                                                                                                                         11; Mismatches
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Pred. No. 1.6;
16; Mismatches
                                                                                                                                                                                                                                                                                                            Score 84; DB
Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                              Length 255
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US-09-880-748-1199
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                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-880-748-1199
                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
SEQ ID NO.1199
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1199, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ruben et al. TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 257
                                                                                                                            Local Similarity
les 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 10.8%;
Local Similarity 28.6%;
                                          107 VTARWGMDVWGQGTLVTVSSGGGGGGGGGGGGGGG------GSAQAVLTQPSSASGTP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 ILTGYYMGSAFDQWGKGTLVTVSSGGGGSGGGGGGGGGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 SGAPGQRVTISCTGNSSNIGAGYEVHWYQLV 184
    83
                                                                                    22 VVPQWG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 RKSE-TTITOSGYGNGADVGQGAD-NYDQLV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 VVSGSALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
  -TTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA-DQWNAKNSDITVGQYGGNNAAL 125
                                                                                                                              Conservative
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                                                                                                                                              10.7%; Score 83; DI
25.8%; Pred. No. 2;
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                                                                                                                              13;
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Pred. No. 1.8;
13; Mismatches
                                                                                  -GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSB
                                                                                                                              Mismatches
                                                                                                                                                                    DB 10; Length 253;
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                                                                                                                              Gaps
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Db 157 GQRVTISCSGSSSNIGSNVINWYQQLPRTAPKLLIHTNDQRPSGVPDRFSGSKSGTSGTL 216

Search completed: March 11, 2004, 19:18:38

Job time : 24.6 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          Database :
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Maximum DB seq length: 2000000000
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Perfect score:
PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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776
                                                                                                                                                                                                                                                                            283366 seqs, 96191526 residues
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                             283366
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# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result	Score	Query Match	% Query Match Length DB	Ú	IJ	tion
1	682	87.9	:	2	JC6039	fimbrin protein ag
2	682	87.9	151	N	AI0635	major curlin chain
ω	521				S70788	curlin protein csg
4	499.5	64.4			D90806	curlin major subun
S	499.5	64.4			H85665	hypothetical prote
0	109	14.0			842136	
7	109	14.0			E95965	hypothetical glyci
æ	102	13.1			T26667	
9	98	12.6			E70663	
10	95	•		N	E70946	PPE
11	94	12.1		N	T21956	hypothetical prote
12	•	•		N	AD3143	₩
13		12.0		N	H98144	hypothetical prote
14		12.0		N	F70825	probable PPE prote
15	93.5	12.0		N	S11672	ice nucleation pro
16		11.9	151	N	S70787	curlin nucleator p
1 /	92.5	11.9		۸ (	60806	minor curlin subun
1 0	32.0	11.9		) V	103143	curiti minor chain
20	91.5	11.8	1258	N I	J00188	ice nucleation pro
21	Ψ	•		N	G71518	hypothetical prote
22	90.5	11.7		N	JC6040	fimbrin protein ag
23	90.5	11.7		N	AH0635	nucleation compone
24	90.5	11.7		N	B70987	probable PPE prote
25	89.5	٠		N	S07053	ice nucleation pro
26	89	11.5		N	835327	protein kinase sgg
27	87	•		N	D96010	hypothetical expor
	2					
28	c	11.2		N	E70768	hypothetical glyci

# ALIGNMENTS

				,				
Q	g Q	dg V	Query Maest Lou	C; Function: A; Descripti A; Note: fin C; Keywords: F; 1-20/Doma F; 21-151/Pr	A; Accession A; Molecule t: A; Molecule t: A; Residues: A; Note: sequ C; Genetics: A; Gene: agfA	A, Experimen A, Note: the R, Collinson J. Bacterio A, Title: Pu A, Reference A, Contents:	A;Access A;Residuc A;Residuc A;Cross A;Access A;Molecu A;Residuc	RESULT 1 JC6039 fimbrin 1 C;Specie C;Date: C;Access R;Collin J. Bactes A;Referen
121 NNAALVNQTASDSSYMVRQVGFGNNATANQY 151	61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120 	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 	Query Match 87.9%; Score 682; DB 2; Length 151; Best Local Similarity 90.7%; Pred. No. 1.2e-50; Matches 137; Conservative 2; Mismatches 12; Indels 0; Gaps 0;	C;Function: A;Description: major component of thin aggregative fimbriae A;Description: major component of thin aggregative fimbriae A;Description: major component of thin aggregative fimbriae A;Dote: fimbria C;Keywords: fimbria F;1-20/Domain: signal sequence #status predicted <sig> F;1-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>	A; Accessor: Preliminary A;Molecule type: protein A;Residues: 21-33 <co3> A;Note: sequence extracted from NCBI backbone (NCBIP:45936) C;Genetics: agfA</co3>	A,Experimental source: strain 27655-3b A,Experimental source: strain 27655-3b A;Note: the authors translated the codon ACG for residue 44 as Ile R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W. J. Bacteriol. 173, 4773-4781, 1991 A,Title: Purification and characterization of thin, aggregative fimbriae from Salmonell. A;Reference number: A44898; MUID:91310586; PMID:1677357 A;Contents: 27658	A;Accession: JC6039 A;Accession: type: DNA A;Residues: 1-151 <col/> A;Residues: 1-151 <col/> A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714 A;Accession: PC6015 A;Accession: PC6015 A;Residues: 21-52 <co2></co2>	RESULT 1  JC6039  JC6039  JC6039  Graphorin protein agfA precursor - Salmonella enteritidis  Graphories: Salmonella enteritidis  Graphore: 31-Dec-1996 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999  Graccession: JC6039; PC6015; A44898  RrCOllinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.  J. Bacteriol. 178, 662-667, 1996  Artitle: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.  Areference number: JC6039; MUID:96146512; PMID:8550497

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121

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A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arngvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. Mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                              Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                                                                                                                                                                                                                              A;Cross-references: EMBL:X90754; NID:gl147558; PIDN:ChA62282.1; PID:gl147564
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Rile
A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: csgA protein; major curlin protein
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change
C;Accession: S70788; G64846; S31202; S34560; S34559
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Expression of two csg operons is required for production A;Reference number: S70783; MUID:96414468; PMID:8817489 A;Accession: S70788
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A;Residues: 1-151 <HAM>
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Nature 413, 848-852, 2001

A;Authors: Parry, C:; Quail, M:; Rutherford, K.; Simmonds, M.;

A;Title: Complete genome sequence of a multiple drug resistant

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AI0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-151 < PAR >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: AI0635
C;Accession: AI0635
R;Parkhill, J.; Dougan, G.; Jan
th T.; Connerton, P.; Cronin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major curlin chain precursor [imported] - Salmonella enterica su C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: A10635
                                                                                                                 Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                    ;Status: nucleic
                                                                                                                                             Status: nucleic
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Best Local
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Gene: STY1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                      acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                 acid sequence not
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90.7%;
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in, A.;
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Pred. No. 1.2e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                               shown; translation not
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    Salmonella enterica subsp.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
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                                                                                                                                                                                                           K-12
                                                                                                                                           shown
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; White, N.
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ey, M.;
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A; Molecule type: DNA
A; Residues: 1-152 < HAY>
A; Cross-references: GB:BZ
A; Experimental source: st
C; Genetics:
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                                                                                                                                                                                                                                                                                                                          R;Hayashi, T.; Makino, 1
gasawara, N.; Yasunaga,
DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                         A;Title: Complete genome sequence of enterohemorrhagic E A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: D90806
                                                                                                                                                                                                                                                                                                                                                               C;Date: 18-Jul-2001 #sequence_revision C;Accession: D90806 R;Hayashi, T.; Makino, K.; Ohnishi, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          D90806
                                                                                                                                                                                                                                                                                                                                                                                                                      curlin major subunit CsgA [imported] C;Species: Escherichia coli
                                                                                                                                                 A;Gene:
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A; Molecule type: DNA
A; Residues: 1-133, 'RQRDSGWIW' <OLS3>
A; Cross-references: EMBL:L04979; NID:g290424;
A; Cross-references: strain K-12, substrain
                                                                                                                                                                                                                                                        A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 21-42;44-50 <OLS2>
R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library,
A;Reference number: S34559
A;Accession: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;21-151/Product: curlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type:
A; Residues: 21-4
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Best Local :
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                                MKLLKVÄAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
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                                                                                                                                                                                                                                                                                                                                             Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii,
Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                        Conservative
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ce: strain O157:H7, substrain RIMD
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                                                                                       64.4%;
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69.5%;
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Pred. No. 3e-35;
B; Mismatches
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Pred. No. 4.6e-37;
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QSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG 119

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A;Cross-references: EMBL:L03710
R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene A;Reference number: $03650; MUID:88189811; PMID:3357771
A;Accession: $03650
A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773 <MAR>
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S42136
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                                                                                                                                                                                                          A;Title: Retroviral-type zinc fingers and glycine-rich repeats A;Reference number: S42135; MUID:94051569; PMID:8233798 A;Accession: S42135
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1748 <TAY>
A; Cross-references: EMBL: L03710; NID: g161751; PID: g161752
                                                                                                                                                                                                                                                                                                                                                                                    R;Taylor, F.M.; Martindale, submitted to the EMBL Data | A;Reference number: S42136
                                                                                                                                                                                                                                                                                                                                                                                                                                         cnjB protein - Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Species: 19-Mar-1997 #sequence revision 18-Jul-1997 #text_change 07-Dec-1999
C;Paccession: S42135; S42135; S03650
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A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343<sup>.</sup>
                                                                                                                                                                                                                                                                   R; Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614,
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Nature 409, 529-533, 2001
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Best Local S
Matches 103
Molecule type: DNA
Residues: 236-250,'I',252-255,'N',257-773 <MAR
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F;1501-1514/Region: z
F;1530-1543/Region: z
F;1555-1568/Region: z
F;1579-1592/Region: z
F;1602-1615/Region: z
F;1602-1615/Region: g
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A;Introns: 85/3; 136/1;
C;Keywords: zinc finger
F;1164-1450/Region: 91yc
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A;Molecule type: DNA
A;Residues: 1-2174 <KUR>
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A; Accession: E95965
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A:Gene: SMb21548
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A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GS
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Amp
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.:
A;Title: The composite genome of the legume symbiont Sinorhizobium |
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021) C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
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                                                                                                                                                                       750 GLTLTTQGSHAAGIVAQS-VGGGGGTGGTASSYSAGI--
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                                                                                                                                                                                                                                                                                                                                                                                                        AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGS------ANAA-----
                                                                                 GOYGGNNAA--LVNQTASDSSVMVROVG 141
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GGTGGNGGAGGEVSVSLTDSAIRTGQGG
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Dreano, S.; Federspiel, N.A.; Fisher, R.F..
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Rajandream, M.A.; Rogers, J.; Rutter, Nature 393, 537-544, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A;Reference number: Z20252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Y38E10A.q - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T26667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
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(Residues: EMBL.AL110484; NID:e1542205; PIDN:CAB54408.1; COSS-references: EMBL.AL110484; NID:e1542205; PIDN:CAB54408.1;
                                                                                                                                                                                                                                                                                                                                                            ;Cross-references: GB:Z83860; GB:AL123456; NID:g3261681; PIDN:CAB06165.1; PID:e290763;
;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Date: 17-Jul-1998 #sequence_revision;Accession: E70663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: CESP:Y38E10A.q;Introns: 105/2; 174/1; 248/1; 372/3; 436/3
                                                                                                                                                                                                                                                                                                                  Gene:
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Best Local
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  132 DSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSDARKSETTITQSGYGNGAD----VGQGADNYDQLVTRVVT-----HEMAHADQWNAKN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRSVGFGAQQFGGSQFARPIPAGGGGGGGGGGGGGGGGGGGG--
                                              FGNAGNINTGF-
                                                                                     YGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALV---NQTAS 131
                                                                                                                                                                                SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGAGGGGAGGGKAGGAKNSASYGSSANEVKSVGFG----AQQY 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDITYGQYGGNNAALVNQTAS--DSSVMVRQVGFGNNATANQY 151
                                                                                                                                      SGTGNIG----FGNSGNNNIGFENSG-DGNIGFFNSGDGN-
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                               12.6%;
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28.8%;
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Pred. No. 1;
16; Mismatches
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Pred. No. 0.44;
4; Mismatches
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probable
C;Species
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                           A;Residues: 1-407 <WIL>
A;Cross-references: EMBL:Z74033; PIDN:CAA98477.1;
A;Experimental source: clone F38B7
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A;Accession: T21956
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                                                                                                                                                                                                                              A; Introns: 12/1; 57/3; 124/2; 163/1; 330/3
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;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003;
;Accession E70946
                                                                                                                                                                                                                                                                       ;Gene: CESP:F38B7.3
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Best Local (
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Gene: PPE
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442 SFNVGFQNTGFGNSGAGN
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Mycobacterium tuberculosis
                       61
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                                                                                                                                               34;
                                                                                                                                                                    Similarity
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SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQMNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA
                                                                FGSGILAGSLLGYGLGSMWGGHHSYGGWGGGYGGGG------YGMAG---GYY 293
                                                                                                      FAAIVVSGSALA-GVVPQWGG------GGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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ilarity 27.4%;
Conservative 1
                                                                                                                                               Conservative
                                                                                                                                                                    12.1%; Score 94; DB 2; 25.8%; Pred. No. 1.4;
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Pred. No. 1.7;
14; Mismatches
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                                                                                                                                                 Mismatches
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                                                                                                                                                 43;
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                                                                                                                                                                                     Length 407
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hypothetical protein AGR_L_228 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002 C;Accession: H98144 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.
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ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Teference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: H98144
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C;Genetics:
A;Gene: AGR_L_228
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A; Residues: 1-145 < KUR>
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                                                                   64;
                                                                                                                                                                                                                                                                                                          PID:g15158413; GSPDB:GN00170
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GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD---NY--

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probable PPB protein - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Species: Mycobacterium tuberculosis

C;Accession: F70825

C;Accession: F70825

C;Accession: F70825

C;Connor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go

C;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, S37-544, 1998

A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Aitle: Deciphering the biology of Mycobacterium tuberculosis from the complete

A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                            ice nucleation protein - Xanthomonas campestris
C;Species: Xanthomonas campestris
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1:
C;Accession: S11672
                                                                                                                                                                                                                                                                                                                                                           RESULT 15
S11672
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                                                                          A;Molecule type: DNA
A;Residues: 1-1567 <ZHA>
A;Cross-references: EMBL:X52970; NID:g48531; PIDN:CAA37140.1; PID:g48532
C;Superfamily: ice nucleation protein
                                                                                                                                                                      Mol. Gen. Genet. 223, 163-166, 1990
A,Title: Conserved repetition in the ice nucleation gene A,Reference number: S11672; MUID:91080859; PMID:2259339
A,Accession: 311672
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A;Experimental source: strain H37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
42;
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          GNTGNNNIGIGLTGSNQIGFGGLNSGSGNIGFGNSGTGN
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21;
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                Score 93.5;
Pred. No. 6
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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    SwissProt_42:*
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    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emoedy L., Mueller K.-M., T)
"Purification and characterization of thin,
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Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA,
the structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
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-- FUNCTION: CURLIN IS THE STRUCTURAL
-- COILED SURFACE STRUCTURES THAT ASSE
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SPECIES=S.enteritidis; STRAIN=27655-3B;
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-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-I- FUNCTION: STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                               MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emcedy L., Trust T. "Purification and characterization Salmonella enteritidis.";
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"The Crl protein activates cryptic
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"A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region
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                                                                                                                                                                                                                  SEQUENCE OF 21-40.
STRAIN=K12 / YMEL;
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STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
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                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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 TEMPERATURES FIBRONECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                 complete genome sequence nce 277:1453-1474(1997).
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                                                                                                                                                                                                                                                         nding to the 12.7
3:137-155(1996).
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(Rel. 34, Last sequence up
(Rel. 41, Last annotation
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                                                                                                                                                           Russell D.G., Normark genes for curli format coli HB101.";
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Fimbria; Signal; Complete
SIGNAL 1 20
SIGNAL 21 151
           MEDLINE-21074935; PubMed-11266551;

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Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
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Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Major curlin subunit precursor.
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EMBL; X90754; CAA62282.1; -.
EMBL; AE000205; AAC74126.1; -.
                                                                                                                                                                                                                                                                                                                        Whilch G.A., Keen J.E., Elder R.O., "Mutations in the csgl promoter associated with variations in expression in certain strains of Escherichia coli O157:H7.", Appl. Environ. Microbiol. 67:2367-2370(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSGA OR Z1676 OR ECS1420.
Escherichia coli O157:H7.
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=0157:H7 / I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteríaceae;
NCBI_TaxID=83334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=0157:H7 / ATCC 43895;
MEDLINE=21218556; PubMed=11319125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / R.
STRAIN=21156231;
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01-NOV-1990
16-OCT-2001
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MEDILINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Hayashi T., Makino K., Ohnishi M., Kurokawa C., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Romplete genome sequence of enterohemorrhagic Escherichia coli o157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. B:11-22(2001).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROW TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
         MEDLINE-91080859; PubMed=2259339;
Zhao J., Orser C.S.;
"Conserved repetition in the ice nucleation
Xanthomonas campestris pv. translucens.";
                                                                                                            Xanthomonas campestris (pv. translucens).
Bacteria, Proteobacteria, Gammaproteobacteria,
Xanthomonadaceae; Xanthomonas.
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EMBL; AE005315; AAG55788.1; -.
EMBL; AP002554; BAB34843.1; -.
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223:163-166(1990)
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Tobe T.,
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MBL outstation -
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Best Local S
Matches 42
STRAIN=K12 / MG1655;
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                              MEDLINE=96414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of
fibronectin- and congo red-binding curli polymers in Escheric
                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Minor curlin subunit precursor
CSGB OR B1041 OR Z1675 OR ECS1419.
Bscherichia coli, and
Escherichia coli, O157:H7.
                                                     SEQUENCE
                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=K12 / MC4100;
                                                                                                                                                                                          Bacteria, Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                               CSGB_EC
P39828;
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Pfam; PF00818; Ice nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION;
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UENCE 1567 AA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTYSTAllization in supercooled water.
SUBCELLULAR LOCATION: Outer membrane (By similarity).
DOWAIN: CONTAINS 153 IMPERRECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANEOUS: A STRICTURAL MODEL IS SUGGESTED IN WHICH THE IC
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no way.
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w; C8B451D959ECAD63 CRC64;
            Bloch
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PIR; PIR; PIR;

; C90806; C90806. ; G85665; G85665. ; S70787; S70787.

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EMBL; X90754; CAA62281.1; --
EMBL; AB000205; AA074125.1;
EMBL; D90741; BAA35831.1;
EMBL; AB005315; AA655797.1;
EMBL; AB002554; BAB34842.1;
                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
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                                                                                                                                                                                                                                                                                                                                                                                               of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-0157:H7 / RIMD 0509952;

MEDLINE-21156231, PubMed=11258996;

MEDLINE-21156231, PubMed=11258996;

MEDLINE-21156231, PubMed=11258996;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escheri O157:H7 and genomic comparison with a laboratory strain DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99157246; PubMed=7854117;
Arnqvist A., Olsen A., Normark S.;
"Sigma S-dependent growth-phase induction of the csgBA promoter "Sigma Coli can be achieved in vivo by sigma 70 in the abse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature
[5]
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita M., Kanai K., Kashimoto K.
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Masohimoto K.
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
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"The com
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                                                                                                                                                                                                                                                                                                         the nucleoid-associated protein H-NS.";
Microbiol. 13:1021-1032(1994).
FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CUCLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT CEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT
                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                 FIBRONECTIN. THI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence nce 277:1453-1474(1997).
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an email to license@isb-sib.ch)
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Fimbria;
                                                                                                                                     InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 51.
PRINTS; PR00327; ICENUCLEAIN,
PROSITE; PS00314; ICE_NUCLEAINON; 34.
Ice_nucleation; Repeat; Outer_membrane.
                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Michigami Y., Watabe S., Al "Cloning and sequencing of uredovora.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=KUIN-J; PubMed=7764866; MEDLINE=94264407; PubMed=7764866; Data H.,
                                                                                                                                                                                                                                                            PIR; JC2143; JC2143.
HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                                                             EMBL; D14992; BAA03636.1;
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MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE IN NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Ice nucleation proteins enal crystallization in supercooled water. SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family.
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Signal; Complete proteome.
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                                                                                             1034 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 35, Created)
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                      11.8%;
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MINOR CURLIN SUBUNIT.
MW; B18D266B964014B8 CF
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5; Mismatches
                   Score 91.5; DE 
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                                                                                                                                                                                                                                                                                                                                                                                                               CIYSTAILIZATION IN SUPERCOOLED WATER.

-!- SUBCELLULAR LOCATION: Outer membrane.

-!- DOMAIN: CONTAINS 126 INFERENCE REPEATS OF A CONSENSUS OCTAPEFTII.

-!- A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESII.

PERIODICITY IS SUPERINFOSED.

-!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE.

NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene
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Pfam; PF00818; Ice nucleation; 65.
PRINTS; PR00377; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 45.
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                              SEQUENCE
                                                                                                                          ICe nucleation; Repeat; Outer membrane.

DOMAIN 162 1217 OCTAPEPTIDE PERIODICITY
                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The consensus sequence of ice nucleation proteins herbicola, Pseudomonas fluorescens and Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erwinia herbicola.
                                                                                                                                                                                                                                       EMBL; M26382; AAA24823.1;
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                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                             JQ0188; JQ0188.
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161
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                                                       46;
                                                                      Similarity
IATYGSTLSGTHQSQLIAGYGSTETAGDSSTLIAGYGSTGTAGADSTL-VAGYGSTQTA-
                          IVVSGSALAGVVPQW--GGGGNHNGGGNSS------GPDSTLSIYQYGSANAAL
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                                                                                                               1258 AA;
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RESULT 9
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O84418;
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Stephens R.S., Kalman S., Lammel C.J., R.
Mitchell W.P., Olinger L., Tatusov R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=D/UW-3/Cx;
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                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis.";
Science 282:754-759(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis.
Bacteria; Chlamydiae;
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Pfam; PF02415; Chlamydia PMP; 4.
TIGRFAMs; TIGR01376; POMP_repeat; 1.
                                                                                                                                                                                                                                                       PHCI-2DPAGE; 084418; -
                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of an obligate intracellular pathogen
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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                                                                           IIEIANNKATDVGGGA-----YVKGTLTCENSHRLQFLKNSSDKQGGGIYGEDNITLSNL
                                                                                                               NADAWASSSPOSGSGATTVSNSGDSSSGSDSDTSETVPATAKGG-GLYTDKNLSITNITG
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                                                                                                                               SGSALAGVVPQWGGGGN--HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT-
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ne protein pmpB precursor
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RESULT 10
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RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica servara Typhi CT18.";
Nature 413:848-852(2001).
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Matches
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EMBL; AE016840; AA069400.1; -.
EMBL; ASD16840; AA069400.1; -.
Fimbria; Signal; Complete proteome.
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-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-COILED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AV
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
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Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blatther F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi st
and CT18.";
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STRAIN=Ty2 / ATCC 700931;
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28-FEB-2003 (Rel. 41, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
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Enterobacteriaceae; Salmonella.
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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Matches 36
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J. Bacteriol. 178:662-667(1996).

I. FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI, CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                           StyGene;
Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P55226;
01-OCT-1996
01-OCT-1996
28-FEB-2003
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MEDLINE-98117058; PubMed-9457880;
MEDLINE-98117058; PubMed-9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                          EMBL; AJ002301; CAA05316.1; -.
EMBL; AE008749; AALZ0073.1; -.
EMBL; U43280; AAC43598.1; -.
PIR; JC6040; JC6040.
                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S. enteritidis; STRAIN-27655-3B;
MEDLINE=96146512; PubMed=550497;
COllinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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CSGB OR AGFB OR STM1143.
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Enterobacteriaceae; Salmonella.
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i; Signal; Complete p
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22 151
38 151 AA; 16182 M
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ITQSGYGNGADVGQ-GADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQ
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                      Conservative
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                                                                                                    Score 90.5; DB Pred. No. 0.53; 7; Mismatches
                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                               noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                                                                                                     DB 1; Length 151;
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Pfam; PF00818; Ice nucleation; 69.
PRINTS; PR00327; ICENUCLEATIN.
PR00317; ICE NUCLEATION; 49.
Ice nucleation; Repeat; Outer membrane.
DOMAIN 162 1281 OCTAPEFTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- FUNCTION: Ice nucleation proteins enable bacteria to crystallization in supercooled water.
-I- SUBCELULAR LOCATION: Outer membrane (By similarity).
-I- DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSEN OCTAPERTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE REGIONAL 48-RESIDUE RERIODICITY IS SUPERIMPOSED.
-I- SIMILARITY: Belongs to the bacterial ice nucleation p
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleation activity.";
FEBS Lett. 258:297-300(1989).
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Bacteria; Proteobacteria; Gammapro
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01-FEB-1991
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                                                                                                                                                                                                                                                          modified and this statement
entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECISS=M.bovis; STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
Garnier T. Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
                                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh; MEDLINE=22206494; PubMed=12218036;
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10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical glycine-rich protein Rv2098c/MT2159/Mb2125c.
RV2098C OR MT2159 OR MTCY49.38C OR MB2125C.
Mycobacterium tuberculosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YK98_MY
Q10707;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
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                                                                                                                                                                                                                                                                                                                                                                                                                              frameshift in position 59. Ref.1 sequence has been cnecked by authors in Ref.1 and they report that no errors have been found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY.

CAUTION: Ref.1 sequence differs from that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                      AE007065;
BX248341;
MT2159; -.
                                                                                                                                                                   Z73966; CAA98228.1; ALT_FRAME
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                                                                                                                     AAK46440.1;
CAD96978.1;
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                                                                                                                                                                                                                                                                                         is not removed
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TubercuList; Rv2098c; InterPro; IPR000084; 1

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                                                                                                                                                                                                                         InterPro; IPR006025; Pept M_Zn_BS
InterPro; IPR001577; Peptidase_M8
Pfam; PP01457; Peptidase_M8; 1.
                                                                                                                                                                                                                                                                                                                 EMBL; M60048; AAA29244.1; -. HSSP; P08148; 1LML.
                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Webb J.R., Button L.L., McMaster R.W. "Heterogeneity of the genes encoding of Leishmania donovani.";
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P23223;
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Eukaryota; Euglenozo
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                                                                                                                                                                                                                                                                                               MEROPS; M08.001;
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(Major surface
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FUNCTION: Has an integral role during the infectic in the mammalian host.
CATALYTIC ACTIVITY: Preference for hydrophobic respl' and basic residues at P2 and P3'. A model nona cleaved at -Ala-Tyr-1-Leu-Lys-Lys-COPACTOR. Binds I zinc ion per subunit (By similar SUBCELLULAR LOCATION: Attached to the membrane by SIMILARITY: Belongs to peptidase family M8.
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sin precursor (EC 3.4.24.36) (Cell
sce glycoprotein) (GP63 protein) (P
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1979 MW; 12C8630C59CA0C13 CRC64;
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                                                                                                                                Glycoprotein; Meion; GPI-anchor;
ACTIVATION PEPTIDE.
LEISHMANDLYSIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                POTENTIAL.
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                                               This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed during development of Leishm. promastigotes to an infectious form."; J. Biol. Chem. 267:1888-1895(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=90205976; PubMed=2320059;

Miller R.A., Reed S.G., Parsons M.;

"Leishmania gp63 molecule implicated in cellular arg-01y-Asp sequence.";
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NCBI_TaxID=44271;
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01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation (Cell surface protease)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surfa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Three distinct RNAs for the surface protease gp63 expressed during development of Leishmania donovani
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                                                                                                                                                                                                                                                                               FUNCTION: Has an integral role during the infection of macropha in the mammalian host.

ATTIVITY: Preference for hydrophobic residues at Pl a Pl' and basic residues at P2 and P3'. A model nonapeptide is P1' and basic residues at P2 and P3'. A model nonapeptide is Cleaved at -Ala-Tyr-|-Leu-Lys-Lys-
COPACTOR: Binds 1 zinc ion per subunit (By similarity).

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Attached to the memora SIMILARITY: Belongs to peptidase family M8.
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C P08148; PL5906;

O1-AUG-1988 (Rel. 08, Created)

T 01-APR-1990 (Rel. 14, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

Leishmanolysin precursor (EC 3.4.24.36) (Cell su

Color surface glycoprotein) (GP63 protein) (Pro
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[3]
GPI-ANCHOR.
MEDLINE=91009116; PubMed=2145267;
Schneider P., Ferguson M.A.J., McConville M.J.,
Homans S.W., Bordier C.;
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Eukaryota; Euglenozoa;
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                                                                                                                                  "Molecular
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; P08148; 1LML.
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                                                                                                                       L.L., McMaster W.R.; ular cloning of the major surface antigen of leishmania."; Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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171:589-589(1990)
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PROSITE; PS00142; ZINC_PROTEASE; 1.

Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;

Hydrolase; Signal; Cell adhesion; GPT-anchor; 3D-structure; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@eisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y00647; CAA68673.1; -. PIR; PL0221; PL0221. PDB; 1LML; 17-SEP-97. MEROPS; M08.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95406217; PubMed=7675700; MEDLINE-95406217; PubMed=7675700; Schlagenhauf E., Etges R., Metcalf P.; Schlagenhauf E., Etges R., Metcalf P.; Schlagenhauf E., Etges R., Metcalf P.; Schlagenhauf E., Etges R., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.; Schlagenhauf E., Etges G., Metcalf P.;
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InterPro; IPR001577; Peptidase_M8
Pfam; PF01457; Peptidase_M8; 1.
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MEDLINE=98416698; PubMed=9739094;
Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P1 and basic residues at P2 and P3. A model nonapeptide is cleaved at -Ala-Tyr-1-Leu-Lys-Lys-.

COFACTOR: Binds 1 zinc ion per subunit.

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. PTM: THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS A FULLY SATURATED, UNBRANCHED 1-O-ALKYL CHAIN (MAINIX C24.0) AND A MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0, C14:0, C16:0, AND C18:0).

SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e Leishmania major promastigote surface protease.";
Biol. Chem. 265:16955-16964(1990).
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     POTENTIAL.
ACTIVATION PEPTIDE.
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SQ SEQUENCE 602 AA; 63953 MW; 982EF3245D87C43E CRC64;
Query Match 11.2%; Score 87; DB 1; Length 602;
Best Local Similarity 89.5%; Pred. No. 4.8;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 85 ADNYDQLVTRVVTHEMAHA 103
Db 251 ASRYDQLVTRVVTHEMAHA 269

Search completed: March 11, 2004, 18:34:57
Job time: 6.3 secs
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB DB	ID
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w	538	69.3	149	N	Q7X240
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υ	421.5	54.3	150	N	Q7X237
o	305.5	39.4	76	N	Q54069
7	122	15.7	29	N	Q983J5
œ	115	14.8	139	16	Q8EIH3
9	110	14.2	130	16	Q89JI4
10	109.5	14.1	502	16	Q8EIH4
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11.8	11.8	11.9	11.9	11.9	11.9	11.9	11.9	11.9	12.0	12.0	12.0	12.0	12.0				12.2	12.2	12.2			12.4	12.4	12.6	12.6	13.1	13.1	13.4
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# ALIGNMENTS

Qy 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151	Qy 61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG	Qy 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ	Query Match 86.7%; Score 673; DB 2; Length 152; Best Local Similarity 89.4%; Pred. No. 3.7e-47; Matches 135; Conservative 3; Mismatches 13; Indels 0;	SQ SEQUENCE 152 AA; 15401 MW; 9DA7DADC2364B006 CRC64;	NON_TER 152 152	RL Infect. Immun. 65:5320-5325(1997).	cells.";	Salmonella typhimurium SR-11 with mouse small intestinal	thin, aggregative fimbriae promotes interaction	Sukupolvi S.S	MEDLINE=98053981; PubMed=9393832;		OC Enterobacteriaceae: Salmonella.	Salmonella typhimurium.	_	01-JAN-1998 (TrEMBLrel. 05, Last	01-JAN-1998 (TrEMBLrel. 05, Created)	033802;	ID O33802 PRELIMINARY; PRT; 152 AA.	033802
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"Production of Cellulose and Curli Fimbriae by Members of th
Enterobacteriaceae Isolated from the Human Gastrointestinal
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515701; CAD56675.1;
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Fec4;
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Bacteria; Proteobacteria;
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EMBL; AJ515700; CAD56672.1; -.
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Bacteria; Proteobacteria;
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Jogaj X., Bokranz W., Nimtz M., Romling U.;
Production of Cellulose and Curli Fimbriae by Members of the Family
Production of Teclated from the Human Gastrointestinal Tract.";
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Citrobacter.
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Pred. No. 3.2e
17; Mismatches
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Enterobacter sakazakii.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Enterobacter.
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MEDINB=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., S
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.I.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome
of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                     NCBI_TaxID=28141;
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EMBL; AJ515702; CAD56678.1; -.
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"Virulence of Salmonella enteritidis in chickens correlates
colony morphology and expression of SEF17 fimbrise.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                               GNHXGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADN--
                                                                                                                                                                                                           GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQQADNYD
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76 AA;
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(TrEMBLrel. 13, Created)
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(TrEMBLrel. 16, Last annotation update)
nit monomer (Fragment).
                                                                                                                                                                                                                                           Conservative
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                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                    7704 MW;
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4; Mismatches
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Pred. No. 9.
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Q8EIH3;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., DeBoy R.T., Deterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.; Fraser C.M.
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MEDLLINE=99314153; PubMed=10386375;

La Ragione R.M., Collighan R.J., Woodward M.J.;

"Non-curliation of Escherichia coli 078:K80 isolates associated IS1 inserti on in csgB and reduced persistence in poultry infect FEMS Microbiol. Lett. 175:247-253(1999).

EMBL; AJ131756; CAB45380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
Alteromonadaceae; Shewanel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shewanella oneidensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shewanella oneidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22297686; PubMed=12368813;
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SO0866; -.
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                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                              EMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGN 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
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Matches 39
                                       Heidelberg J.F., Paulsen T.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Sott J., Beanan M., Brinkac L., Daugherty S., Meboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vanathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Wueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanalla oneidensis."
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01-MAR-2003 (TrEMBLrel 23,
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Q94821; P92146; P92145; P9
01-FEB-1997 (TTEMBLEG1. 02
01-FEB-1997 (TTEMBLEG1. 02
01-OCT-2003 (TTEMBLEG1. 25
                                                                                                                                                                                                                                                                         PROSITE;
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             "Retroviral-type zinc fingers and glycine-rich repeats encoded by cng, a Tetrahymena gene active during meios Nucleic Acids Res. 21:4610-4614(1993).

EMBL; X06462; CAB37323.1; -.

EMBL; L03710; AAC37171.1; -.

PIR; S42136, S42136.

HSSP; P05888; 1AAF.

GC; GC:0003676; Francleic acid binding; IEA.
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Pfam; PF00098; zf-CCHC; 7
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MEDLINE=88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; SO0865;
Hypothetical p
SEQUENCE 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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SM00343; ZnF
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$M00343; ZNF C2HC; 7.

$$M00343; ZNF CCHC; 7.

$$; P$50158; ZF CCHC; 7.

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                                                                                                                                                                                         Similarity
      QTGGGWGSNDNQQQ
                                    GADVGQGA-DNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ--YGGNNAA
                                                                                                                      QWGGGGNHNGG----GNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT----QSGYGN
                                                                                      OFGGGGNSNGGOSWGTSSGSDWN----
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Best Local S
Matches 40
                                                                                                                  Q8Y106;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable hemagglutinin related protein.
RSC0887 OR RS06116.
Ralstonia solanacearum (Pseudomonas solanacearum)
Bacteria; Proteobacteria; Betaproteobacteria; Bur
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Q22UU8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR002016; Peroxidase.
InterPro; IPR002173; PfkB.
Pfam; PF03797; Autotransporter; 1.
PROSITE; PS00435; PEROXIDASE 1; 1.
PROSITE; PS00583; PEROXIDASE 1; 1.
PROSITE; PS00583; PEKD KINASES 1; 2.
Plasmid; Hypothetical protein; Complete proteome.
Plasmid; Hypothetical protein; Complete proteome.
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"The complete sequence of the 1,683-kb pSymB megaplasmid fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL; ALGO3645; CAC49389.1; -.
PIR; E95965; E95965.
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RB0989 OR SWB21548.
RRizobium meliloti (Sinorhizobium meliloti).
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
  STRAIN=GMI1000;
                             SEQUENCE FROM N.A.
                                                                                                             Burkholderiaceae;
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GO:0004601; F:peroxidase activity; IEA
GO:0006979; P:response to oxidative str
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Pred. No. 5.1;
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                                                                                                                                          Burkholderiales;
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RESULT 14

QBXSD6

ID QBXSD

ID QBXSD

AC QBXSD

AC QBXSD

DT 01-MA

DT 01-OC

DE Proba

GN RSP055

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A Chandler M., Cholsne N., Claudel Renard C., Cunnac S., Demange N.
A Chandler M., Cholsne N., Claudel Renard C., Cunnac S., Demange N.
A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
A Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Meissenbach J., Boucher C.A.;
Tenome sequence of the plant pathogen Ralstonia solanacearum.";
Multiple M., Mincker P., Levy M.,
Meissenbach J., Boucher C.A.;
Tenome sequence of the plant pathogen Ralstonia solanacearum.";
Mature 415:497-502(2002).
Meissenbach J., Boucher C.A.;
Tenome sequence of the plant pathogen Ralstonia solanacearum.";
Meissenbach J., Boucher C.A.;
Tenome sequence of the plant pathogen Ralstonia solanacearum.";
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QBXSD6; (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable hemaggluttinin-related protein.
RSP0540 OR RS06117.
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Plasmid megaplasmid.
Bacteria, Proteobacteria; Betaproteobacteria; Bur
Burkholderiaceae; Ralstonia.
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Pfam; PF05860; Haemagg_act; 1.
PROSITE; PS01070; NUCLEASE_NON_SPEC;
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EMBL; AL646061; CAD14589.1; -.
EMG; GO:0004519; F:endonuclease
GO; GO:0003576; F:nucleic acid
GO; GO:0003576; F:nucleic acid
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Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
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Plasmid;
SEQUENCE
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Infect. Immun. 65:5320-5325(1997).
EMBL; AJ000514; CAA04150.1; -
SEQUENCE 179 AA; 19318 MW; A2BCCB648B3C0B0B CRC64;
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MEDLINE=98053981; PubMed=9393832;

Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian

Normark S.J., Rhen M.;

"Expression of thin, aggregative fimbriae promot
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01-JAN-1998 (TrEMBLrel. 05,
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                  133 SSVMVRQ 139
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13.7%; Score 106.5;
Similarity 29.5%; Pred. No. 15;
43; Conservative 19; Mismatches
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3552 AA; 352934 MW; C5432AABE2CCF59C CRC64;
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length: 2000000000
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# ALIGNMENTS

#### RESULT 1 AAB36352 ID AAB3 XX AAB3 AC AAB3 XX AAB3 AC A 05-APR-1999; 05-APR-2000; 2000WO-CA000356 WO200060102-A2 Synthetic. Salmonella enteritidis. vaccine; immune response; Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; 26-FEB-2001 AAB36352; AAB36352 standard; WPI; 2000-672631/65. 12-OCT-2000 Escherichia coli. AgfA::PT3#7 amino acid sequence (UYVI-) UNIV VICTORIA Doran JL, (first entry) 99US-0127888P protein; Collison immunogen 151 SK, SEQ ID NO:24 Кау WW;

The present invention describes a recombinant agfA gené (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene homologous species; (3) directing recombination of a recombinant gene homologous species; (3) directing recombination of a recombinant gene

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

N-PSDB; AAC64628.

Disclosure; Page 138; 139pp; English.

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RESULT 2
AAB36347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Biterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                  N-PSDB; AAC64623.
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Pred. No. 1.6e-68;
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Escherichia coli.
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                                                                05-APR-1999;
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(UYVI-) UNIV VICTORIA
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Best Local Similarity
Matches 143; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene
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                                        Salmonella
                                                                                               Salmonella; AgfA; vaccine
                                                                                                                                                                        AgfA sequence
                                                                                                                                                                                                                                             25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                        AAR74625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important foor directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                      AAR74625 standard; protein; 151
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(first en
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Pred. No. 4.2e-61;
0; Mismatches 0
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                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                             Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response Salmonella in animals (e.g. food producing animals) and humans. (Updat on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
WPI; 2000-672631/65
                                                                  05-APR-1999;
                                                                                      05-APR-2000; 2000WO-CA000356
                                                                                                                                                      Salmonella enteritidis.
                                                                                                                                                                                                                                   26-FEB-2001
                                                                                                                                                                                                                                                         AAB36341;
                                                                                                                                                                                                                                                                              AAB36341 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151
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                      White AP,
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                                                                                                            12-OCT-2000
                                            (UYVI-) UNIV VICTORIA
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                      Doran JL,
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                                                                99US-0127888P
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                       Collison SK,
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                       Kay WW;
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(Updated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombinant gene CC back into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the complymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for cell-citing an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to complete feel to the carrier fimbrial subunit for directing an immune response continuous and subunit proteins are usually strong communication which may be important for directing an immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                            Misc-difference
                                                                                                     Salmonella
                                                                                                                                        Enteropathogenic bacteria;
                                                                                                                                                                                   Salmonella
                                                                                                                                                                                                                         25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                       AAW23570 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid finbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 135; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                     enteritidis
                                                                                                                                                                              enteritidis 27655-3b agfA.
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(first entry)
                                          Location/Qualifiers
                  /note= "Encoded by GCC"
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                                                                                                                                        enterobacteria; S.enteritidis;
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Pred. No. 4.1e-60;
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RESULT 7
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Best Local
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                            05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                           Salmonella enteritidis.
                                                                                                                                                                                                                                                                                             vaccine; immune response;
                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36346 standard;
                                                                                 12-OCT-2000
                                                                                                                                      WO200060102-A2
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                                                                                                                                                                                                               Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enteropathogenic bacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA INNOVATION &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                            amino acid sequence SEQ ID NO:12
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Pred. No. 5.2e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                         gene replacement;
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5.2e-60;
11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC directing recombination of a recombinant gene into the chromesome of the chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating a replacement segment or segments of foreign amino acid golymer comprising a recombinant AgfA comprising a replacement segment or segments of foreign amino acid golymer comprising a recombinant AgfA comprising a recombinant AgfA comprising a recombinant AgfA comprising a recombinant AgfA comprising a recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for golymer into the expression of recombinant AgfA protein which is useful for comprising an immune response in an animal. In a finbrial presentation comprises the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live cagainst the inserted epitope, and hybrid fimbria are usually strong compressive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 134;
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Best Local
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                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                         AgfA::PT3#8 amino acid sequence SEQ ID NO:26
                                                                                                                                                                               AAB36353 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 151 AA,
                                                                                                   26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein useful for eliciting
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                                                                                                                                                                                                                                                                                   NNAALVNYDQLVTRVVTHEMAHA------
                                                                                                                                                                                                                                                                                                                         -----NYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                 (first entry)
response; immunogen
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                          directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid dequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is polymer into the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response
                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                        Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 138; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                 the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                   immunogens, which may be important for directing an immune respagainst the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                    nexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA
121
                                                                                                                                                                                                                                            124;
                                                                            61
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                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                    HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                           MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doran JL,
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                        ΑA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0127888P
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                                                                                                                                                                                                                                                          78.6%;
82.1%;
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                                                                                                                                                                                                                                                                                                                                                              the present
                                                                                                                                                                                                                                                             Score 609; DB 3;
Pred. No. 4.2e-52;
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay WW
                                                                                                                                                                                                                                                                              Length 151
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ID AAB3
                                                                                                                                                                                                                          CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the CC homologous species; (3) directing recombination of a recombinant gene combinant gene gene combinant gene combinant gene gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combin
                                                                                               Matches
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant agfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein useful for eliciting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AgfA::PT3#6 amino acid sequence SEQ ID
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                                                                                               Local Similarity
les 128; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-672631/65
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                             MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                         151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; 151 AA
                                                                                                                   78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collison
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                                                                                            Score 609; DB 3;
Pred. No. 4.2e-52;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expresses recombinant AgfA
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                                                                                                                                       Length 151;
                                                                                            Indels 46;
                                                                                            Gaps
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comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for cell-cell and immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbria protein sees soth the immunogenicity and adhesion properties relevant for an efficient live vaccine, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which encodes foreign epitope or antigen, protein useful for eliciting immune respo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC64625.
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Matches 124; Conservative
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of the homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombinatin and a recombination of a recombination of a recombination of a 
                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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82.1%;
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Pred. No. 8.2e-52;
5; Mismatches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kay
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign D sequence which encodes a foreign epitope or antigen. Also describe

described

Disclosure; Page 138; 139pp; English.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

AAC64630.

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RESULT 13
AAB36348
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WPI; 2000-672631/65
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                                                                                                                                                                  05-APR-1999;
                                                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis.
                                                                                                                                                                                                                                                                                  12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence

    use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
assembly system of strains of Salmonella, Escherichia coli and

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                                                  Doran JL,
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                                                                                                                                                                  99US-0127888P
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81.5%;
                                                     Collison
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                                                  SK,
                                                     Kay WW;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                   121 HEMAHANQTASDSSVMVRQVGFGNNATANQY
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81.5%;
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Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; immunogen

Escherichia coli CsgA amino acid sequence SEQ ID NO:7

26-FEB-2001

(first entry)

vaccine; immune response;

WO200060102-A2 Escherichia coli.

12-OCT-2000

05-APR-2000; 2000WO-CA000356

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 151 AA;
                      E. coli CsgA subunit 15 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 135; 139pp; English.
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                                                             04-DEC-2003
                                                                                                     ABR82651
                                                                                                                                          ABR82651 standard; protein; 151
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70.2%;
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Search completed: March Job time: 45.9 secs

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Matches
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                                                                                                                                                                                                                                                                   The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a ma selected from sequences shown in ABR82642, ABR82640-49. The peptide antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmon or Shigella infection. The peptide that is immobilized on a solid su is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. C. 15 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated peptide capable of binding a mammalian plasma prouseful in the manufacture of a medicament for the prevention a treatment of a bacterial infection, such as Escherichia coli, or Shigella infections.
                                                                                                                                                                                                                                          Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2002; 2002GB-00002275
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                             HEMAHANQTASDSSVMVRQVGFGNNATANQY
                                                                           SDARKSETTITQSGYGNGADVGÓGADNSTIELTQNGFRNNATIDQWNAKWYDQLVTRVVT
GNGAAVDOTASNSSVNVTQVGFGNNATAHQY
                                                           TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
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Pred. No. 4.2e-44;
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US-09-186-387-2
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US-09-186-4738-3
US-08-864-038A-3
US-09-186-473-171
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	הנקתנונו
34, App	71, App	4, Appl	4, Appl:	4, Appl:	4, Appl:	4, Appl:		4, Appli	5005, Ap	73, App	6, Appl:	<ol><li>Appl:</li></ol>	6, Appl	41, App	42, App.	7973, A	

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RESULT 1
US-08-233-788A-59
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6931
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Applicat:
Patent No. 5635617
PATENT INFORMATION:
Query Match
Best Local Similarity
Matches 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
CCLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: COllinson, Karen S.
APPLICANT: Clouthier, Sharen C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION NUMBER OF SEQUENCES: 61
CORRESPONDENCES: 61
                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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STREET: 6300 Columb
CITY: Seattle
STATE: Washington
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5. 5635617
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Score 689; DB 1; Length 151
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2; Mismatches 11; Indels
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RESULT 3
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              Sequence 8, Application US/09196387 Patent No. 6277613
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Best Local Similarity
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GENERAL INFORMATION:
GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 26-API CLASSIFICATION: 43:
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: King, Joshua
REGISTRATION NUMBER: 35,570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                          82
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                                                                                                                                                                                                          22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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                                                                                                                                                                                                                                                                  99;
                                                                                                                                             GQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDS 133
                                                                                                                   GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 112
                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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Collinson, Karen S.
Clouthier, Sharon C:
Clouthier, Sharon C:
AVENTION: METHODS AND COMPOSITIONS FOR DETECTION
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N: 435
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William W.
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Pred. No. 1.7e-42;
2; Mismatches 11; Indels
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US-09-841-835-8
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Best Local (
                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: de Lan
APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                             TITLE OF INVENTION: A PROTEIN THAT BINDS TITLE OF INVENTION: OF USE THEREOF NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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APPLICATION NUMBER: 0
FILING DATE: June 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 673 amino acids
       CITY: Hackensack
STATE: New Jersey
                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
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Similarity 28.4%;
42; Conservative 16
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GY: linear
                                          411 Hackensack Avenue,
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Smith, Su
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Pred. No. 1.1;
16; Mismatches
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                                          4th Floor
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Best Local Similarity
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LENGTH: 673 amino acids
TYPE: amino acid
                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 60,742
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICANT: Smith, Susan
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CLASSIFICATION:
IOR APPLICATION DATA:
                                                                                                                                                                                                            COUNTRY: USA
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28.4%; Pred. No. 1.1;
stive 16; Mismatches
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)ER: 600-1-230 CIP1
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                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION UNMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 949 amino acids
TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CORRESPONDENCE ADDRESS:
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                                                                       TELECOMMUNICATION INFORMATION:
                                TELEFAX:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/841,835 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 411 Hackensack Avenue, 4th Floor
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                                                    TELEPHONE:
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Local Similarity 28.4%;
es 42; Conservative 16
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Smith, Susan
                                    201-343-1684
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SEQ ID NO:
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Pred. No. 1.8;
16; Mismatches
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US-09-196-387-2
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US-09-196-387-2
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Query Match
Best Local Similarity
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APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino aci
                                                                MOLECULE TYPE:
HYPOTHETICAL:
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APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 949 amino acids
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                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                  TOPOLOGY:
                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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TOPOLOGY: linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Score 90.5;
Pred. No. 2.
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Pred. No. 1.
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               DB 3;
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               Length 1327;
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US-09-841-835-2
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE:
HYPOTHETICAL:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
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ADDRESSEE: Klauber & Jackson
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG-------DVSRVKRLVDA--- 204
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                           65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLYTRVVT 120
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                                                                                        VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                       Score 90.5; DE Pred. No. 2.8; 16; Mismatches
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US-09-972-115A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application Patent No. 6001592
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09972115A Patent No. 6599728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/972.115A CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: US 60/128,577 PRIOR FILING DATE: 2000-04-10 PRIOR APPLICATION NUMBER: US 60/129,123 PRIOR APPLICATION NUMBER: US 60/129,123 PRIOR FILING DATE: 1999-04-13 NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Fiatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Geron Corporation APPLICANT: Gregg, Morin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 080/003C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                             APPLICANT: KUNIO NAKASHIMA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
TITLE OF INVENTION: TO SAID POLYPEPTIDE
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1327
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Word Perfect 6.1
URRENT APPLICATION DATA:
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                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG-----DVSRVKRLVDA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                   514-01
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                                                                                                                                                                                                               Tsu-city
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                                                                                                                                                              Mie-prefecture
: JAPAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ANVNAKDMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                   Isshinden
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                                                                                                                                                                                                                                                          812-5 Hirano
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                                                                                                3.50 inch,
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; Pred. No. 2.8;
16; Mismatches 61;
                                                                                                  1.44 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
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US-09-198-452A-171
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                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 171
LENGTH: 1156
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 171, Application US/09198452A Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment-
TITLE OF INVENTION: chereof and uses thereof, in particular for the diagnosis, prev
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/198,452A CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: May 28, PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: F-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: peptide
LOCATION: from 1 to 738
IDENTIFICATION METHOD: 1
                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
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916
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                                                                                                                               32;
                           95 NGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSS 134
                                                                                              44 TLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTI------ELTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
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                                                              TVSPEDYAAVQAALA--AYVRKHESLIV-STYGLGAQEGQTSSKVTTLMRDLHAVEELVE
                                                                                                                                 Conservative
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VETYRLNRSDQILHRV--HSVLHSHLRDSDSS 947
                                                                                                                                               11.2%; Score 87; 32.0%; Pred. No.
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Pred. No. 1
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                                                                                                                                 Mismatches
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                                                                                                                                               5.1;
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6.
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                                                                                                                                 34; Indels
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                                                                                                                                                                  Length 1156;
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126 ANQTASDSSVMVRQVGFGNN 145

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US-09-336-447A-15
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                                                                                                                                                                                                                     ; ORGANISM: Moraxella catarrhalis US-09-336-447A-15
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                                                                                                                                                               Query Match
Best Local
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LENGTH: 339
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/09336447A Patent No. 6310190
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                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: AMCY:024
CURRENT APPLICATION UMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HANSEN, APPLICANT: AEBI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-252-991A-32096
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PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                             LENGTH: 889
                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
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                                                                       69
                                                                                                           28
                                80 DVGQG-----ADNSTIELTQNGFRN----NATID---QWNAKNYDQLVTRVVTHEMAH 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQ----
                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KVAAFAAIVVSGSALAGVVPQWGG------GGNHNGGGNSSGPDSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
34; Conserv
FVGGGYKNLAEGDNATI---AGGFANLAEGDNATIAGGFENRAEGIDSVVSG-----GY 179
                                                                                                         GGGNHNGGGNSSGPDSTLSIYQ---YGSANAALALQSDARKSETTITQSGY-----GNGA 79
                                                                     GAGRHNNVGGSAHHSGILGGWKNTVNGYTSAIVGGYGNETQGDYTFVGGGYKNLAKGNYT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAAAVSNGQYSTAGSAASQTSTGNTTVNSANYAYGGTY 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MACIVER, ISOBEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEBI, CHRISTOPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPE, LESLIE D.
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERIC J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US 60/074,788
1998-02-18
UMBER: US 60/094,190
1998-07-27
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSVLQSGYGNTLNNYSNPNTASLSNSANNVSGNLGVNV-AAGNFNQQKND 163
                                                                                                                                                               10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.9%; Score 84.5; I
21.5%; Pred. No. 1.8;
tive 32; Mismatches
                                                                                                                                              16;
                                                                                                                                          Score 83; DB 4;
Pred. No. 8.9;
6; Mismatches 5
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RESULT 15
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US-07-731-157A-2
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             Sequence 2, Application US/08541780 Patent No. 5935831
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                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/731,157
FILING DATE: 19910509
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 90200962
APPLICATION NUMBER: EP 90200962
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER PH.D., BARBARA
REGISTRATION NUMBER: 32,750
REPERENCE/DOCKET NUMBER: GBRO-027
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 720 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Mutated beta-lactam acylase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palan
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415-857-0663
                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                107
                                                                                                                                             90 IELTQNGFRNNATIDQWNAK------NYDQLVTRVVTHEMAHANQTASDSSVMVRQV 140
                                                                                                                                                                             58 HIYGVDAPSAFYGYGWAQARSQGDNILRLYGEAR----
                                                                                                                                                                                                           37 NSSGPDSTLSIYQYGSANA-----ALALQSDARKSETTITQSGYGNGADV-GQGADNST 89
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                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                               VWLLTNGVPERA---QOWYAQQSPDFRANLDAFAAGI----NAYAQQNPDDISPDVRQV 158
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Pred. No. 9
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Search completed: March 11, 2004, 18:44:53 Job time: 13.4 secs
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.8
Matches 46; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157
FILING DATE: BP 90200962
APPLICATION NUMBER: EP 90200962
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: RAE-VENTER PH.D., BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-027/00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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                                                                                         107 VWLLTNGVPERA--QQWYAQQSPDFRANLDAFAAGI----NAYAQQNPDDISPDVRQV 158
                                                                                                                                 90 IELTQNGFRNNATIDQWNAK-----NYDQLVTRVVTHEMAHANQTASDSSVMVRQV 140
                                                                                                                                                                                58 HIYGVDAPSAFYGYGWAQARSQGDNILRLYGEAR--
                                                                                                                                                                                                                        37 NSSGPDSTLSIYQYGSANA-----ALALQSDARKSETTITQSGYGNGADV-GQGADNST 89
                                                                                                                                                                                                                                                                         2 LRVLHRÄASALVMATVIGLAPAVAFALAEPTSTPQAPIAAYKPRSNEILWDG----YGVP 57
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25.8%; Pred. No. 9.5;
ative 17; Mismatches
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Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-156-761-9343

US-10-289-762-171

US-10-156-761-8763

US-10-156-761-11721

US-09-880-748-1165

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US-09-880-748-1168
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US-09-841-835-10
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US-10-032-585-7876
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              Sequence 20638, A
Sequence 876, App
Sequence 8, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 9343, Ap
Sequence 171, Ap
Sequence 17121, Ap
Sequence 11721, Ap
Sequence 1136, Ap
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76.5	77	77	77	77	77	77.5	77.5	78	78	78	78	78.5	78.5	79	79	79	80	80	80	80	80	80.5	80.5	80.5	81	81	81	81.5	82	
9.9	9.9	9.9	9.9	9.9	9.9	10.0	10.0	10.1	10.1	10.1	10.1	10.1	10.1	10.2	10.2	10.2	10.3	10.3	10.3	10.3	10.3	10.4	10.4	10.4	10.5	10.5	0	10.5	10.6	
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US-08-779-457-49	US-09-815-242-12996	US-10-108-605-303	US-09-880-748-1013	US-09-880-748-1010	US-09-880-748-2127	US-10-259-194A-68	US-09-880-748-1554	US-09-820-843A-21	US-09-880-748-1281	US-09-880-748-1466	US-09-880-748-1130	US-08-834-666A-6	US-10-156-761-9625	US-09-813-214A-9	US-09-912-020-364	US-09-880-748-1122	US-10-246-330-4	US-09-793-306-146	US-09-880-748-1153	US-09-880-748-2098	US-09-996-194-16	US-10-233-553-11	US-10-156-761-12824	US-10-233-553-23	US-10-369-493-9134	US-09-912-020-299	US-09-880-748-1494	US-10-156-761-11972	US-09-880-748-1226	
Sequence 49, Appl	12996	Sequence 303, App	1013,	Sequence 1010, Ap	2127,	68,	Sequence 1554, Ap		1281	Sequence 1466, Ap	Sequence 1130, Ap	Sequence 6, Appli	Sequence 9625, Ap	Sequence 9, Appli	Sequence 364, App	Sequence 1122, Ap	Sequence 4, Appli	Sequence 146, App		Sequence 2098, Ap		Seguence 11, Appl	Sequence 12824, A	Sequence 23, Appl	Sequence 9134, Ap	Sequence 299, App	Sequence 1494, Ap	Sequence 11972, A	Sequence 1226, Ap	

## ALIGNMENTS

US-10-369-493-20638

GENERAL INFORMATION:

Sequence 20638, Application US/10369493 Publication No. US20030233675A1

```
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory G.
APPLICANT: Glater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 50/360,039
PRIOR APPLICANTS NUMBER: US 60/360,039
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
19
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                                                                                                                                                                                              7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                   AAFAADSNTVYLNOTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                  14.3%; Score 111; DB 15; Length 445; 25.5%; Pred. No. 0.006; :lve 25; Mismatches 68; Indels 3
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US-09-841-835-8
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US-10-032-585-7876
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Publication No. US20030180953A1
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
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                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                        ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., Davi
                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 688
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                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
   NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                           APPLICATION NUMBER:
                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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Charles, F
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Smith, Susan
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                                                                                     INFORMATION FOR SEQ ID NO:
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                                               SEQUENCE CHARACTERISTICS
LENGTH: 949 amino acids
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MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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                                                                                                         FILING DATE:
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STATE: New Jersey
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STREET: 41
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TELEFAX: 201-343-1684
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Smith, Susan
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> Match 11.7%; Local Similarity 28.4%; 205 ----ANVNÁKDMAGRKSSPLHFAAGFG 227 121 HEMAHANQTASD----SSVMVRQVGFG 143 158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG---99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157 65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120 6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64 16; 600-1-230 CIP1 Score 90.5; Pred. No. 1 Mismatches DB 9; 61; Indels 29; Length 673; DVSRVKRLVDA--- 204 Gaps

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/196,387 ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION: SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS TITLE OF INVENTION: OF USE THEREOF NUMBER OF SEQUENCES: 12 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Application US/09841835 411 Hackensack Avenue, Klauber & Jackson US/09/841,835 10: 4th Floor Version #1.30

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                                                                       Matches
                                                                                                        Query Match
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Best Local
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APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/841,835
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                      Local Similarity
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TELEFAX: 201-343-1684
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                                  6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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411 Hackensack Avenue, 4th Floor
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                                                                                      11.7%;
28.4%;
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                                                                    ; Score 90.5; D; Pred. No. 2.9; 16; Mismatches
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US-09-972-115A-8
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                                                                                                                                                                                                                         Sequence 4, Application US/1019937
Publication No. US20030190739A1
GENERAL INFORMATION:
APPLICANT: Christenson, Erik
APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
APPLICANT: McElligott, David L.
APPLICANT: McElligott, David L.
APPLICANT: McElligott, David L.
APPLICANT: McElligott, David L.
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SEQ ID NO 8
FRICTH: 1327
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SOFTWARE: PatentIn Ver. SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                           FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
PRIOR FILING DATE: 2000-06-28
                                             PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
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PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A Second Mammalian Telomerase FILE REFERENCE: 080/003C CURRENT APPLICATION NUMBER: US/09/972,115A CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: US 60/128,577 PRIOR FILING DATE: 2000-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
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APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Piatyszek A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ANVNAKDMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ANVNAKDMAGRKSSPLHFAAGFG 227
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28.4%; Pred. No. 2.9;
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9343
EXECUTE: 438
                                                                                                           RESULT 9
US-10-289-762-171
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Sequence 171, Application US/10289762
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fraç
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local :
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
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ORGANISM: Homo sapiens
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Local Similarity 28.4%; Pred. No. 2.9;
1es 42; Conservative 16; Mismatches
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                                                                                                                                                                                      -----ALLPWDAKNFDKI 127
                                                                                                                                                                                                                                                       KKVLQPELDKFEEQTGIKVKLEVVPWSDLLNRILTATTSGQGPDVLNIGNTWSASLQATG
                                                                                                                                                                                                                                                                                                                            MRSIRAAAVGAVTMSLALAASAC----GGSSTGGGSNDSP-KTLT-YWASNQGASIAVD
                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALA--
                                                                                                                                                                                                                    FRNNATIDOWNAKNYDOL 114
                                                                                                                                                                                                                                                                                              ---LQSDARKSE-----
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                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 11.4%; Score 88.5; DI 24.6%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                        ----TTITQSGYGNGADVGQGADNSTIELTQNG
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US-10-156-761-11721
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   Sequence 11721, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
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GENERAL INFORMATION:

APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCS: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILLING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 171
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                / Match 11.1%; Score 86; DB Local Similarity 30.2%; Pred. No. 2.3; Des 38; Conservative 10; Mismatches
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358
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                                        126 ANQTAS 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 TLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTI-----ELTQ
                                                                                                                                                                                                                        8 AFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 11.2%; Score 87; DB Similarity 32.0%; Pred. No. 5.5;
SARTGS
                                                                                     -TEWLVGASSGGDDGGGGGTCTAAQLLGNNGFESGAT--TWTAS-----SDVITNSSGE 357
                                                                                                                                TTITQSGYGNGADVGQGADNSTIE--LTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAH 125
                                                                                                                                                                          AFFATSTFGS---GRVAFWGDSSPIDDGTGQSGNTLYDGWNDTGATNAALALNA-----
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363
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106 ATTGALDMWGRGTLVTVSSGGGGGGGGGGGGG---

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                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-880-748-1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Streptomyces avermitilis US-10-156-761-11721
                                                                                                                                                                                               SEQ ID NO 1136
LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1136, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11721
                                                                               Query Match 10.8%;
Best Local Similarity 24.5%;
                                                              Matches
                                                                                                                                                                                                                                                                                                      PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-66-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLECTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ruben et al.
TITUE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
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                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 271
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/293,499
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/277,379 FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 AAGATRKKTWTVCVDAWRVPLGMHIETRDVS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 SGSAPSGGRADPGRAHGGSPTPSVSSGGGGGGGGGGGTSTGGSATL-----GGPÄALSV 176
18 ALAGVVPOWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 -- GFRNNAT---- IDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 QSDARKS-----ETTITQSGYGNGAD-----VGQ-GADNSTIELTQN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 SGSALAG------VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STPVREASDKRWCEKVTVSFHNTGGGAARSGTVTFGTHIIGALGIDWATIESTEDLPVPI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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; Pred. No. 1.2;
18; Mismatches
                                                          19; Mismatches
                                                                             Score 84; DB 10; Length 254; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                            61; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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NUMBER OF SEQ ID NOS: 3239
SEQ ID NO 1165
LENGTH: 254
TYPE: PRT
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
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                                                                                                                                                                                                                                                                                                                                                              US-10-156-761-13168
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US-09-880-748-1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/21,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
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APPLICANT: Ruben et al.
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               Sequence 13168, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/293,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 VITGLQAEDEADYYCQSYDLSLTGRNYVFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 VVT----HEMAHANQTASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 QTITISCTGSDSNIGAGYDVHWYQHLPGTAPKLLIYVNTNRPSGVPDRFSGSKSGTLASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 ATTGALDMWGRGTLVTVSSGGGGSGGGSGGG------GSAQAVLTQPSSVSGTPG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 VITGLOAEDEADYYCOSYDLSLTGRNYVFGS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 VVT----HEMAHANQTASDSSVMVRQVGFGN 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 TTITQSGYGNGADVGQGAD-----NSTIELTQNGFRNNATIDQWNAKNYDQLVTR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 TTITQSGYGNGADVGQGAD-----NSTIELTQNGFRNNATIDQWNAKNYDQLVTR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 ALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
37; Conserv
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PRIOR APPLICATION NUMBER: JP 20
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 15109
SEQ ID NO 13168
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                                                                   ; SEQ ID NO 15; LENGTH: 889; TYPE: PRT; ORGANISM: Moraxella catarrhalis US-09-952-267-15
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US-09-952-267-15
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                                                                                                                                                                                                                                                                                   Query Match 10.7%; Score 83; DB 10; Length 889; Best Local Similarity 27.9%; Pred. No. 10; Matches 39; Conservative 16; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09952267
Publication No. US20030032772A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.8%; Score 83.5; Disest Local Similarity 24.6%; Pred. No. 2.8; Matches 43; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HANSEN, I
APPLICANT: AEBI, CI
APPLICANT: COPE, LI
APPLICANT: MACIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/952,267
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/336,447
PRIOR FILING DATE: 1999-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISCE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
  180
                                             126 ANQTASDSSVMVRQVGFGNN 145
                                                                                          129 FVGGGYKNLAEGDNATI---AGGFANLAEGDNATIAGGFENRAEGIDSVVSG-----GY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 ILLSIGGAA--AGIDLSSSAVADRFVATIVP-LLKKYNFDGIDIDIETGLVGSGN 174
                                                                                                                                         80 DVGQG-----ADNSTIELTQNGFRN----NATID---QWNAKNYDQLVTRVVTHEMAH 125
                                                                                                                                                                                         69
                                                                                                                                                                                                                                    28 GGGNHNGGGNSSGPDSTLSIYQ----YGSANAALALQSDARKSETTITQSGY-----GNGA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 IELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD-----NST 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 WTPITDSRIAAHGYNVINAAFPV---IRSDGTALWEDGMDTGVKVATPAEMCQAKASGQT 122
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ANOATGESSTV---AGGSNN 196
                                                                                                                                                                                         GAGRHNNVGGSAHHSGILGGWKNTVNGYTSAIVGGYGNETQGDYTFVGGGYKNLAKGNYT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRLLAVALTAAVLTPLSIATAPTASAADTCAVKSRPSGKVLQGYWENWDGSSNGVHPPFG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEBI, CHRISTOPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERIC J.
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                                                                                                                                                                                                                                                                                      51; Indels 34;
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                                                                                                                                                                                                                                                                                   Gaps
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Search completed: March 11, Job time: 25.6 secs

2004, 19:18:39

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Run on:
                                                                                                                OM protein - protein search, using sw model
March 11, 2004, 18:24:14; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec
                                                                                                                                                                                                 GenCore version 5.1.6
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Title: Perfect score: Sequence: US-09-543-407-24 775

Scoring table: 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues

Searched:

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. 1	Score 690	? ?   <del>5</del> 4		22 🖁	ID JC6039 AI0635	Description fimbrin protein ag
ω κ	533	68.8	151	N	S70788	major curiin co curlin protein
4.	11.		152	N	90806	
ហ			152	ν	H85665	hypothetical
6	101	•	409	N	T20847	hypothetical
7	99	12.8	1748	N	S42136	cnja prot
89	æ	•	151	N	JC6040	fimbrin protein
9	98.5	12.7	151	2	AH0635	nucleation compone
10	o,		151	N	S70787	curlin nucleator
11	σ	•	151	N	C90806	
12	σ		151	N	G85665	curlin minor
13	w	12.1	552	N	D70604	probable PPE
14	N	11.9	440	N	AD1539	probable sugar ABC
15	N	11.9	1028	N	A56038	μ.
16	'n	11.9	1213	N	S16356	ovo protein
17	90	11.6	145	N	AD3143	conserved hypothet
18	90	•	145	N	H98144	hypotheti
19	90	•	347	N	B39112	merozoite
20	89.5	٠	256	N	T03371	glycine-rich
21	89	•	262	N	S00275	tail fiber prote
22		٠	573	N	C86266	F3F19.21 protein
23	89	•	2174	Ŋ	E95965	hypothetical
24	88.5		321	N	A47369	RNA-binding
25	87	11.2	590	_	A45621	leishmanolysin (EC
26	87		599	N	B42049	leishmano
27	87	٠	599	N	A44951	leishmano
28	87	•	602	_		leishmano
ပ္	87	-1			PL0221	

4 4	43	42	41	40	39	38	37	36	S	34	ω ω	32	31	30
82.5	83	83.5	83.5	84	84	84.5	85	85	85	85.5	96	86	. 87	87
10.6	10.7	10.8	10.8	10.8	10.8	10.9	11.0	11.0	11.0	11.0	11.1	11.1	11.2	11.2
382	639	1635	423	764	439	340	967	575	401	438	582	447	1537	1537
N	<b>N</b>	N	N	ν	N	N	N	N	N	N	N	N	N	N
F90892	C42049	AI0452	T19581	H71607	AC1182	A83401	S66852	S35327	C88571	T35789	F70675	G84687	C81558	F86509
nypornerical proce probable outer mem	leishmanolysin (EC	hemolysin [importe	hypothetical prote	hypothetical prote	probable sugar ABC	hypothetical prote	hypothetical prote	protein kinase sgg	protein C05B5.3 (i	probable secreted	probable PPE prote	probable disease r	conserved hypothet	CT147 hypothetical

## ALIGNMENTS

Ş	B 8	B &	Quer Best Matc	C; Key C; Key F;1-2 F;21-:	A;Gen C;Fun A;Des	A;Status: I A;Molecule A;Residues: A;Note: sec C:Genetics:	A;Refi A;Coni A;Acci	A;Not R;Col J. Ba A;Tit	A;ACC A;Mol A;Res	A; Mol A; Res A; Cro	A;Tit. A;Ref	R;Col	C;Dat	JC6039 fimbri	DECITE OF
121 HEMAHANQTASDSSYMVRQVGFGNNATANQY 151 :	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120 	1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 	Query Match 89.0%; Score 690; DB 2; Length 151; Best Local Similarity 91.4%; Pred. No. 4.7e-51; Matches 138; Conservative 2; Mismatches 11; Indels 0; Gaps 0;	F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat>	A;Gene: agfA C;Function: A;Description: major component of thin aggregative fimbriae	A;Status: preliminary A;Molecule type: protein A;Residues: 21-33 <co3> A;Note: sequence extracted from NCBI backbone (NCBIP:45936) C:Genetics:</co3>	A;Reference number: A44898; MUID:91310586; PMID:1677357 A;Contents: 27655 A;Accession: A44898	on A K.H. tion	A;Accession: P-6015 A;Molecule type: protein A;Residues: 21-52 <co2> A;Experimental source: strain 27655-3b</co2>	A;Molecule type: DNA A;Residues: 1-151 <col/> A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714	A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A;Reference number: JC6039; MUID:96146512; PMID:8550497 A:Accession: JC6039		C.)Species: Salmonella enteritique C:)Date: 31-Dec-1996 #Bequence revision 31-Dec-1996 #text_change 08-Oct-1999 C.)Cococcion. TC6030. DC6015. TA4898	GEOORIA GEORGIA Fimbrin protein agfA precursor - Salmonella enteritidis	

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A,Experimental source: strain Ki2, substrain W3110
A,Mote: the nucleotide sequence was submitted to the EMBL Data Library, Auc R,BBlattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A,Title: The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUID:97426617; pMID:9278503
A,Accession: G64846
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Nilternate names: csgA protein; major curlin protein
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01
C;Accession: $70788; 664846; $31202; $34560; $34559
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production A;Reference number: $70783; MUID:96414468; PMID:8817489
A;Accession: $70788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      curlin protein csgA precursor - Escherichia coli (strain
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A;Residues: 1-151 <HAM>
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A; Residues: 1-151 < PAR>
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A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0635
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                  ;Residues: 1-151 <BLAT>
;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1;
;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1;
;Experimental source: strain K-12, substrain MG1655
;Experimental source: strain K-12, substrain MG1655
;Experimental source: strain K-12, substrain MG1655
;Experimental source: strain K-12, substrain MG1655
;Experimental source: strain K-12, substrain MG1655
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;Experimental source: strain K-12, substrain MG1655
;Experimental source: strain K-12, substrain MG1655
;Experimental source: strain MG1655
;Experimen
                                                                                                                                                                                                                        Status: nucleic acid sequence not
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                                                                                                                                                                                          Molecule type: DNA
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Best Local
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Pred. No. 4.7e-51
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ies, R.M.; Dowd,
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                                                                                                            PID:g1787279
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MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL

QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVV MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGHHGGGGNNSGPNSELNIYQYGGGNSALAL

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R;Hayashi, T.; Makino, gasawara, N.; Yasunaga, DNA Res. 8, 11-22, 2001
                                                                                                                                                                                     A,Title: Complete genome sequence of enterohemorrhagic Escherichia A,Reference number: A99629; MUID:21156231; PMID:11258796 A,Accession: D90806
                                                                                                                                                                                                                                                                                    curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, su
C;Species: Escherichia coli
C;Date: 18-7ul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: D90806
                                                                        A;Gene:
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A;Cross-references: EMBL:L04979; NID:g290424;
A:Experimental source: strain K-12, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Olsen, A.N.; Arnqvist, A.M. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number:
A; Accession: S31202
A; Molecule type: DNF
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A; Accession: S34559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i)Description: major component of wild-type curli; interaction between CsgA and Note: curli are thin, coiled fibers expressed on the surface of Escherichia co and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers;1-20/Domain: signal sequence #status predicted <SIG>
          Matches
                      Query Match
Best Local Similarity
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                                                                        ECs1420
          104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TDARNSDLTITOHGGGNGADVGQGSDDSSIDLTORGFGNSATLDOWNGKNSEMTVKQFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                   Makino, K.; Ohnishi,
Kasunaga, T.; Kuhara,
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
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                    66.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.8%;
      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
Score 511.5; DB 2;
Pred. No. 4.6e-36;
"" matches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 533; DB 2;
Pred. No. 7.1e-38;
                                                                                                                                                                                                                                                     M.; Kurokawa, K.; Ishii S.; Shiba, T.; Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     October 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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W3110
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                                                                                                                                                                                                                                                                                                                                  coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                      Ishii,
     Indels
                                Length
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                                    152;
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Shinagawa,
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                                                                                                                     GSPDB:GN00154
   1;
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                                                                                                                                                                                                                       coli
   Gaps
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hypothetical protein csgA [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 C;Species: Escherichia coli (c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: H85665
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-409 <WIL>
A;Residues: 1-409 <WIL>
A;Cross-references: EMBL:Z69383; PIDN:CAA93412.1; GSPDB:GN00022; CESP:F13E9.
A;Experimental source: clone F13E9
                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F13B9.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T20847
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                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A;Reference number: Z19332 A;Accession: T20847
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R; McMurray, A.
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A;Experimental source: strain O157:H7, substrain EDL933
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A;Introns: 32/1; 275/3; 337/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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Best Local S
Matches 104
                                                                                                                                                  ;Superfamily:
                                                                                                                                                                                                          Gene: CESP:F13E9.4
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Best Local
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                                   15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG
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                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QADARNSDITITQHGGGNGADVGQGSDDSSIDITQRGFGNSATLDQWNGKDSHMTVKQFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGNGAAVDQTASNSTVNVTQVGFGNNATAHQY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THEMAHANQTASDSSVMVRQVGFGNNATANQY 151
SGOQASGSMNSFGGOGGYGONONGFGGOSGFSGOSGWGSNSLSSANSNGNNNOG--SSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      loricrin
                                                                         Conservative
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                                                                 13.0%; Scu.
23.3%; Pre
----ive 26;
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                                                                                         Score 101; DB
Pred. No. 0.4;
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Pred. No. 4.6e-36;
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                                                                                                                                                                                                                                                                                                                                                                                 February
                                                                         Mismatches
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                                                                                                             DB 2;
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                                                                                                             Length 409
                                                                         Indels
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Best Local
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A; Molecule type: DNA
A; Residues: 1-1748 <TAY>
A; Residues: 1-1748 <TAY>
A; Cross-references: RMBL:L03710; NID:g161751; PID:g161752
A; Cross-references: EMBL:L03710; NID:g161751; PID:g161752
R; Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
Nucleic Acids Res. 21, 4610-4614, 1993
A; Title: Retroviral-type zinc fingers and glycine-rich repeats in A; Reference number: $42135; MUID:94051569; PMID:8233798
A; Accession: $42135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Genetic code: SGC5
A;Introns: 85/3; 136/1; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 708/3; 777/3;
C;Keywords: zinc finger
E;1164-1450/Region: glycine-rich
F;1451-1464/Region: zinc finger CCHC motif
F;1478-1491/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1530-1543/Region: zinc finger CCHC motif
F;1579-1592/Region: zinc finger CCHC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-1
A;Residues: EMBL:L03710
A;Cross-references: EMBL:L03710
R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A;Reference number: S03650; MUID:88189811; PMID:3357771
A;Accession: S03650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773
A;Cross-references: EMBL:X06462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1626-1748/Region: glycine-rich
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1723 ----WGSNNQAS 1730
                                                                                                                                                                                                                                                 1640 QFGGGGNSNGGQSWGTSSGSDWN
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                        QTGGGWGSNDN-----QQQQNENTGGGGWGSSN-
                                                                                                                                                                             GADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMV 137
                                                                                                                                                                                                                                                                                                         QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT----QSGYGN
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                                                          ROVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATA 148
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Pred. No. 3.1;
16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1748;
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RESULT
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fimbrin prote
C;Species: Sa
C;Date: 31-De
C;Accession:
   curlin nucleator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleation component of curlin monomers [imported] - Salmonella C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AH0635
                                                                                                                                                                                                                                                                                          A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Parkhill, J.; Dougan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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J. Bacteriol. 178, 662-667, 1996
A;Title: Salmonella enteritidis agfBAC operon encoding thin,
A;Reference number: JC6039; MUID:96146512; PMID:8550497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: agfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:U43280; NID:g1184712; A;Experimental source: strain 276755-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: JC6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type:
                                                                                                                                                                                                                                                                                                                                        ;Molecule type: DNA;Residues: 1-151 <PAR>
                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                          Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.; Moule, S.; O'Gaora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Note:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keywords: fimbria
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                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                NGFRNNATIDOWNAKNYD-OLVTRVVTHEMAHANOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                  GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                                                                                                                                                    GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST----IELTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGGNNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGFRNNATIDQWNAKNYD-QLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 signal sequence #status
ct: fimbrin protein agfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              minor component of thin aggregative fimbriae ae bind to fibronectin, plasminogen, tissue plasminogen
   protein
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                                                                                                                                                                                                                                                                                                                        GB:AL513382;
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 csgB
                                                                                                                                                                                                                                     12.7%;
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                                                                             -AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
 precursor
                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                   PIDN: CAD08267.1; PID: g16502314; GSPDB: GN00176
                                                                                                                                                                                                                                       Score 98.5;
Pred. No. 0
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7; Mismatches
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K.D.; Thomson, N.R.;
                                                                                                                                                                                                                       Mismatches
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#status predicted <MAT>
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 Escherichia
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coli
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(strain
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                                                                                                                                                                                                                     19;
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K-12
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                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <HAY>
                                                                                                                                                                                                                                                                                                   C;Species: Escheric
C;Date: 18-Jul-2001
C;Accession: C90806
                                                                                 A;Gene:
                                                                                                                                                                                                A; Reference number: A; Accession: C90806
                                                                                                                                                                                                                                                 gasawara, N.; Yasunaga,
DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                               R;Hayashi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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Matches
                                             Query Match
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              30;
                               Similarity
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              Conservative
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                              12.5%;
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minor curlin subunit precursor CsgB [imported] -
C;Species: Escherichia coli
                                                                                                                                                                           A; Title: Complete genome sequence of enterohemorrhagic Escherichia A; Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: minor component of wild-type curli; interaction between CsgA and CsgB A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli the and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Au;
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A;; Rose, D.J.; Mau, B.; Shao, Y.
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A;Title: Expression of two csg operons is required for A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli A; Reference number: A64720; MUID:97426617; PMID:9278503
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Cross-references: GB:BA000007; PIDN:BAB34842.1, PID:g13360879; GSPDB:GN00154 Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                   Date: 18-Jul-2001 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGSSNRAK-IDQTGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY
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                                                                                                                                                                                                                                                              K.; Ohnishi,
, T.; Kuhara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.5%; Score 96.5; DB 2; 25.6%; Pred. No. 0.31; tive 24; Mismatches 46;
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                                                                                                                                                                                                                                                              Kurokawa, R
Shiba, T.;
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                                                                                                                                                                                                                                                              C.; Ishii, K.;
Hattori, M.;
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24;

Mismatches

46; ν,

17;

Gaps

4

Score 96.5; DB Pred. No. 0.31;

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Length 151;

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Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70604
                                                                                                                                                                                                                                         A;Residues: 1-552 <COL>
A;Residues: 1-552 <COL>
A;Cross-references: GB:292774; GB:AL123456; NID:g3261729; PIDN:CAB07133.1; PID:g1877289
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, ; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: G85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Escherichia coli
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                                                                                           Query Match
Best Local S
Matches 41
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Best Local Similarity
  353
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                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSANAALALQSDARKSE----TTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAPGIAAAAGYDLANSEYNFAVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQ
  SGSGNIGVENTGANTLVP--
                                           SGSALAGV-----VPQWGGGGNHNGGGNSSGPD---STLSIYQYGSANAALALQSDA
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                                                                                                                                                                                            Phaseolus
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                                                                                        Score 93.5; DB 2; Length 552; Pred. No. 2.4; 1; Mismatches 58; Indels 3
  -GDLNNLGVGNSGNANIGFGNAGVLNTGFGNASILNTGLG
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lanta, E.;
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LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD

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probable sugar ABC tr
C;Species: Listeria i
C;Date: 27-Nov-2001 #
C;Accession: AD1539
                                                                                                                                                                                                                                                                                                                 DNA-binding protein ovo - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_chan C;Accession: A56038 R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.;
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AD1539
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
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                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-1028 <GAR>
A;Cross-references: GB:U11383; NID:g520526;
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A;Title: Multiple products from the shavenbaby-ovo gene A;Reference number: A56038; MUID:95021209; PMID:7935398
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A;Cross-references: GB:AL592022; PIDN:CAC96084.1; PID:g16413303; GSPDB:GN00178
A;Experimental source: strain Clip11262
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.; Dominguez-Bernal, G.; Duchaud, E.; Du
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A;Accession: A56038
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                                                                                     A;Cross-references: FlyBase:FBgn0003028
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Matches 40
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    Conservative
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23.8%; Pred. No. 2
                        11.9%;
26.7%;
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    14;
                        Score 92.5;
Pred. No. 5
    Mismatches
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Mismatches
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urand, L.; Dussurget, O.;
                                                                                                                                                     PIDN: AAB60216.1; PID: g520527
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; Entian, K.D.;
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Voss, H.; W
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Search Job ti	Db	8	Дb	8	DЬ
Search completed: March 11, 2004, 18:42:11 Job time : 11.3 secs	148 HHHQHNNNNNNNGGQTSMMGHPFYGGNPSA 177	123 MAHANQTASDSSVMVRQVGFGNNATA 148	105GGNGYINCGGVG-GENNSLDGNNLLNEASVSNYNESNSKFHNHH 147	63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHE 122	

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Result
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-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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SPECIES-S. enteritidis; STRAIN=27655-3B;
MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emoedy L., Mueller K.-M., T;
"Purification and characterization of thin,
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Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA,
the structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
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J. Bacteriol. 173,4773-4781 (1991).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Riley M., Collado-Vides J., Riley M., Collado-Vides J., Riley M., Collado-Vides J., Riley M., Collado-Vides J., Riley M., Collado-Vides J., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., Riley M., R
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STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
                                                                                                                               MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emoedy L., Trust T Purification and characterization
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STRAIN=K12 / YMEL;
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"The RpoS sigma factor relieves
repression of csgA, the subunit
Escherichia coli.";
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Enterobacteriaceae; Eschei
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(Rel. 34, Last sequence up
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SIMILARITY:

BELONGS TO THE CSGA/CSGB FAMILY.

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RESULT 3
CSGA ECO57
ID CSGA ECO57
AC Q33U<sup>2</sup>4;
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Best Local S
Matches 106
                       STRALM-0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

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28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
Escherichia coli 0157:H7.
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Fimbria;
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NCBI_TaxID=83334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria;
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A -> E (IN REF. 1).
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Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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ccheв 27;
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                               Escherichia coli O157:H7.",
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Best Local S
Matches 104
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SEQUENCE FROM N
STRAIN=0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yohashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tot Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasu Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RComplete genome sequence of enterohemorrhagic Escherichia co O157:H7 and genomic comparison with a laboratory strain K-12. DNA Res. 8:11-22(2001).

-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AN TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; H856
Fimbria;
MEDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wa: Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                             Q8Z7M3;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                        CSGB
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                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                 NCBI_TaxID=601;
                                                                                                                                                                                                              Enterobacteriaceae;
                                                                                                                                                                                                                                    Bacteria;
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                                                                                                                                                                                                                                    Proteobacteria;
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152
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                                                                                                                                                                                                                                    Gammaproteobacteria;
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MAJOR CURLIN SUBUNIT.
77777004DDE91243 CRC64;
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Pred. No. 1.5
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on update)
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ka M., Tobe
N., Yasunaga 7
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K-12.";
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RESULT 5
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Matches 34
SPECIES=S.typhimurium; STRAIN=SR-11; MEDLINE=98117058; PubMed=9457880; Romling U, Bian Z., Hammar M., Sierralta W.D., Normark S. "Curli fibers are highly conserved between Salmonella typh Escherichia coli with respect to operon structure and regu D. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                CSGB_SALTY STAN
P55226;
01-OCT-1996 (Rel. 3
01-OCT-1996 (Rel. 3
28-FEB-2003 (Rel. 4
                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602, 592;
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                      Salmonella typhimurium, and Salmonella enteritidis.
                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
Minor curlin subunit precursor (Fimbrin SEF
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@sisb-sib.ch).
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Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

Burland V. Kodoyianni V., Schwartz D.C., Blattner F.R.;

Burland V. Kodoyianni V., Schwartz D.C., Blattner Typhi st
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Quail M.A., Rutherf
Whitehead S., Barre
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Krogh A., Larsen T.S., Leather S., Moule S., O'O
Quail M.A., Rutherford K., Simmonds M., Skelton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of a enterica serovar Typhi CT18."; Nature 413:848-852(2001).
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- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLICOLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TELERONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPON
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AE016840; AAO69400.1; -.
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y2 / ATCC 700931;
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28.8%;
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Pred. No. 0.09
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CSGB_ECOLI
STANDARD; PRT; 151
P39828;
01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence upda
28-FEB-2003 (Rel. 41, Last annotation up
Minor curlin subunit precursor.
CSGB_OR_B1041 OR_Z1675 OR_ECS1419.
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Best Local
           Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Escherichia
NCBI_TaxID=562, 83334;
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SEQUENCE FROM N.A.
SPECIES=S typhimuri
NCBI_TaxID=562,
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                                                       Escherichia coli, and Escherichia coli 0157:H7.
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SIGNAL 1 21 POTENTIAL.
CHAIN 22 151 MINOR CURLIN
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EMBL; AE008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
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MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Ban
"Salmonella enteritidis agfBAC operon encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).
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MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney B.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
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- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
- COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY F
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TC
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
CURLIN MONOMERS.
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                                       Gammaproteobacteria;
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Pred. No. 0
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COFC5430E6DD361D CRC64;
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SEQUENCE FROM MC4100;
STRAIN=K12 / MC4100;
STRAIN=K12 / MCDLINE=96414468; PubMed=8817489;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of "Expression of two csg operons is required for production of "Expression of two csg operons is required for production of "Expression of two csg operons is required for production of "Expression" and congo red-binding curli polymers in Escherichia
                                                                 Arnqvist A., Olsen A., Normark S.;

"Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coli can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";

Mol. Microbiol. 13:1021-1032(1994).

-I- FUNCTION: CUBLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROW TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21156231; PubMed-11256796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Hayashi T., Makino E., Ohnishi M., Kurokawa K., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apodaca J., Anantharaman T.S., Lin J., Welch R.A., Blattner F.R., "Genome sequence of enterchaemorrhagic
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MEDLINE=21074935; PubMed=11206551;
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Science 277:1453-1474(1997).
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                       CURLIN MONOMERS
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P51521; Q9XZU4;
01-OCT-1996 (Re
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                          This
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-Oregon-R;

MEDLINE=91293102; PubMed=1712294;

MEDLINE=91293102; PubMed=1712294;

Mevel-Ninio M.T.M., Terracol R., Kafatos

"The ovo gene of Drosophila encodes a zin

for female germ line development.";

EMBO J. 10:2259-2266(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavenbaby-ovo gene region melanogaster: relationship to genetic complexity."; Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovo protein (Shaven OVO OR SVB.
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MEDLINE=95021209; PubMed=7935398;
MEDLINE=95021209; PubMed=7935398;
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EMBL; AE000205; AAC74125.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                 FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF ILINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.
SUBCELLILAR IOCATION: Nuclear (potential).

DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING COGENESIS. STORED IN THE IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINENT OF THE GERM LINE PRECURSOR POLE CELLS.

SIMILARITY: Contains 4 C2H2-type zinc fingers.
                          SWISS-PROT entry is copyright. It is produced
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EG12621; csgB.
Signal; Complete proteome.
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
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InterPro; IPR007087; Znf_C
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EMBL; X59772; CAB36921.1; ALT_SEQ.
PIR; A56038; A56038.
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entities requires a license agreement (See http://www.isb-
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                      095272;
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                                                            HHHOHNNNNNNGGOTSMMGHPFYGGNPSA 177
                                                                                                                           LLKVAAFAAIVVSGSALAGVVPQWCGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
                                                                                                 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHE
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26.7%;
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity and can modify TRF1, and thereby regulation of telomere length.
-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20556282; PubMed=10988299;
Chi N.-W., Lodish H.F.;
"Tankyrase is a Golgi-associated mitogen-activated properties is a Golgi-associated mitogen-activated probabitrate that interacts with IRAP in GLUT4 vesicles.
J. Biol. Chem. 275:38437-38444 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nicotinamide + {ADP-D-ribosyl} (N+1) acceptor.
-!- SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with the cytoplasmic domain of LNPEP/Otase in SLC2A4/GLUT4-vesicles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith S., de Lange T.;
"Cell cycle dependent localization of the to nuclear pore complexes and centrosomes.
J. Cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cook B.D., Dynek J.N., Chang W., Shostak "Role for the related poly(ADP-Ribose) po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
MEDLINE=21602874; PubMed=11739745;
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TNKS OR TINI OR TINI OR PARPL.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human telomeres.",
1. Cell. Biol. 22:332-342(2002).
- FUNCTION: May regulate vesicle
                                                                                                                                                                                                                                                                                                                                                                            · TISSUE
                                                                                                                                                                                                                   PTM: Upon insulin-stimulation, phosphorylated on serine residues by MAPK kinases.

PTM: ADP-ribosylated (-auto).

SIMILARITY: Belongs to the PARP family.

SIMILARITY: Contains 15 ANK repeats.

SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binds to the N-terminus of telomeric TRF1 via the ANK repeats. SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi a with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TNKS is found in the nucleus, associated with TRF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: May regulate vesicle trafficking and modulate subcellular distribution of SLC2A4/GLUT4-vesicles. Has I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=095271-2; Sequence=VSP_004538, VSP_004539;
Note=No experimental confirmation available;
SSUE SPECIFICITY: Ubiquitous; highest levels in testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=095271-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
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                     Noved. Usage by and for (See http://www.isb-sib.
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at human telomeres.";
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                                                                                                                                            a collaboration - MBL outstation
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SMART; SM00248; ANK; 17.

SMART; SM00454; SAM; 11.

PROSITE; PS50008; ANK REPEAT; 15.

PROSITE; PS50297; ANK REP REGION; 1.

PROSITE; PS50105; SAM DOMAIN; 1.

Transferase; Glycosyltransferase; NAD; Golgi stack; Telomere;

Transferase; Glycosyltransferase; NAD; Golgi stack; Telomere;
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EMBL; AF082558; AAC79843.1;
EMBL; AF082559; AAC79844.1;
HSSP; Q00420; IAWC.
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                                                                                                                                                                                                                                         VARSPLIC
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Pfam; PF00536; SAM; 1.
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                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002110; ANK. InterPro; IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0000781; C:chromosome, telomeric region; IDA.
GO:0003950; F:NAD ADP-ribosyltransferase activity; IDA.
GO:0005515; F:protein binding; IPI.
GO:0007004; P:telomerase-dependent telomere maintenance;
205
                    121
                                          158
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                                                                                                                              l Similarity 28.4
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                                                                           VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS
                   HEMAHANQTASD----SSVMVRQVGFG 143
                                          GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG-
                                                              KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
                                                                                                       VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
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ANVNAKDMAGRKSSPLHFAAGFG 227
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                                                                                                                             Score 90.5; DB Pred. No. 5.6; L6; Mismatches
                                                                                                                                                                                                                                                                                   POLY-HIS.
POLY-PRO.
POLY-SER.
                                                                                                                                                                                                                                                                                                                   SAM.
                                                                                                                                                                                  E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1184.
                                                                                                                                                                                                                /FTId=VSP 004538.
Missing (In isoform 2).
/FTId=VSP 004539.
H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
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RESULT 9 MSA2\_PLAF2

STANDARD;

PRT;

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RESULT 10
VG38_BPT2
ID VG38_BPT2
AC P07875;
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CHAIN
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=70150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M59765; AAA29691.1; -. PIR; B39112; B39112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSA2_PLAF2 STANDARD; PRT; 347 AA (03646; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erythrocyte.
-!- SUBCELLULAR LOCATION: Attached to the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: May play a role
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3PI-anchor; Merozoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malaria; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smythe J.A., Coppel R.L., Kemp D.J., Anders R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001136; MSA 2.
Fam; PF00985; MSA 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural diversity in the Plasmodium falciparum merozoite surface
                                                                                                                                       182
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                                                                                                                                                                                 VVTHEMAHANQTASDSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                           AGNGAGNGAGNGAGNGAVASAGNGAVASAGNGAVASAGNGAVAERSSSTPATTTTT
                                                                                                                                                                                                                                                                    ETTITQSGYGNGA--DVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQ-----LVTR
                                                                                                                                                                                                                                                                                                                   AGNGAVASAGNGAGNGAGNGAGNGAGNGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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HYDROPHOBIC, REMOVED DURING
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
(MSA-2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                                                                                                       71;
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Best Local
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01-NOV-1991
01-NOV-1991
10-OCT-2003
                                  Webb J.R., Button L.L., McMaster k.w. "Heterogeneity of the genes encoding of Leishmania donovani.";
                                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (
                                                                                 MEDLINE=92107220;
                                                                                               STRAIN=LV9
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                   Leishmania donovani
Eukaryota; Euglenoz
                                                                                                                                                                                          endopeptidase)
                                                                                                                                                                                                                                                                                                      LEIDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF05268; GP38; 1.
Fiber protein; Phage re
SEQUENCE 262 AA; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87283911; PubMed=3302276;
Riede I., Drexler K., Eschbach M.L., Henning U.;
"DNA sequence of genes 38 encoding a receptor-recognizing bacteriophages T2, K3 and of K3 host range mutants.";
J. Mol. Biol. 194:31-39(1987).
-i- FUNCTION: V938 is at the tip of the long tail fibers a the phage recognition site for the cellular receptor.
-i- MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA v
T4-like viruses
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Viruses; dsDNA viruses,
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01-AUG-1990
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InterPro; IPR007932; Tail_fibre_GP38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
Biochem. Parasitol. 48:173-184(1991). FUNCTION: Has an integral role during in the mammalian host.
                                                                                                                                    ryota; Euglenozoa;
TaxID=5661;
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1990 (Rel. 15,
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                                                                                                                                                                                                                                                                                        STANDARD;
                                                                PubMed=1762629;
L.L., McMaster R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25801 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recognition.
rean1 MW; 0567366918F6C745 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                 Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89; DB 1; Length 262;
Pred. No. 1.2;
9; Mismatches 38; Indels
                                                                                                                                                                                                    3.4.24:36) (Cell surface protease) (GP63 protein) (Promastigote surface
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            infection
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                                                    glycoprotein
            of macrophages
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RESULT 12
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                                                 Leishmania chagasi.
Eukaryota; Euglenozoa;
EUSI_TaxID=44271;
                                                                                                                                                                                                                                                                            LEICH
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METAL
ACT_SI
 MEDLINE=90205976;
                   SEQUENCE FROM N.A.
                                                                                                                             endopeptidase).
                                                                                                                                         01-ARR-1990 (Rel. 14, Created)
01-ARR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (
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CHAIN
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InterPro; IPR001577; Peptidase
Pfam; PF01457; Peptidase_M8; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 p1 and basic residues at P2 and P3. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-CPACTOR: Binds 1 zinc ion per subunit (By similarity). SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchol SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                           TEICH
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PubMed=2320059;
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                                                                        Kinetoplastida;
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ZINC (CATALYTIC) (
EXINILARITY SYSIMILARITY                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 87;
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ZINC (CATALYTIC) (BY SIMILARITY).
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                                                                        Trypanosomatidae; Leishmania
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"Leishmania
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                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zymogen;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M80672; AAA29238.1; -. EMBL; M28527; AAA29235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed during development of Leishm. promastigotes to an infectious form."; J. Biol. Chem. 267:1888-1895(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00782; ĽSHMANOĽYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptidase M8.
Pfam, PF01457; Peptidase M8; 1.
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                                                                                                                                                                               LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92112918; PubMed=1370484;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic pl' and basic residues at P2 and P3'. A model r cleaved at -Ala-Tyr-| Leu-Lys-Lys-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to peptidase family M8.
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le implicated in cellular adhesion lacks an
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MEDLINE-95406217; PubMed-7675788;
Schlagenhauf E., Etges R., Metcalf P.;
"Crystallization and preliminary X-ray diffraction studies
leishmanolysin, the major surface metalloproteinase from Le
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"Structure of the glycosyl-phosphatidylinositol membrane the Leishmania major promastigote surface protease.";
J. Biol. Chem. 265:16955-16964(1990).
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"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
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Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                      EMBL; Y00647; CAA68673.1;
                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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SIMILARITY: Belongs to peptidase family M8.
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PL0221; PL0221
1LML; 17-SEP-9
                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration -
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                                                                                                                                  non-profit institutions as long
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el. 14, Last sequence update)

el. 42, Last annotation update)

precursor (EC 3.4.24.36) (Cell

glycoprotein) (GP63 protein) (I
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InterPro; IPR001577; Peptidase M8.
Pfam; PF01457; Peptidase M8; 1.
PRINTS; PR00782; LSHMANOIYSIN.
PROSITE; PS00142; ZINC PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Hydrolase; Metalloprotease; Glycoprotein; 3D-structure; Lipoprotein.
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SEQUENCE FROM N.A.
STRAIN=MNYC/BZ/62/M379;
MEDLINE=93149206; PubMed=8426614;
Medlina-Acosta E., Karess R.E., Russell D.G.;
"Structurally distinct genes for the surface mexicana are developmentally regulated.";
                                                                                      Leishmania mexicana.
Eukaryota; Euglenozoa;
NCBI_TaxID=5665;
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(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
sin C1 precursor (EC 3.4.24.36) (C
ace glycoprotein) (GP63 protein) (ce)
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                                                                                                               Trypanosomatidae; Leishmania.
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Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Zymogen; Signal; Cell adhesion; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEROPS; M08.001; -.
GlycoSuiteDB; P43150; -.
InterPro; IPR006025; Pept M
InterPro; IPR001577; Peptida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest
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or send an email to license@isb-sib.ch).
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PRINTS; PR00782; LSHMANOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X64394; CAA45733.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ol. Biochem. Parasitol. 57:31-46(1993).

I- FUNCTION: Has an integral role during in the mammalian host.

I- CATALYTIC ACTIVITY: Preference for hydrony and basic residues at P2 and P3'.

Cleaved at -Ala-Tyr-(-Leu-Lys-Lys-.

COPACTOR: Binds 1 zinc ion per subunit
                                                                                                                                                                                                           Local Similarity
les 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amastigote forms.
SIMILARITY: Belongs to peptidase family M8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                               253
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                                                                                                                                             ASRYDOLVTRVVTHEMAHA
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(Rel. 39, Last sequence update)
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89.5%;
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Matches 45
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CHAIN
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InterPro; IPR005346; Autotransporter.
Pfam; PF03797; Autotransporter.
                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THE 120 KDA SUFFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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                                                                                                                                                                                                                                                                                                      TIGRFAM8;
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Rickettsiaceae; Rickettsieae;
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SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By similarity).
SUBCELLULAR LOCATION: Cell wall. This bacterium is covered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
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601
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                                                                                                                                           VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK
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SSLTNAQTLTISGT---
                           EMAHANQTASDSSVMVRQVGF--GNNATANQY 151
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ilarity 29.6%;
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                                                                                                                                                                                                                               168097 MW;
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-IGIIGANNTTLGQF
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Pred. No.
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ompB); 32 kDa beta peptide)
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1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 March 11, 2004, 18:23:54; Search time 30.5 Seconds (without alignments) 1562.074 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1017041 seqs, 315518202 residues
sp_invertebrate:*
sp_mammal:*
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sp_organelle:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12	11	10	9	80	7	σ.	5	4.	w	2	_	Result No.
99	99.5	100	100	101	103	104	109	122	122	385	431.5	508.5	553	591.5	681	Score
12.8	12.8	12.9	12.9	13.0	13.3	13.4	14.1	15.7	15.7	49.7	55.7	65.6	71.4	76.3	87.9	Query
1748	171	362	151	409	362	7716	139	502	29	76	150	152	149	150	152	Query Match Length
σ	16	16	N	ű	16	16	16	16	N	Ŋ	N	16	N	N	N	DB
Q94821	Q89JI3	Q8EV84	Q7X238	Q19414	Q89D03	Q7UWZ8	Q8EIH3	Q8EIH4	Q9S3J5	Q54069	Q7X237	QBCW63	Q7X240	Q7X243	033802	Ü
Q94821 tetrahymena	Q89ji3 bradyrhizob	Q8ev84 mycoplasma	Q7x238 enterobacte	Q19414 caenorhabdi	Q89d03 bradyrhizob	Q7uwz8 rhodopirell	Q8eih3 shewanella	Q8eih4 shewanella	Q9s3j5 escherichia	Q54069 salmonella	Q7x237 enterobacte	Q8cw63 escherichia	Q7x240 citrobacter	Q7x243 citrobacter	O33802 salmonella	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
90.5	90.5	91	91.5	91.5	92.5	92.5	92.5	92.5	92.5	92.5	93	93	93.5	93.5	93.5	93.5	93.5	94	94.5	95.5	95.5	95.5	95.5	96	96	96.5	6	98
11.7	11.7	11.7	11.8			11.9		11.9	11.9	11.9	12.0	12.0	12.1	12.1	12.1	12.1	12.1	12.1	12.2	12.3	12.3	12.3	12.3	12.4	12.4	12.5		12.6
1209	152	191	1615	1422	1354	1351	1222	1222	440	348	3552	3501	623	552	552	453	453	179	453	1286	624	160	151	157	154	160	151	713
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Q89CK5	Q7X241	QBTFA6	Q9KKA8	Q8EFU3	Q8MPN4	Q8SX56	6TBL8	Q9W4F0	Q92DG1	093397	Q8XSD6	90,1480	Q8VIY0	Q7TW76	P96840	Q9NGF7	Q9NGF6	033801	Q9N6M8	Q841Y5	QBNIV1	QBCW64	Q7X244	Q88HG0	Q89JI5	Q83RU7	Q7UCZ1	Q9N8N5
Q89ck5 bradyrhizob	Q7x241 citrobacter	Q8tfa6 saccharomyc	Q9kka8 rickettsia		Q8mpn4 drosophila	Q8sx56 drosophila	Q8t819 drosophila	Q9w4f0 drosophila	Q92dg1 listeria in	093397 cyprinus ca	Q8xsd6 ralstonia s	Q8y106 ralstonia s	Q8viy0 mycobacteri	Q7tw76 mycobacteri	P96840 mycobacteri	Q9ngf7 drosophila	Q9ngf6 drosophila				Q8niv1 neurospora	Q8cw64 escherichia	Q7x244 citrobacter	. Q88hg0 pseudomonas	Q89ji5 bradyrhizob	Q83ru7 shigella fl	Q7ucz1 shigella fl	Q9n8n5 trypanosoma

# ALIGNMENTS

ą	뮍	Ą	DЬ	ð	===	ŞQ	FT	3 2	RI	RT	RT	₽	R.A	25	RP	RN	õ	8	8	SO	2	DE	ΡŢ	DI	D1	AC	Ħ	O3
121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	61 SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNAKNYDQLVTRVVT 120	1 MKLLKVAAFAAIVVSGSAVAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	Query Match 87.9%; Score 681; DB 2; Length 152; Best Local Similarity 90.1%; Pred. No. 2e-46; Matches 136; Conservative 3; Mismatches 12; Indels 0; Gaps 0;	SEQUENCE 152 AA; 15401 MW; 9DA7DADC2364B006 CRC64;	NON_TER 152 152	σ	•	Salmonella typhimurium SR-11 with mouse small intestinal epithelial	"Expression of thin, aggregative fimbriae promotes interaction of		Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,	MEDLINE=98053981; PubMed=9393832;	SEQUENCE FROM N.A.	[1]	NCBI TaxID=602;	Enterobacteriaceae; Salmonella.	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	Salmonella typhimurium.		n (Fragment).	(TrEMBLrel. 19, Last	(TrEMBLrel. 05,	-1998 (TrEMBLrel.	033802;	O33802 PRELIMINARY; PRT; 152 AA.	RESULT 1

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RESULT
Q7X243
ID 243
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AC Q7
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Matches 119
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.", Infect. Immun. 72:4151-4158 (2003).

EMBL; AJ515701; CAD56675.1; -.
SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
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01-OCT-2003
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Citrobacter sp. Fec2.
Bacteria; Proteobacteria; Gamma; Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria;
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Q7X243;
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78.8%;
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Pred. No. 2.3e
L2; Mismatches
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                                                                       Score 553; DB 2;
Pred. No. 2.5e-36;
5; Mismatches 21;
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RESULT 5
Q7X23
ID Q7X2
AC Q7X2
AC Q7X2
AC Q7X2
DT 01-0
DT 01-C
DT 01-C
Curl
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MEDLINE=22388234; PubMed=12471157;

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Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515702; CAD56678.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cox J.M., Eglezos S., Woolcock J.B.;
"Virulence of Salmoneella entertidis in chickens correlates colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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                      Escherichia coli.
Bacteria; Proteob
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STRAIN-SE30;
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Enterobacteriaceae; Salmonella.
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  Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                             GNHXGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST
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                        Proteobacteria;
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                      Gammaproteobacteria; Enterobacteriales;
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Last annotation update)
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Pred Mismatches
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Pred. No. 2.1e-23;
D; Mismatches 1
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RESULT 8
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01-MAR-2003
01-MAR-2003
01-MAR-2003
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Red T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Meyer T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
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MEDLINE-99314153; PubMed=10386375;
La Ragione R.M., Collighan R.J., Woodward M.J.;
La Ragione R.M., Collighan R.J., Woodward Sistemated with "Non-curliation of Escherichia coli 078:K80 isolates associated with Inserti on in csg8 and reduced persistence in poultry infection."
FEMS Microbiol. Lett. 175.247-253(1999).
EMBL, AJ131756; CAB45380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete SEQUENCE 502 AA; 52441 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conserved hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the dissimilatory Shewanella oneidensis.";
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NCBI_TaxID=70863;
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                                                                                                                                                                                                                                                    29 GGNHNG----
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  ELV-AFATGEDNSIEISQEGDANFAYVDATGN
                                               EMAHANOTASDSSVMVRQVGFGN----NATAN
                                                                                                                                                DARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTH
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                                                                                                 KOKGDSNGAEFOVWGDSNDVDLKORGDANFATFGAYGTDNDFDLSSKGDNN
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27.0%;
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RESULT 10
Q7UWZB
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DT 01-OC
DT 01-OC
DT Hypot
GN RB166
OS Rhodc
OC Bacte
OC Planc
OX NCB1
RN I[1]
RA SEDUF
RC STRAJ
RA G10ec
RA Ludwin
RT Strai
RI Proc.
DR ENTA;
KW Hypot
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Best Local S
Matches 34
       Query Match
                                                  Hypothetical protein; SEQUENCE 7716 AA;
                                                                                                                                                                                Gloeckner F.O., Kube M., Bauer M., Teel:
Ludwig W., Gade D., Beck A., Borzym K.,
Schlesner H., Amann R., Reinhardt R.,
                                                                                                                                       strain 1
                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Planctomycetes; Planctomycetaceae; Pirell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Bisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                MEDLINE=22735913; PubMed=12835416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003
01-OCT-2003
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01-MAR-2003
01-MAR-2003
                                                                                                                                                           "Complete genome sequence of
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=117;
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Nat Riotechnol. 20:1118-1123(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7UWZ8;
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01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Minor curlin subunit CsgB, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22297686;
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NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shewanella oneidensis.
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                                                                                        Natl. Acad. Sci. U.S.A. 100:8298-8303(2003)
BX294135; CAD72214.1; -.
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Pred. No. 0.28
19; Mismatches
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                                          D391A25BD96405C0 CRC64;
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m K., Heitmann
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01-NOV-1996
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Q89D03;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                        F13E9.4 protein.
                                                                 Caenorhabditis elegans.
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EMBL, AP005962; BAC52907.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAMENO T., Nakamura Y., Sato S., Minamisawa K., Uchiur Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kav Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRLFLATTAAVAIATSALAQSSP---STSNSNPSTTQRQPDSTSTTPSSSTPSGSAQTNP
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362 AA; 39058 MW;
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Pred. No. 2.6;
14; Mismatches
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8; Mismatches
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1da T., Yamada
                                  Rhabditoidea;
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RESULT 13
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Matches 35
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Matches 37
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EMBL; AJ515702; CAD56677.1;
                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                            Enterobacteriaceae; Enterobacter.
NCBI_TaxID=28141;
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Bacteria; Proteobacteria;
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InterPro; IPR003677; Oncho
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Science 282:2012-2018(1998).
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T20847; T20847.
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37; Conserv
                                                                                                      Similarity
                                                                    AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT
                                                                                                                                                                                                                                                                                                                                                                                                                           NNKSLTTNQINEQ---ASNWASANSVQAQYIQYETNRSA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGN--GADVGQGADNSTIE---LTQNGFRNN--------ATIDQWNAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGQQASGSMNSFGGQGGYGQNQNGFGGQSGFSGQSGWGSNSLSSANSNGNNNQG--SSSG
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ITODGYGNSAKIIQKGSGNRANITQYGTQKTAVVVQ----KQSQMAIRVI 149
                      ITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNYDOLVTRVV 119
                                              AQIRQEGSKLLSVVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YONNOGRHOGOGGGHSSSSNSVMSNNGYSSNSGYGNNNGPTPSFLNNVSSSAAQDYYNIV
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                                                                                                                                         15985 MW; F0B82BD2A27882B7 CRC64;
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31.8%;
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Last annotation update)
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Pred. No. 1.6;
L2; Mismatches
                                                                                                                                                                                                                                                                                                                                             Created)
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Pred. No. 4.3;
6; Mismatches 66
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RESULT 15
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Q89JI3;
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01-JUN-2003
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Q8EV84;
01-MAR-2003
01-MAR-2003
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                                                                                                                                                                                                                                                                                                       Bradyrhizobium japonicum.
Bacteria; Proteobacteria;
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PROSITE; PS00013; PROKAR_LIPOPROTEIN;
Lipoprotein; Complete proteome.
SEQUENCE 362 AA; 38547 MW; 8DA27F:
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Yosahino C., Horino A., Shiba T., Sasaki T., Horino R., Shiba T., Sasaki T., I
"The complete genomic sequence of Mycoplasma I
intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
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                                                                                                                                                             EMBL;
                                                                                                                                                                                    "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
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                                                                                                                                                             AP005954; BAC50565.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGS-ALAGVVP-----QWGGGGGNHNGGGNSSG-----PDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSV--MVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLSIYQYGSANAALALQSDARKSETTITQSG-----YGNGADVGQGADNSTIEL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTESTFKGD-TYETWSAKVGDKKGT-----YAQASKQLDIKSINDLETQLGDSNN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPTIKKEVSLSGALSKIYDANKSTSDLIAEDIKANPTNYFDNGEALKDLIKDATVSVNGG
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                                                                                               AA;
                                                                                               17448 MW;
                                                                                                                                                                                                                                                                                       a A., iu.
M., Shimpo s
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24,
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   Score
Pred.
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                                                                                               995DB08C01498381 CRC64;
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   99.5;
No. 2;
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ki T., Hattori M.;
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                                                                                                                                                                                                                                                   symbiotic bacterium
                                                                                                                                                                                                                                                                                                                 M., Kawashima K., Wada T., Yamada
                                                                                                                                                                                                                                                                                                                                                                               Uchiumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                Length 171;
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Matches	40; Conservative 21; Mismatches 63; Indels 31; Gaps 4;	
¥	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	
ŏ	40 MRKLFFASVAVLALSSAAQAA	
¥	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVT 116	
ੱ ਹ	79 NGLTNDSSSTTQIGILNGASTMQGTSSPSLNNVSTVNQAGVQNSATTGQVAFGNNGSAIT 138	
₹	117 RVVTHEMAHANQTASDSSVMVRQVGFG-NNATANQ 150	
ğ	139 QNSFGPPALQNNSASVGQLSFGINTSTVSQ 168	
earch compob time :	earch completed: March 11, 2004, 18:40:45	

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Minimum DB
Maximum DB
                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                             seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          March 11, 2004, 18:13:53; Search time 45.9 Seconds (without alignments) 929.514 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-543-407-26
782
                                                                                                                                                                                                                                                                                                                                                          1586107 seqs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                               A_Geneseq_29Jan04:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compus
                                                                                          geneseqp1980s:*
geneseqp2000s:*
                 geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
                                                                         geneseqp2001s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compugen Ltd
                                                                                                                                                                                                                                                                                                                       1586107
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No. 1 2 2 3	Score 782 709 692 692	Query Match 100.0 90.7 88.5	Length 151 151 151	ผมผม	ID AAB36353 AAB36350 AAR74625 AAB36341	Description Aab36353 Ag Aab36350 Ag AAb36350 Ag AAb363615 Ag AAb363615 Ag
ი თ	687 675		151 151	ພ ພ	AAW23570 AAB36349	Aaw23570 Aab36349
7	617		151	w	AAB36354	
80	614		151	ω	AAB36346	
9	612		151	w	AAB36347	
10	609		151	w	AAB36352	
11	109	76.9	151	W	AAB36351	
12	600		151	w		
13	577		151	ω	AAB36348	
14	523	•	151	ω	AAB36343	
15	518	•	151	7	ABR82651	
16	507		120	N	AAR62761	
17	507		120	N	AAW23569	
18	445	56.9	142	N	AAR52664	
19	373		122	N	AAR52663	
20	188	٠	45	ω	AAB36316	
21	132	16.9	22	w	AAB36318	
22	123	٠	23	w	AAB36321	
23	123		23	w	AAB36326	
24	123	15.7	23	ω	AAB36338	
S T						

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 138; 139pp; English.

<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26
96	96	96	96.5	96.5	97.5	97.5	98.5	100	100	100	100	100	102	105	107	111	111	111	112
12.3	12.3									12.8							14.2		14.3
19	19	19	468	447	1028	850	738	3300	943	943	943	943	26	597	151	22	22	22	151
w	w	w	w	w	4	4	N	σ	N	N	N	N	7	4	w	ω	ω	w	w
AAB36328	AAB36336	AAB36323	AAG29727	AAG29728	ABB62708	ABB65764	AAW56163	ABU36445	AAY39175	AAY39032	AAW81745	AAW64378	ABR82649	AAU08231	AAB36342	AAB36337	AAB36327	AAB36322	AAB36344
Aab36328	Aab36336	Aab36323	Aag29727	Aag29728	Abb62708	Abb65764	Aaw56163	Abu36445	Aay39175	Aay39032	Aaw81745	Aaw64378	Abr82649	Aau08231	Aab36342	Aab36337	Aab36327	Aab36322	Aab36344
Salmonel.	Salmonell	Salmonell	Arabidops	Arabidops	Drosophil	Drosophil	New DNA &	Protein e	M. tubero	M. tuberc	M. tuberc	Mycobacte	E. coli V	Polypepti	Salmonell	Salmonell	Salmonel	Salmonel	Escherich

# ALIGNMENTS

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WPI; 2000-672631/65.
N-PSDB; AAC64629.
                                                                                                                                                                                         WO200060102-A2
                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                           Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                         AAB36353;
                                                                                                                                                                                                                                                                                     AAB36353 standard;
                                                                                                                           White AP,
                                                                                                                                                    05-APR-1999;
                                                                                                                                                                05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                             12-OCT-2000.
                                                                                                                                                                                                                             vaccine; immune response; immunogen
                                                                                                                                                                                                                                               AgfA::PT3#8 amino acid sequence SEQ ID NO:26
                                                                                                                                                                                                                                                            26-FEB-2001
                                                                                                                                       (UYVI-) UNIV VICTORIA.
                                                                                                                           Doran JL,
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                    99US-0127888P
                                                                                                                                                                                                                                                                                     protein; 151 AA
                                                                                                                           Collison
                                                                                                                           SK,
                                                                                                                           Kay WW;
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RESULT 2
AAB36350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 151; Conservative (
Recombinant agfA gene having which encodes foreign epitope protein useful for eliciting
                                                                                                                   N-PSDB; AAC64626.
                                                                                                                                               WPI; 2000-672631/65.
                                                                                                                                                                                                White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                 05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                          (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AgfA::PT3#5 amino acid sequence SEQ ID NO:20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36350 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 AA;
                                                                                                                                                                                                                                                                                                              99US-0127888P
                            having a segment replaced by a foreign DNA sequence epitope or antigen, expresses recombinant AgfA
                                                                                                                                                                                             Collison SK, Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
  immune
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Pred. No. 2.3e-67;
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  response in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC directing recombination of a recombinant gene into the chromosome of the Chomologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native CC back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant Agfa protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to 50,000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live cracine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response cC against the inserted epitope, and hybrid fimbriae are easy and cCC inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                         Salmonella
                                                                                                                                                                                                                                                        Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
26-JUN-1995
                     (UYVI-) UNIV VICTORIA INNOVATION (KING/) KING J.
                                                                           26-APR-1993;
                                                                                                             26-APR-1994;
                                                                                                                                                  10-NOV-1994
                                                                                                                                                                                    WO9425598-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR74625 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively, (2)
                                                                                                                                                                                                                                                                                              AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SDARKYDQLVTRVVTHEMAHA------GQGADNSTIELTQNGFRNNATIDQWNAKNSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune respons Salmonella in animals (e.g. food producing animals) and humans. (Upo on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                       WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1999;
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                                                                                                                   Disclosure; Page 135; 139pp; English.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong vaccine, the carrier fimbrial subunit proteins are usually strong vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of filmbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
Collinson SK,
                                                                                                                                                                                                                                                                                    Salmonella
                                                                                                                                                                                                                                                                                                                                                          Salmonella
                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW23570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW23570 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 151 AA;
                                                                                                                                         03-JUN-1997
                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                       Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                   (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                      26-APR-1993;
                                                                                                         26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the exemplification of the present invention
                                                                                                                                                                            JS5635617-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                    enteritidis
                                                                                                                                                                                                                                                                                                                                                          enteritidis 27655-3b agfA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                      93US-00054452
Kay ww,
                                                                                                         94US-00233788
                                                                                                                                                                                                                                Location/Qualifiers 123
                                                                                                                                                                                                             /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.5%;
Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 692; DB 3;
Pred. No. 1.1e-58;
2; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
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RESULT 6
AAB36349
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Best Local Similarity
               Recombinant
                                         N-PSDB; AAC64625.
                                                     WPI; 2000-672631/65
                                                                               White AP,
                                                                                                                               05-APR-1999;
                                                                                                                                                         05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                     12-OCT-2000
                                                                                                                                                                                                                                                                  Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                    Escherichia
                                                                                                                                                                                                                                                                                                     Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                              WO200060102-A2
                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#4
                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                           AAB36349 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-309886/28.
N-PSDB; AAT74142.
                                                                                                                                                                                                                                                                                           vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 7; 85pp;
binant agfA gene
encodes foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136;
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                                                                                                        VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                            Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                    COLL
                                                                                                                                                                                                                                                                                                                             amino acid sequence SEQ ID NO:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.9%; ilarity 90.1%; Conservative
                                                                                                        VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                 99US-0127888P
                                                                                                                                                                                                                                                                                         response;
                                                                                                                                                                                                                                                                                                    chromosomal gene replacement; fimbrin; epitope;
having a segment replaced by a epitope or antigen, expresses r
                                                                              Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                        immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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Pred. No. 3.3e-58;
2; Mismatches 13
                                                                              XS,
                                                                            Kay ww
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
         foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
        DNA sequence
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                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                           Local
106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                       106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                     136;
                                                                                                                          61 LVTRVVTHEMAHA-------GYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
                                                                                          46 LVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ
                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPD-
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                         86.3%;
                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                Score 675; DB 3;
Pred. No. 4.7e-57;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                     Indels
  151
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                                                                                                                                                                                                                                                                                   Gaps
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# RESULT 7 AAB36354 ID AAB3

AAB36354 standard; protein; 151

A

AAB36354;

26-FEB-2001 (first entry)

AgfA::PT3#9 amino acid sequence SEQ ID NO:28

Salmonella; agfA; chromosomal gene replacement; fimbrin; vaccine; immune response; 1mmunogen epitope;

Salmonella enteritidis

Escherichia coli.

WO200060102-A2 Synthetic

12-OCT-2000

05-APR-2000; 2000WO-CA000356

which

99US-0127888P

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RESULT 8
AAB36346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation eliciting an immune response in an animal. In a fimbrial presentation conjunction, the hybrid fimbrian protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 128; Conser
                  Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                     AgfA::PT3#1 amino acid sequence SEQ ID NO:12
                                                                                               26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assembly system of strains of Salmonella, Escherichia coli and Enterobacterlaceae for the production of fimbriae comprising recombinant AgfA, CogA and AgfA-homologue fimbrin subunits, respectively, (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAC64630
vaccine; immune response; immunogen
                                                                                                                                                                           AAB36346 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 138; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence which encodes a for (1) use of thin aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification
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                                                                                                                                                                                                                                                                         98
                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                             58
                                                                                                                                                                                                                                                                                               RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA-----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                         RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vention describes a recombinant agfA gene (I) where a gene has been replaced by a segment of a foreign DNA encodes a foreign epitope or antigen. Also described in aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                         protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.9%;
73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 617; DB Pred. No. 1.8e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
.8e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                              151
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                                                                                                                                                                                                                                                                                                                                                                                           back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigen an animal. In a fimbrial presentation system the heterologous antigen an animal. In a fimbrial presentation of 100,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong manunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and in expensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      Sequence
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Escherichia coli.
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                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                    LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
NNAALVNYDQLVTRVVTHEMAHANNATANQY
                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                       Conservative
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80.8%;
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                                                                                                                                                                                                                                                                         Score 614; DB 3;
Pred. No. 3.5e-51;
                                                                                                                                                                                                                                                       Mismatches
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RESULT

AAB36347

AAB36347 standard;

protein; 151 AA

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                                                                                                                                                 AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively, (2)
CC directing recombination of a recombinant gene into the chromosome of the
CC homologous species, (3) directing recombination of a recombinate
CC copy of that gene; and (4) eliciting a recombinate response in an animal,
CC comprising separating an amino acid polymer comprising a recombinant AgfA
CC protein containing a replacement segment or segments of foreign amino
CC acid sequence or sequences grown on a Salmonella, E. coli or
CC Enterobacteriaceae host cell, from the host cell and introducing the
CC polymer into the animal in conjunction with a carrier or diluent. (1) is
CC useful for the expression of recombinant AgfA protein which is useful for
CC cliciting an immune response in an animal. In a fimbrial presentation
CC system the heterologous antigens, are presented in high numbers (up to
CC sonogenicity and adhesion properties relevant for an efficient live
CC vaccine, the carrier fimbrial subunit proteins are usually strong
C1 immunogenis, which may be important for directing an immune response
CC against the inserted epitope, and hybrid fimbriae are easy and
CC inexpensive to purify in large amount. The present sequence is given in
CC the exemplification of the present invention
                                                                         Matches
                                                                                        Query Match
Best Local
                                                                                                                                               Sequence
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Escherichia coli.
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                                                                     Similarity 81.
                                                                                                                                               151 AA;
                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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l for eliciting immu
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                                                                                        78.3%;
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                                                                 Score 612; DB
Pred. No. 5.5e
5; Mismatches
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                                                                     e 612; DB 3; I
. No. 5.5e-51;
ismatches 23;
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            directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sees set both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
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  against the inexpensive
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inserted epitope, and hybrid to purify in large amount. The
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        The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CegA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino
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                                                                                                                                                                                                                                                                                                                                                                       Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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82.1%;
                                                                                                                                                                                                                                                                                                                                                                          Collison
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                                                                                                                                                                                                                                                                                                                                                                          SK,
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엺
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.1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
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ID AAB36
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the argument if the transfer of the present sequence is given in the argument is to present sequence.
                                                                                                                                            WPI; 2000-672631/65.
N-PSDB; AAC64631.
                                                                                                                                                                                                                                                    05-APR-1999;
                                                                                                                                                                                                                                                                                05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                         WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I)
                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                     Escherichia
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                                                                                                                                                                                         Doran JL,
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                                                                                                                                                                                                                                                    99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.9%;
                                                                                                                                                                                          Collison
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Pred. No. 6.3e-50;
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                                                                                                                                                                                         Kay WW
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Recombinant agfA gene having a segment replaced by a foreign which encodes foreign epitope or antigen, expresses recombing protein useful for eliciting immune response in animal.

antigen, expresses recombinant une response in animal.

DNA sequence

Disclosure; Page 139; 139pp; English.

The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign D sequence which encodes a foreign epitope or antigen. Also describe

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC back into the chromosome of the homologous species, replacing the native C copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a Carrier or diluent. (1) is CC useful for the expression of recombinant AgfA protein which is useful for CC useful for the expression of recombinant agfA protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation System the heterologous antigens are presented in high numbers (up to 10,000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response consists the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local .
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  White AP, Doran JL,
                                                                                                  05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                              WO200060102-A2
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                                                    (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                     Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36348 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                           vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        assembly system of strains of Salmonella, Escherichia coli and enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation
assembly system of strains of Salmonella, Escherichia coli a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                         immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid sequence SEQ ID
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81.5%;
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Pred. No. 7.8e-50;
4; Mismatches 24
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RESULT 14
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Best Local S
Matches 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                     Escherichia
                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin;
                                                                                                                                                                                                                                                   26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                              vaccine;
                                                                                                                                                                                                        Escherichia coli CsgA amino acid sequence SEQ ID NO:7
                                                                                                                                                                                                                                                                                                                                  AAB36343 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 136; 139pp; English
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                                                                                                                                              immune
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                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                           response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.8%;
                                                                                                                                              immunogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches 104
                   E. coli CsgA subunit 15 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                        04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                ABR82651
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                                                                                                                            standard; protein; 151
                                                                                                                                                                                                                          GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
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Pred. No. 2e-42;
8; Mismatches
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Matches 103
                                                                                                                                                                                                                                                                                                  The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.
                                                                                                                                                                                                                                                     Sequence 151
                                                                                                                                                                                                                                                                                    protein to bind
15 kDa protein
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GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                                                 MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
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A COMPOSITIONS FOR A 701 Fifth Avenue 701, Version #1.25 0, Version #1.25 788A 3.403C2	08-728-470-9 08-719-641-9 08-728-470-10 08-719-641-10 08-617-697-9 08-617-697-10 09-543-6181-5434 08-458-0228-6 08-331-5158-2 09-336-4478-9 09-336-4478-9 07-876-280-2 07-876-280-2 07-675-772-2 08-158-232-2 08-158-232-2 08-304-626-2	
R DETECTION	sequence sequence	
	nce 9, Appli nce 9, Appli nce 10, Appli nce 10, Appli nce 10, Appli nce 5434, Ap nce 6, Appli nce 2, Appli nce 2, Appli nce 17, Appli nce 2, Appli nce 2, Appli nce 2, Appli nce 2, Appli nce 2, Appli nce 2, Appli nce 2, Appli nce 2, Appli	

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RESULT 3
US-09-056-556-204
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US-08-233-788A-57
Sequence 204, Application US/09056556 Patent No. 6350456 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
TELLEPHONE: (206) 622-4900
TELLEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 57, Application US/08233788A
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                Local
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                                                                                                                                             GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                    GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
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                                                                                                                                                                                                                                                                                                                                                                                                       120 amino acids
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87.5%;
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Pred. No. 2.1e-42;
2; Mismatches 12; Indels
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Matches
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                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622,4900
                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,55
                                                                               TITLE OF INVENTION:
                                                                                                                                     APPLICANT:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                   APPLICANT:
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                             ADDRESSEE:
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                                                                            Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
NVENTION: COMPOUNDS AND M
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         6300 Columbia Center, 701 Fifth Avenue
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Dillon, Davin C.
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Dillon, Davin C.
VENTION: COMPOUNDS AND METHODS FOR THE PREVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                             SEED and BERRY LLP
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                                                                                                                                                                                                                                           Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.8%; Score 100; 26.0%; Pred. No. 0.
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Mismatches
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                                                                               METHODS
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                                                                               FOR DIAGNOSIS
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                                                                                                                    SOFTWARE: Pa
SEQ ID NO 131
LENGTH: 943
Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6572865
                                                                                                                                                                        PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-1
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1996-0
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/477,135A
CURRENT FILING DATE: 2000-01-03
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Pentides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
                                                                                                                                                                                                             PRIOR APPLICATION NUMBER:
                                                                           TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 05-MAY-199
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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              12.8%; Score 100; DB 26.0%; Pred. No. 0.2;
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12; Mismatches
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                               DB 4; Length 943;
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52;
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Indels
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US-09-072-967-204
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TOPOLOGY:
US-09-072-967-204
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                                                                                                                                   Matches
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                      STRANDEDNESS:
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504 GEGNAGDENOGFANT----
                                                                  464 GSGNIGVFNVGSGSLGNYNIGSGN------LGIYNIGFGNVGDY-------NV 503
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                                 74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN------ 121
                                                                                                  16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
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Lodes, Michael J.
Hendrickson, Ronald C.
HENDRICON COMPOUNDS AND M
NVENTION: AND DIAGNOSIS O
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                                                                                                                                                                                                                                                                     943 amino acids
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                                                                                                                                   Conservative
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Vedvick, Thomas S.
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Dillon, Davin C.
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                                                                                                                                                   Score 100; DB 4; Length 943; Pred. No. 0.2;
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 ---GNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 553
                                                                                                                                   Mismatches
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                                                                                                                                   52; Indels
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US-08-864-038A-3
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Best Local 9
                                                                                                                                                                                         Matches
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APPLICANT: Kunio
                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 15-July
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                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                              CELL TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
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504 LGGGSAAAAAAAAAAASGGGGRALRRALRROMRGGGSAAA 543
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5. 6001592
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                                                          ---LAAALAAAGAGGGLGGGGGGGALAAALAAAGAGGGGFGGLGGL
                                                                                      TRVVTHEMAHAGYGNGADVGQGADNSTIELTQ-----NGFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                           LLKSSASASASASASAG
                                                                                                                                                   LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLV
                             YGGNNAALVNOTASDSS-----VMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 953-7733
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                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                             peptide
from 1 to 738
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ION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

ION: CONTAINING SAID CDNA, HOST CELLS TRANSPORMED WITH SAID

ION: CONTAINING SAID CDNA, HOST CELLS TRANSPORMED WITH SAID

ION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

ION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
                                                                                                                                                                                                  12.6%;
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Pred. No. 0.2;
11; Mismatches
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US-09-328-352-4764
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                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
LENGTH: 975
TYPE: PRT
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GENERAL INFORMATION:
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4764, Application US/09328352 Patent No. 6562958
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09336447A Patent No. 6310190
                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                               ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: AMCY:024
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TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Moraxella catarrhalis
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                                                                                                                                                                                                      Local Similarity es 37; Conserv
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                                                       338 NSFTLIGNSS---SSSVNTAPTTTSNTVNDNDTID--NGNSGGTGSGSGNGSGDGLLNGA 392
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                                                                                                                                                                15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
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ASDSSVMVRQVGFGN 144
                                                                                      ----YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
                                                                                                                           NGTGDSG-VSALGGSGNGSGDGAGNGIASGNGBHNYGIGNGNGDDVDITAPITGVLNISG 337
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FISKE, MICHAEL J
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                                                                                                                                                                                                                      Score 91.5; DI Pred. No. 1.4;
                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                          SEQ ID NO 26438
LENGTH: 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6167, App
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26438, Application US/09252991A Patent No. 6551795
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LENGTH: 273
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                                                                                                                                                                                            Matches
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc J. I
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
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                                                                                                                366 ILSHEVSVAAVGQANAAGDGSGQVHVAQGPAGANASDSNGVTIVQQQPAVDLAAGANGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 TVGQYGGNNAALVNQTASDSSV--MVRQVGF 142
                                      426 AVQSQSGANIGSGANGISVVQSQNGANIGAGASDISVVQSQNSPNIGSGVNGVTVVQSQN
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                                                                          64 RVVTHEMAHAGYG------NGADVGQGADNSTIELTQN-----GFRNNATIDQWN
                                                                                                                                                    13 VVSGSALAGVVPQWGGGGNHNG------GGNSSGPDSTLSIYQYGSANAALYDQLVT
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  AKN----SDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MARC J. Rubenfield et al.

VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                            11.0%; Score 86; DB 4; Length 1415; 23.9%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.3%; Score 88; DB 4; Length 273; 28.5%; Pred. No. 0.6;
                                                                                                                                                                                          21; Mismatches
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US-09-841-835-8
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Sequence 8, Applicati
Patent No. 6506587
GENERAL INFORMATION:
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APPLICANT: de Lan
APPLICANT: Smith,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,221
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
APPLICANT: de Lange, APPLICANT: Smith, Susan
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS
TITLE OF INVENTION: OF USE THEREOF
TITLE OF TOTAL STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 673 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                         62 -VTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                       6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQL---
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                                                                                                                                                      Application US/09841835
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29.6%; Pred. No.
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                                                         TO TRF1 AND METHODS
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RESULT 14
US-09-196-387-10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
                                                                                                           ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                APPLICATION NUMBER: FILING DATE:
CLASSIFICATION:
                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                  ADDRESSEE:
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ה''ח 627761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
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                                                                                                                                                                                    New Jersey
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411 Hackensack Avenue,
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Pred. No. 7.
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                                                              Version
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US-09-841-835-10
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GENERAL INFORMATION:
APPLICANT: de Lan
APPLICANT: Smith,
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                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                   TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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REFERENCE/DOCKET NUMBER: 600
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411 Hackensack Avenue, 4th Floor
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Smith, Susan
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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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2: /cgn2-6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2-6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2-6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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7: /cgn2-6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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Match
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd
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 15 US-10-369-493-20638

9 US-09-793-306-146

9 US-09-996-634-131

10 US-09-997-182-131

10 US-09-997-181-131

10 US-09-997-181-231

10 US-10-193-002-199

14 US-10-193-002-199

15 US-10-369-493-20619

10 US-09-952-267-5

10 US-09-952-267-5

10 US-09-952-267-5

11 US-10-233-53-23

14 US-10-233-53-11

14 US-10-185-990-11

15 US-10-369-493-18460
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Sequence 20638, A
Sequence 131, App
Sequence 131, App
Sequence 131, App
Sequence 131, App
Sequence 199, App
Sequence 204, App
Sequence 20619, A
Sequence 2, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 11, Appl
Sequence 10, Appl
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10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.1	10.1	10.2	10.2	10.2	10.2	10.2	10.2	10.3	10.3	10.4	10.4	10.5	10.5	10.5	10.5	10.5	10.5	10.5	0	10.7	10.9	11.1
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US-10-374-780A-336	US-10-225-067-102	US-10-225-068-48	US-08-834-666A-6	US-10-389-566-1139	US-09-880-748-1840	US-09-880-748-1556	US-10-369-493-9713	US-09-880-748-1494	US-09-882-227-522	US-10-029-386-31982	US-10-369-493-9134	US-10-156-761-14828	US-09-738-626-3535	US-10-238-075-1549	US-10-238-075-749	US-09-996-194-16	US-10-246-330-4	US-09-952-267-13	US-10-199-937-4	US-09-972-115A-8	US-09-841-835-2	US-10-369-493-20166	US-09-841-835-10	US-09-841-835-8	US-10-094-749-2987	US-10-009-823A-10	US-10-156-761-11286	US-09-810-264-28	US-10-369-493-12420
336,	102	Sequence 48, Appl	Sequence 6, Appli	1139,	1840,	1556,	9713,	1494,	Sequence 522, App		Sequence 9134, Ap	Sequence 14828, A		Sequence 1549, Ap	Sequence 749, App	16,	4	13	Sequence 4, Appli	8	Sequence 2, Appli	Sequence 20166, A	Sequence 10, Appl	Sequence 8, Appli		Sequence 10, Appl	Sequence 11286, A	Sequence 28, Appl	Sequence 12420, A

## ALIGNMENTS

RESULT 1 US-10-369-493-20638

QY 51 GSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN 110	Qy 7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIXQY 50	Query Match 14.9%; Score 116.5; DB 15; Length 445; Best Local Similarity 27.5%; Pred. No. 0.0019; Matches 46; Conservative 20; Mismatches 60; Indels 41; Gaps 6;	; FEATURE: ; NAME/KESY: unsure ; LOCATION: (1)(445) ; OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-20638	; SEQ ID NO 20638 ; LENGTH: 445 ; TYPE: PRT ; ORGANISM: Rhodopseudomonas palustris	; FILE REFERENCE: 38-10(52052)B ; CURRENT APPLICATION NUMBER: US/10/369,493 ; CURRENT FILING DATE: 2003-02-28 ; PRIOR APPLICATION NUMBER: US 60/360,039 ; PRIOR FILING DATE: 2002-02-21 ; NUMBER OF SEQ ID NOS: 473.74	; APPLICANT: Slater, Steven C. ; APPLICANT: Goldman, Barry S. ; APPLICANT: Chen, Xianfeng ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES	; Sequence 20638, Application US/10369493 ; Publication No. US20030233675A1 ; GENERAL INFORMATION: ; APPLICANT: Cao, Yongwei ; APPLICANT: Hinkle, Gregory J.

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US-09-996-634-131
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PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILLING DATE: 2000-01-03
PRIOR PELICATION NUMBER: 08/990,823
PRIOR FILLING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILLING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILLING DATE: 1995-06-15
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                                                                                                                                                                                                                                                                                                                                                            Sequence 131, Application US/09996634 Patent No. US20020172684A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 146
LENGTH: 597
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                                                                                                                                                                                                           FILE REFERENCE: 61260
CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
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Patent No. US20020098200A1
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                                                                                                                                                                                                                                                                                     APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences
TITLE OF INVENTION: immunostimulatory Peptides
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TITLE OF INVENTION: Of Tuberculosis
FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR APPLICATION NUMBER: US 60/23,828
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443 NOS-----VGFGNAGTLN
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RESULT 5
US-09-997-181-131
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US-09-997-182-131
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LENGTH: 943
TYPE: PRT
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PRIOR FILLING DATE: 2000-01-03
PRIOR PELICATION NUMBER: 08/990,823
PRIOR FILLING DATE: 1997-12-15
PRIOR FILLING DATE: 1997-12-15
PRIOR PELICATION NUMBER: 08/96/10375
PRIOR APPLICATION NUMBER: 60/000,254
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
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CURRENT FILING DATE: 2001-11-28
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TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                              ---NAALVNQTASDSSVM----VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                       GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY
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Pred. No. 0.
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Application US/09997181 o. US20030049269A1

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RESULT 6
US-10-193-002-199
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US-09-997-181-131
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Publication No. US20030135026A1
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PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
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CURRENT FILING DATE: 2001-11-28
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                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                       CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                  ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFGNAGDFNQGFANT-----GNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS
                                                                                                                                                                  COUNTRY: USA
ZIP: 98104-7092
APPLICATION NUMBER: US/10/193,002 FILING DATE: 10-Jul-2002
                                                                                                                                                                                                                                                                                                                                               Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campos-Neto, Antonia
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                                                                                                                                                                                                                                                                                                                                    TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                   350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 100; DB Pred. No. 0.22;
                                                                                                                                                                                                                                                    701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52;
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RESULT 7
US-10-084-843-204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
APPLICANT: Ree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 199:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION = CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
APPLICATION DATA: 105-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                       Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Monald C.
TITLE OF INVENTION: COMPOUNDS AND M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 199:
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                              STATE: Washington
                                                                                                                                                                                                                                                                                                                     CITY: Seattle
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TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                         ZIP: 98104-7092
                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Maki, David J
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Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                                                                                                        355
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Pred. No. 0.22;
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                                                                                                                                                                                                                                                                                                                                           701
                                                                                                                                                                                                                                                                                                                                           Fifth Avenue
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SEQ ID NO 20619
LENGTH: 486
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                    Query Match
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                            FEATURE:

NAME/KEY: unsure

LOCATION: (1).. (486)

OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 204: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              Local
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mes 40; Conserv
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                          145 -----VIIHTAAVGGRPRGALISQG--NLLI------AQSSLVDAWRLTEADVNLGM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY--
                                                                                                                            86
                                                                                                                                                                11 AIVVSGS----ALAGVVPQWGGGGNHNGGGNSSGP-----DSTLSIYQYGSANAAL 57
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                                                                                                                                                                                                           l Similarity
37; Conserv
                                                                                                                        SVVVAGTDYRDIVAGVLPSLGGVKKAYAIGDGSGPFAPFKDLASDTPFSAPEFGAADGF-
                                                                                 YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG- 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---NAALVNQTASDSSVM---VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
  -QYGGNNAALVNQTASDSSVM 136
                                                                                                                                                                                                                            12.6%; Score 98.5; DB 15; 25.7%; Pred. No. 0.14;
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                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                           Indels
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Query Match
Best Local Similarity
"~*~hes 34; Conserve
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Sequence 21, Application US/09820843A

Publication No. US20030039963A1

GENERAL INFORMATION:
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                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENCTH: 354
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: Q63915
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Council of Scientific and Industrial TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-09-12 PRIOR APPLICATION NUMBER: 09/336,447 PRIOR FILING DATE: 1999-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/952,267
CURRENT FILING DATE: 2001-09-12
                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: PPE
NAME/KEY: misc_feature
OTHER INFORMATION: gi|1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: AMCY:024
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                                                                                                                                                                                                           ORGANISM: M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDEMEURG, ROSS A.
APPLICANT: FREDEMEURG, ROSS A.
FITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 AGGSHNQATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 V----NOTASDSSVMVRQVGFGNNATAN 149
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ON: gi|1781260
                                     11.8%; 27.6%;
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                     12;
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                 Score 92; DB Pred. No. 0.42
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                                                       DB 10; Length 354;
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                     43;
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                     Indels
                     34;
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RESULT 12
US-10-233-553-11
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; ORGANISM: Homo sapiens US-10-233-553-11
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Publication No. US2003015285A1
GENERAL INFORMATION:
APPLICANT: NIPPON SHINYAKU CO.,LTD.
APPLICANT: HIRABAYASHI, Kazuko
APPLICANT: YANO, Junichi
TITLE OF INVENTION: Method of examining the efficacy of therapy with nucleic
FILE REFERENCE: B-345
FILE REFERENCE: B-345
                                                                      CURRENT APPLICATION NUMBER: US/10/233,553
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: JP 2001-267385
PRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 11
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Matches
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LENGTH: 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NIPPON SHINYAKU CO., LTD.
APPLICANT: HIRABAYASHI, Kazuko
APPLICANT: YANO, Junichi
TITLE OF INVENTION: Method of examining the efficacy of therapy with nucleic acid
FILE REFERENCE: B-345
CURRENT APPLICATION NUMBER: US/10/233,553
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: JP 2001-267385
PRIOR FILING DATE: 2001-09-04
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                                                         LENGTH: 894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 GGGG-----NHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGN 77
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Query Match
Best Local Similarity
Watches 42; Conserv:
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US-10-185-990-11
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US-10-185-990-10
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                                                                                                                                    APPLICANT: Pan, Jae-Gu
TITLE OF INVENTION: JAE GU PAN ET AL
FILE REFERENCE: 02589:000100
CURRENT APPLICATION NUMBER: US/10/185,990
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
                                                                                                                                                                                                                                                          Sequence 11, Application US/10185990 Publication No. US20030073109A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 1621
TYPE: PRT
ORGANISM: BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/10185990 Publication No. US20030073109A1 GENERAL INFORMATION:
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Best Local (
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CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 11
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TITLE OF INVENTION: JAE GU PAN
FILE REFERENCE: 02589.000100
                                                                                       ORGANISM: Bacillus subtilis
                                                                                                         TYPE: PRT
                                                                                                                     LENGTH: 1626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 NAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI 113
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               Conservative
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                              11.3%;
27.1%;
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27.1%; Pred. No. 6.3;
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27.1%; Pred. No. 1
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               21;
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              Score 88.5; DE Pred. No. 6.3; 21; Mismatches
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                                           Length 1626;
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               11;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: DLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 18460
LENGTH: 1649
TYPE: PRT
ORGANISM: Lactococcus lactis
US-10-369-493-18460
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Search completed: March 11, 2004, 19:18:39 Job time : 24.6 secs
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US-10-369-493-18460
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Best Local Similarity
Matches 44; Conserv
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                                                                                                                                               115 VGQYGGNNAALVNQTASDSSVMV, 137
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                                                                                                      766 GGNYG---QAGVETIAGDSTVNV 785
                                                                                                                                                                                                712 EGGGYT---ATTKWGNTTAQVNQGQVNWFLSGGSWGDLYNTG---SATVNVYNGYINAIT 765
                                                                                                                                                                                                                                                                                                    655 WGGGGTVWTYRQAFLQNGNSYLIHNNDIARWTYGGQSNGSQVGNS---YNILNGAIVDTL 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GSALAG-----VVPQWGG---GGNHN--------GGGNSSGPDSTLSIYQYGSA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 NAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                      62 VTRVVTHEMAHAGYGN-GADVGQGADN-----STIELTQNGFRNNATIDQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                     26 WGGGGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSTLSGDNHSRLIAGYGSNETAGNHSDLIAGYGSTGTAGYGSTQTSGEDSSLTA-GYGST 241
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   11.2%; Score 87.5; DB 15; Length 1649; 30.8%; Pred. No. 8.1; tive 10; Mismatches 46; Indels 43;
                                                                                                                                                                                                                                                                                                                                               ----HNG------GGNSSGPDSTLSIYQYGSANAALYDQL 61
                                                                                                                                                                                                                                                                                                                                                                                              46; Indels 43; Gaps
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Title:
Perfect score:
Sequence:
                                                                            Database :
                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                          Searched:
PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-543-407-26
782
                                                                                                                                                                                                                                                                                                                                                                                                                                                            March 11, 2004, 18:24:14; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec
                                                                                                                                                                                                                                                                                      283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                    283366
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# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.

•				,	!	
	leighmanolygin (EC	B42049	v	лоо	12.0	9
ۇ -	cell surface antiq	E97857	N	652	12.1	95
	outer membrane pro	JC1340	N	1651	12.2	95.5
B	probable disease r	G84687	N	447	12.3	96.5
	probable PPE prote	E70663	N	615	12.4	97
ঠ	ovo protein - frui	S16356	N	1213	12.5	97.5
	DNA-binding protei	A56038	N	1028	12.5	97.5
뭐	probable PPE prote	D70575	N	3300	12.8	100
	hypothetical prote	E97835	N	1655	13.1	102.5
ঠ	ice nucleation pro	S11672	N	1567	13.1	102.5
	probable PPE prote	D70604	N	552	13.1	102.5
	ice nucleation pro	JQ0188	N	1258	13.4	104.5
	probable PPE prote	E70946	N	590	13.4	105
_	probable PPE prote	F70825	N	645	13.5	105.5
	ice nucleation act	JC2143	N	1034	13.6	106
F);	nucleation compone	AH0635	N	151	13.7	107
F;1	fimbrin protein ag	JC6040	N	151	13.7	107
C;1	ice nucleation pro	S07053	N	1322	13.7	107.5
A;1	curlin minor chain	G85665	N	151	14.3	112
	minor curlin subun	C90806	N	151	14.3	112
C;I	curlin nucleator p	S70787	N	151	14.3	112
A; C	hypothetical glyci	E95965	N	2174	14.5	113
0,0	hypothetical prote	H98144	N	145	14.6	114.5
A;1	conserved hypothet	AD3143	N	145	14.6	114.5
A; F	hypothetical prote	H85665	N	152	64.1	501.5
A;1	curlin major subun	D90806	N	152	64.1	501.5
A;s	curlin protein csg	S70788	2	151	66.9	523
A; A	major curlin chain	AI0635	N	151	88.5	692
A,c	fimbrin protein ag	JC6039	2	151	88.5	692
A; F			i			
A .	Description	ID	BB	Match Length	Match	Score
4 :					>	

nuclear pore compl	A54831	N	1317	11.4	89.5	5
trfA protein	T14004	N	1390	11.5	90	14
hypothetical	T26667	N	586	11.5	90	ü
probable PPE	E70969	N	3716	11.6	90.5	42
ice nucleation pro	SNPSO	_	1200	11.6	90.5	11
probable PPE	A70762	N	678	11.6	91	ö
probable PPE	F70675	N	582	11.7	91.5	39
cnjB protein	S42136	Ň	1748	11.8	92	8
probable PPE	B70520	N	1436	11.8	92	37
probable PPE	B70663	N	354	11.8	92	8
probable PPE	B70987	N	1053	11.8	92.5	35
probable PPE prote	B70524	N	963	11.8	92.5	34
leishmanolysin	C42049	N	639	11.8	92.5	33
protein kinase	S35327	N	575	11.8	92.5	32
hypothetical glyc:	E70768	N	434	11.9	93	ĭ
Leishmanolysin	A44951	N	599	12.0	94	30

# ALIGNMENTS

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A;Title: The complete genome sequence of Escherichia coli K-12 A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: G64846
                                                                                                                                                                                                                                                                                              A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library,
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland,
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70788; G64846; S31202; S34560; S34559
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
      A;Cross-references: GB:AB000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. Mol. Microbiol. 7, 523-536, 1993
                                                                                                                        A; Molecule type: DNA
A; Residues: 1-151 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Hammar, M.; Arnqvist, A.; Bian, Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg ope
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds A;Title: Complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the complete genome sequence of a multiple drug resingly and the com
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                                                                                                                                                                                     A;Status: nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
A;Experimental source: strain K12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-151 < HAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    curlin protein csgA precursor - Escherichia coli (strain K-12)
N,Alternate names: csgA protein; major curlin protein
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C;Genetics:
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A;Molecule type: DNA
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Best Local S
Matches 137
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No. 3.6e-51;
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· White, N.; J
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V.; Riley,
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ey, M.;
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60
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A;Statue. F.
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-152 <HAY>
A;Residues: GB:BA000007; PIDN:BAB34843.1;
A:Cross-references: GB:BA000007; PIDN:BAB34843.1;
A:Cross-references: GB:BA000007; PIDN:BAB34843.1;
                                                                                                                                                                                                                                                                         DNA Res. 8, 11-22, 2001
A,Title: Complete genome sequence of enterohemorrhagic Escherichia
A:Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                    curlin major subunit CsgA [imported] -
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 21-42;44-50 <OLS2>
R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Lib
A; Reference number: S34559
A; Accession: S34559
                                                                                                                                                                                                                                                                       A;Accession: D90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Description: major component of wild-type curli; interaction between CsgA and CsgB A,Noce: curli are thin, coiled fibers expressed on the surface of Escherichia coli th and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424;
A;Experimental source: strain K-12, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;21-151/Product: curlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-133, 'RORDSGWLW'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type:
A; Residues: 21-4:
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                                                                                                                                                                                                                                                                                                                                                                                             Accession: D90806
                                                                                   Query Match
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                                             102;
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MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALYD
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Masunaga, T.; Kuhara, S.;
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                                          Conservative
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                                                            64.1%; Score 501.5; DB 2
67.1%; Pred. No. 3.4e-35;
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                                          19;
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Pred. No. 5.3e-37;
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8; Mismatches
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                                          Mismatches
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Shiba, T.; Hattori,
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W3110
                                                                               DB 2;
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                                          30;
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                                                                               Length
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M.; Shinagawa, H.
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  59
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QLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG

119

MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL

1

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A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics: A;Gene: csgA
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
AD3143
                                                                                                                                                                                                                                                                                        C;Date: 11-Jan-2002 #sequence_revision 11-Jar C;Accession: AD3143 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                     A, Molecule type: DNA
A, Residues: 1-145 < KUR>
                                                                                                                                                                                                     ster, E.W.

A;Title: The Genome of the N

A;Reference number: AB2577;

A;Accession: AD3143
                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein csgA [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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Best Local S
Matches 102
                                                                                                                    Cross-references: GB:AE008689; PIDN:AAL45562.1; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                       Status: preliminary
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102; Conser
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 39;
                   Similarity
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                                                                    linear chromosome
 Conservative
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                 14.6%;
25.2%;
                                                                                                                                                                                                                       Natural Genetic Engineer Agrobacterium tumefaciens C58; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                          Biddle,
 26;
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Score 114.5; DB Pred. No. 0.0088; Mismatches 5
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Pred. No. 3.4e-35;
9; Mismatches 30;
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                                                                                                                                                                                                                                                                                                                                              R.; Monks,
                                                                                                                                                                                                                                                                          P.; Jung, M.; Krespan,
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D.; Kutyavin,
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                                DB 2;
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 59;
                                                                                                                                     PID:g17743277;
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imalanta, E.;
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Indels
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                                                                                                                                                                                                                                                                          W.; Perry, M.; Gordon-Kamm,
                                   145;
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Potamousis,
 31;
                                                                                                                                      GSPDB:GN00187
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hypothetical protein AGR_L_228 [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_c;Accession: H98114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
H98144
                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Goodner, B.; Hinkle, G.; Gattung, S.;
A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
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A; Residues: 1-145 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Genome Sequence of the Plant Pathogen and Biotechnology A; Reference number: A97359; MUID:21608551; PMID:11743194
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                                                                                                                                                                                                                                                                               position:
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                                  116 GOYGGNNAALVNOTASDSSVMVROVGFGNNATANO
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 97
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                                                                                                                                                                          3 LLKVAAFAAIVVSGSALAGVVPQWGG-----
                                                                                                                                                                                                                              Similarity
 GQFGSNHTTILTQDGNGNIAAGVQVGRGCSANVSQ
                                                                                                      ALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
                                                                                                                                          MIRKSFIASALVALVGLSAAAPAMANDVRIEQYGWSNSAGGAQEGYGNRIRTYQNGGYN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQFGSNHTTILTQDGNGNIAAGVQVGRGCSANVSQ 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLKVAAFAAIVVSGSALAGVVPQWGG--
                                                                                                                                                                                                                                                                                linear chromosome
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                 GB:AE007870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RIVGHQY---GRHNLSAVGQEGHDNYGSTTQNGNRNVAGI---
                                                                      -RIVGHQY---GRHNLSAVGQEGHDNYGSTTQNGNRNVAGI-------
                                                                                                                                                                                                                           14.6%;
                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                               PIDN:AAK88682.1;
                                                                                                                                                                                                            Score 114.5; DB
Pred. No. 0.0088;
6; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                          -GGNHNGGGNSSGPDSTLSIYQYGSANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumefaciens
                                                                                                                                                                                                              31;
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Markelz, B.
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G

RESULT E95965

C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001 hypothetical glycine-rich protein [imported] - C; Species: Sinorhizobium meliloti Sinorhizobium meliloti (strain 1021) mag

P.; Vorholter,

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A,Title: The complete sequence of the 1,683-kb pSymB megaplasmid

A,Reference number: A95842; MUID:21396508; PMID:11481431

A,Accession: E95965

N2-fixing

end

F.J.;

Hernai

A; Status: preliminary

PID:g15140875; GSPDB:GN00167

A; Molecule type: DNA
A; Residues: 1-21/4 < KUR>
A; Residues: 1-21/4 < KUR>
A; Residues: 1-21/4 < KUR>
A; Cross-references: GB: ALL591985; PIDN: CAC49389.1; PID: 91:
A; Cross-references: Strain 1021, megaplasmid pSymB
A; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F.; Finan, T.M.; Long, S.R. Puhler, A.; Abol
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.;
L.; Hyman, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.F
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.;
A; Title: The composite genome of the legume symbiont Sinc Abola, P.; Ampe, F.; Barloy-Hubler S.; Federspiel, N.A.; Fisher, R.F.

, D.H.; Kiss, B.; Komp, C.; Lelaure, S.; Wells, D.H.; Wong, K.; Yeh, K Sinorhizobium meliloti.

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A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence submitted to the EMBL Data Library, August 199
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley,
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           curlin nucleator protein csgB precursor - Escherichia coli (strain K-12) 
N;Alternate names: csgB protein; curlin nucleation component; minor curl 
C;Species: Bscherichia coli 
C;Pate: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2 
C;Accession: S70787; F64846 
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S. 
Mol. Microbiol. 18, 661-670, 1995 
A;Title: Expression of two csg operons is required for production of fib 
A;Reference number: S70783; MUID:96414468; PMID:8817489
                                                                                                                        Ş
                                                                                                                                                                                                                                        A;Description: minor component of wild-type curli; interaction between CsgA and CsgB tri A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <SIG>F;22-151/Product: minor curlin chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: F64846
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S70787
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A;Contents: annotation
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                   A; Gene: csgB
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-151 <BLAT>
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A;Molecule type: DNA
A;Residues: 1-151 <HAM>
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Best Local S
Matches 40
                                                                                                                                                                    Matches
                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278
Experimental source: strain K-12, substrain MG1655
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Similarity 27.0%;
                                        -NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                  GIAAAAGYDLANSEYNFAVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                                      GSANAALYDQLVT--RVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATATAGAGAVGILAOSIGGGGGN---GGNATGGDAGFGSFOIGGGGGG-
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                                                                                                                                                                                                                                                                                                                                                                     23.15
                                                                                                                                                                  Conservative
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                                                                                                                                                                                     14.3%;
29.8%;
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                                                                                                                                                                                   Score 112; DB 2;
Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 113; DB
Pred. No. 0.23;
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                                                                                                                                                                                                    Length 151
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G85665
  C;Species:
C;Date: 30-
                     ice nucleation protein inaA - C;Species: Erwinia ananas
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30-Sep-1991
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77 99 17 51

GIAAAAGYDLANSEYNFAVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS GSANAALYDQLVT--RVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFR----

Conservative

17;

Mismatches

49;

Indels

14;

Gaps

u ;

- NNATIDOWNAKNSDITYGOYGGNNAALVNOTASDSSVMVROVGFGNNATANOY

151

76 86

SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY

#sequence\_revision

30-Sep-1991

#text\_change

26-Aug-1999

Erwinia

ananas

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iller, L.; Grotbeck, E.J.; Davis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                       curiln minor chain precursor, CsgA homolog [importor, Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence revision 16-Feb-2001
C;Paccession: G85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision
                                                                                                                                                                                                      A;Reference number: A85480;
A;Accession: G85665
                                                                                                                                                                                                                         A;Title: Genome sequence of enterohemorrhagic Escherichia coli Ó157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                   R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glassiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: C90806
                                                                                                                                                           A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O157:H7,
                                                                                                  ;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                   Status: preliminary
Query Match
Best Local
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                                                                                                                                          1-151 <STO>
  Similarity
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Yasunaga, T.; Kuhara,
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14.3%;
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Score 112;
Pred. No. 0.
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Pred. No. 0.015;
7; Mismatches 49
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Shiba, T.;
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DB 2
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; Hattori, 
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imalanta, E.;
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                 Length 151;
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M.; Shinagawa,
                                                                                                                                                                                                                                                                                       J.D.; Rose, Potamousis,
                                                                                                                                                                                                                                                                                                                                                14-Sep-2001
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K.; Apodaca
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fimbrin protein agfB precursor - Salmonella enteritidis (;Species: Salmonella enteritidis (;Species: Salmonella enteritidis (;Species: Salmonella enteritidis (;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1 (;Accession: JC6040 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol. 178, 662-667, 1996 J. Bacteriol. 178, 662-667, 1996 A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 A;Accession: JC6040 
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nucleation component of curlin monomers [imported] - Salmonella C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AH0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:U43280; NID:gl184712; PIDN:AAC43598.1; PID:gl184713
A;Experimental source: strain 276755-3b
C;Genetics:
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AH0635
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C;Function:
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R;Abe, K.; W
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FEBS Lett. 258, 297-300,
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Best Local S
Matches 35
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;Residues: 1-1322 <ABE>
;Cross-references: GB:X17316; NID:g296095;
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O, 1989
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Pred. No. 0.039;
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Pred. No. 0.38;
9; Mismatches
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C;Species: Erwinia uredovora
C;Aate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_cha
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C;Aates 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_cha
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R;Michigami, Y:; Watabe, S:; Abe, K.; Obata, H.; Arai, S.
Biotechnol. Biochem. 58, 762-764, 1994
A;Title: Cloning and sequencing of an ice nucleation active
A;Reference number: JC2143; MUID:94264407; PMID:7764866
A;Accession: JC2143
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                   C;Supertamrry: ---
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C; Comment: This protein consists of C; Superfamily: ice nucleation protein
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A: Residues: 1-1034 < MIC>
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C;Date: 30-Sep_1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
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A; Gene: STY1180
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Pred. No. 0.039;
7; Mismatches
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OM protein - protein search, using sw model
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on: March 11, 2004, 18:14:48; Search time 6.3 Seconds (without alignments) 1248.031 Million cell updates/sec

Title: Perfect score: Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5 US-09-543-407-26 782 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151

Total number of hits satisfying chosen parameters: 141681

141681 seqs, 52070155 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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SEQUENCE FROM N.A. SPECIES=S.typhi; STRAIN=TY2 / ATCC 700931;  MEDLINE=25531367, PubMed=12644504;  Deng W., Liou SR., Plunkett G. III, Mayhew G.F., Rose D.J.,  Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;	Davies R.M., Dowd I., White V., Haque A., Hien T.T., Holr V., Leather S., Moule S., O'Ga cd K., Simmonds M., Skelton J [ B.G.; lence of a multiple drug resi ni CT18.";	of Salmonella enterica serovar Tyr  18;  1677608;  mes K.D., Thomson N.R., Pickard D. Bentley S.D., Holden M.T.G., Seba	UENCE FROM N.A.  CIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 70072  LINE-21534948; PubMed=11677609;  Telland M., Sanderson K.E., Spieth J., Clifton S.W., I  Telland M., Forwollik S., Ali J., Dante M., Du F., Hou S  rtney L., Porwollik S., Ali J., Dante M., Grewal N., Mu  nard S., Nguyen C., Scott K., Holmes A., Grewal N., Mu  n E., Sun H., Florea L., Miller W., Stoneking T., Nhan  erston R., Wilson R.K.;	[1] [1] [1] [1] SEQUENCE FROM N.A. SPECIES-S. typhimurium; STRAIN-SR-11; SPECIES-S. typhimurium; STRAIN-SR-11; MEDLINE-98117058; PubMed-9457880; MEDLINE-98117058; PubMed-9457880; ROmling U., Bian Z., Hammar M., Sierralta W.D., Normark S.; "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium; "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and "Curli fibers are highly conserved between Salmonella typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium and typhimurium an	um, d is. eria; ( eria; ( Salmon	55; TT-1996 (Rel. 34, Created) TT-1996 (Rel. 34, Last sequence u TT-2003 (Rel. 42, Last annotation C Curlin subunit precursor (Fimbr OR AGFA OR STM1144 OR STV1181 OR	LT 1 SALTY CSGA_SALTY STANDARD; PRT; 151 AA.

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- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.

- COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERBYTIALLY A
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emoedy L., Mueller K.-M., T.
"Purification and characterization of thin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94013373; PubMed=8104955;
Doran J.L., Collinson S.K., Burian J., Sarl
Munro C.K., Kay C.M., Banser P.A., Peterkin
"DNA-based diagnostic tests for Salmonella
the structural gene for thin, aggregative f
J. Clin. Microbiol. 31:2263-2273(1993).
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regative fimbriae.'
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CSGA_ECOLI
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Obhima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Mocomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
"A 710 b. Forest
                                                              Salmonella enteritidis."
J. Bacteriol. 173:4773-4
-i- FUNCTION: CURLIN IS 7
                                                                                                                                                                                                                             STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1157528;
Arnqvist A., Olsen A., Pfeifer J.,
"The Crl protein activates cryptic
fibronectin binding in Escherichia
Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSGA_ECOLI
P28307;
01-DEC-1992
                                                                                                                        MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emoedy L., Trust T. "Purification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gregor J.
Mau B., S
                                                                                                                                                                                                                                                                                                                                                                                                         corresponding to the 12.7 DNA Res. 3:137-155(1996).
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Expression of two csg fibronectin- and congo
                                                                                                                                                                                                                                                                                                                                                                                                                             "A 718-kb DNA sequence of the corresponding to the 12.7-28.
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"The RpoS sigma factor relieves repression of csgA, the subunit
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MEDLINE=93211294; E
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                                        FUNCTION: CURLIN IS THE STRUCTURAL SUBUNCOILED SURFACE STRUCTURES THAT ASSEMBLE
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                      BELOW
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st A., Bian Z., Olsen A.,
o csg operons is required
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                      CELSIUS.
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / ATCC 43895;
STRAIN=0157:H7 / ATCC 43895;
MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7."
expression in Cartain Strains of Escherichia coli 0157:H7."
expression in Cartain Strains of Escherichia coli 0157:H7."
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28-FEB-2003
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                     MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
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28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
Escherichia coli 0157:H7.
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Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobac
Enterobacteriaceae; Escherichia.
SEQUENCE FROM N.A.
STRAIN=K12 / MC4100;
STRAIN=96414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A.,
"Expression of two csg operons is required
"Expression and congo red-binding curli po
                                                                                                                                                                                                                                                                                                                                                                                          CSGB ECOLI
P39828;
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-i- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. (COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Aiba H., Baba T., Fujita K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
"A 718-kh num" -- T.
                                                                                                                                                                                                                                                                 Arnqvist A., Olsen A., Normark S.;
"Sigma S-dependent growth-phase induction of the c
Escherichia coli can be achieved in vivo by sigma
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STRAIN=0157:H7
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"A 718-kb DNA sequence of the F
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Nature 409:529-533(2001).
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MEDLINE=21074935; PubMed=11206551;
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Mau B., Shao Y.;
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna
Riley M., Collado-Vides J., Glasner J.D., Rode C.I
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1. Microbiol. 13:1021-1032(1994).

1. FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLICULED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TELERONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENTS.
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EMBL; D90741; BAA35831.1; --
EMBL; AE005315, BAAG55797.1; --
EMBL; AE005315, AAG55797.1; --
EMBL; AP002554; BAB34842.1; --
PIR; C90806; C90806.
PIR; G88665; G85665.
PIR; G870787; S70787.
ECOGene; EG12621; C69B.
Finbria; Signal; Complete prot
SIGNAL
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01-FEB-1991 (Re
16-OCT-2001 (Re
Ice nucleation)
                                                                                                                                                                                                                                                                                                              between
                                         Pfam; PF00818; Ice_nucleation; 69.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 49.
                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90092494; PubMed=2599095;
Abe K., Watabe S., Emori Y., Watanabe M., Arai S.
"An ice nucleation active gene of Erwinia ananas.
to those of Pseudomonas species and regions requi:
                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleation activity.";
FEBS Lett. 258:297-300(1989).
                                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=553;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pantoea ananas
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                                                                                                                                                                                                                          send
                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                         CTYSTAILIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSEN
OCTAPEFTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
SIMILARITY: Belongs to the bacterial ice nucleation p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Ice nucleation proteins
                                                                                                                                                       ; X17316; CAA35194.1;
S07053; S07053.
                                                                                                                                                                                                                                                                                                                                                                                                         family.
                                                                                                                                    P06620;
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poTENTIAL.
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  PERIODICITY.
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Best Local
                                        between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The European Bioinformatics Institutes as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                       J. Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTI TEMPERATURES BELOW 37 DEGREES CELSTUS. CURLI CAN E FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION OF SUBUNIT STREEN SUBURITION OF SUBUNIT STREEN SUBURITION OF SUBUNIT STREEN SUBURITION OF SUBURIT STREEN SUBURITION OF SUBURITION OF SUBURITIES SUBURITIES.
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MEDLINE=22531367; PubMed=12644504;

MEDLINE=22531367; PubMed=12644504;

Meng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

"Comparative genomics of Salmonella enterica serovar Typhi st
and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronfin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence up 10-OCT-2003 (Rel. 42, Last annotation Minor curlin subunit precursor. CSGB OR STY1180 OR T1777.
                                                                                                                   This SWISS-PR
                                                                                                                                                                                                                                                                                                                                                                                        Whitehead S., Barrell B.G.; multiple "Complete genome sequence of a multiple enterica serovar Typhi CT18."; Nature 413:848-852 (2001).
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                                                                                                           SWISS-PROT entry is copyright. It is produced throusen the Swiss Institute of Bioinformatics and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
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                                                                       γ
                                                                                                                                                                                            BIND TO
COMPONENT OF
                                                                                                                                                                                                                                      CURLI.
                                                                         and
                                                                                                                   EMBL
                                                                                                                   a collaboration
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                                                                         for
                                                                                                                                                                                                                                      CURLI
                                                                                                                                                                                                                        GROWTH
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RESULT 7
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Best Local
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Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143.
Salmonella typhimurica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fimbria;
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                              McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Courtney L., Porwollik S., Ali J., Dante M., Du F., Ho, Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Ni Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SALTY
                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.typhimurium; STRAIN=SR-11; MEDLINE=98117058; PubMed=9457880; Romling U., Bian Z., Hammar M., Sierralta W.D., Normar Romling U., Bian Z., Hammar M. Seierralta W.D., Normar "Curli fibers are highly conserved between Salmonella Escharichia coli with respect to operon structure and J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                             MEDLINE=96146512; PubMed=8550497; Collinson S.K., Clouthier S.C., D
                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.typhimurium; STRAIN=LT2 / MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhimurium, and Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSGB
                                                                                                                                                                                   "Salmonella enteritidis
                                                                                                                                                                                                                                                           Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                  "Complete
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                               Bacteriol. 178:662-667(1996).
- FUNCTION: CURLIN IS THE STRU
                                                                                     COLLED SURFACE STRUCTURES THAT ASSEMBLE TEMPERATURES BELOW 37 DEGREES CELSIUS. COFIENOMECTIN. THE MINOR SUBUNIT IS THE MUCCURLIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SALTY
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1 21
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                                                                                                                                                                                                                       .enteritidis;
                                                                                                                                                                                                                                                                                  genome
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16254 MW;
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                                                                                                                                                                                                                      STRAIN=27655-3B;
                                                                                  TO THE
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Pred. No. 0.02
17; Mismatches
                                                                                                                                                                                                                                                                                    Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MINOR CURLIN SUBUNIT; 161C54326E573495 CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                  CSGA/CSGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sierralta W.D., Normark
                                                                                                                                                                                                                                                                                                                                                                       SGSC1412 / ATCC
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                                                                                                         SUBUNIT OF THE CURLI. CUEMBLE PREFERENTIALLY AT CIUS. CURLI CAN BIND TO THE NUCLEATION COMPONENT
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                                                                                   FAMILY
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a typhimurium
d regulation."
                                                                                                                                                                                  aggregative
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S., Layman D.,
                                                                                                                    LY AT GROWTH
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICEN PANAN
Q47879;
01-NOV-1997
                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                        -!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF IC-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94264407; PubMed=7764866; Michigami Y., Watabe S., Abe K., Obata H., Ar "Cloning and sequencing of an ice nucleation
        InterPro, IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 51.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 34.
                                                                           EMBL; D14992; BAA03636.1; PIR; JC2143; JC2143.
                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               Biosci. Biotechnol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pantoea ananas (Erwinia uredovora)
Bacteria; Proteobacteria; Gammaprot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fimbria; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               StyGene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U43280; AAC43598.1; -. PIR; JC6040; JC6040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE008749; AAL20073.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ002301; CAA05316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                             redovora."
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBI_TaxID=553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ce nucleation
                                                                                                                                                                                                                                                                                DOMAIN: CONTAINS IMPERFECT REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-REPERIODICITY IS SUPERIMPOSED.
                                                                                                                                                                                                                                                                                                                      FUNCTION: Ice nucleation proteins enal crystallization in supercooled water. SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                               tamily.
                                                               P06620; 1INA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
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                                   IPR000258; Ice_nucleatn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AA;
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                               Biochem. 58:762-764(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16182 MW;
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30.4%;
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                                                                                                                                                                                                   collaboration
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Best Local S
Matches 40
Best Local Similarity
           Query Match
                                                PIR; JQ0188; JQ0188.

HSSP; P06620; IINA.
InterPro; IPR000258; Ice_nucleatn.
InterPro; IPR000258; Ice_nucleation; 65.
Pfam; P700818; Ice_nucleation; 65.
PRINTS; PR00377; ICENUCLEARIN.
PROSITE; P800314; ICE_NUCLEARIN, 45.
Ice_nucleation; Repeat; Outer_membrane.
DOMAIN 162 1217 OCTAPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
SEQUENCE
                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictive use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                                                        "The consensus sequence of ice nucleation proteins herbicola, Pseudomonas fluorescens and Pseudomonas Gene 85:239-242 (1989)
                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erwinia herbicola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990
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                                                                                                                                                         EMBL; M26382; AAA24823.1;
                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90152370; PubMed=2515997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ice nucleation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE
                                                                                                                                                                                                                                                                                                                                           FUNCTION: Ice nucleation proteins enable k crystallization in supercooled water. SUBCELLULAR LOCATION: Outer membrane. DOMAIN: CONTAINS 126 IMPERFECT REPRAIS OF A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE A PERIODICITY IS SUPERIMPOSED.
                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
                                                                                                                                                                                                                                                                                            family
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(Rel. 14,
(Rel. 40,
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                         Prime; Proo818; Ice nucleation; 81.
Primts, PRO0327; ICENUCLEATN.
PROSITE; PSO0314; ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membran SEQUENCE 1567 AA; 152548 MW; C8B4
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16-OCT-2001
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HSSP; P06620; IINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao J., Orser C.S.; "Conserved repetition in the ice nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91080859; PubMed=2259339;
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Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTYSTAILIZATION IN SUPERCOOLED WATER.

SUBCELLULAR LOCATION: Outer membrane (By similarity).

SUBCELLULAR LOCATION: Outer membrane (By similarity).

DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS

OCTAPEPTIDE A.G.Y.G.S.T.L.T; FURTHER ON A 16-RESIDUE AND A

REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

MISCELLANGUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE

NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.

SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Ice nucleation proteins enable
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                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                Outer membrane
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23; Mismatches
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RESULT 11
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Q9KK98; Q9KK98; Q9XC45;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Outer membrane protein B precursor (168 kDa surface-layer protein)

(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rompB)

(romp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                              EMBL; AE008659; AAL03623.1;
EMBL; AF123721; AAF34124.1;
EMBL; AF123726; AAF34129.1;
EMBL; AF149110; AAD39533.1;
                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                       (By similarity).

-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is layer with hexagonal symmetry (By similarity).
                                                                                                                                                                                                                                                                                                                                                                              "The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group. Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roux V., Raoult J.; "Phylogenetic analysis of members of the genus Rickettsia using pene coding the outer-membrane protein rOmpB (ompB)."; Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                              layer with hexagonal symmetry (By similarity).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Indian tick typhus, and Malish 7; MEDLINE=20393643; PubMed=10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fo
Samson D., Roux V., Cossart P., Weissenbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Malish 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stenos J., Walker D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Malish
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                  interPro;
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                                    E97835; E97835
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 IPR006315;
IPR005546;
                                                                                                                                                                                                                                                                                                                                                 THE 32 kDa BETA PEPTIDE MAY SERVE AS
                Autotransport.
Autotransporter
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RESULT 12
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Best Local S
Matches 38
                                                                                                          STRAIN=Oregon-R; PubMed=1712294; MEDLINE=9129102; PubMed=1712294; Mevel-Ninio M.T.M., Terracol R., Kafatos "The ovo gene of Drosophila encodes a zin for female germ line development."; EMBO J. 10:2259-2266 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OVO DANCE PSISZI, 99XZU4, PSISZI, 99XZU4, 101-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation updat 10-OCT-2003 (Rel. 42, Last annotation updat 10-OCT-2016 (Shaven baby protein).
                                                                                                                                                                                                                                                                          Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.;
"Multiple products from the shavenbaby-ovo gene region of
melanogaster: relationship to genetic complexity.";
Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovo protein (Shaven baby protein).
OVO OR SVB.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF I
LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION
SUBCELLULAR LOCATION: Nuclear (Potential)
DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND
ACCUMULATES IN NURSE CELLS DURING OOGENESIS. STORED IN T
BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTIN
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PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Zinc_finger; Metal-binding; DNA-binding;
Transcription regulation.
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requires a license agreement (See
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Pfam; PF00818; Ice_nucleation; 61.
PRINTS; PR00377; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 42.
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Schmid D., Pridmore D., Capitani G.,
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SUBUNIT: MEMBRANE ENVIRONMENT OR AGGREGATION SEEMS TO BE
FOR ICE MUCLEATION ACTIVITY.
SUBCELLULAR LOCATION: Outer membrane (By similarity).
SUBCELLULAR LOCATION: Outer membrane THE CONSENSUS
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
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Best Local S
Matches 36
                                                                                                                                LEICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen;
CHAIN
    endopeptidase).
GP63.
                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (F
                                                                                                   GP63_LEICH
P15706;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMs; TIGR01414; autotrans_barl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer membrane protein B precursor (168 kDa surface-layer (Surface protein antigen) (Cell surface antigen ) (Sca5) (Comp B) (Contains: 120 kDa surface-exposed protein (Surface antigen) (120 kDa outer membrane protein ompB); 32 kDa bet
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB003681; BAA20138.1; -.
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Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
Pfam; PF03797; Autotransporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing of the gene encoding the protein rOmp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).

SUBCELLULAR LOCATION: Cell wall. This bacterium is cover layer with hexagonal symmetry.

SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE
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1656 AA;
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                                                                                                                   STANDARD;
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7 MW; 3132A
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Pred. No. 2.
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                                                                                                                   PRT;
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Mismatches
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                                  (Promastigote
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"Three distinct RNAs for the surface protease gp63 are differentially repressed during development of Leishmania donovani chagasi promastigotes to an infectious form.";

RI J. Biol. Chem. 267:1888-1895(1992).

CC :- FUNCTION: Has an integral role during the infection of macrophages con in the mammalian host.

CC :- CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and C2 in and basic residues at P2 and P3'. A model nonapeptide is C1 cleaved at -Ala-Tyr-|- Leu-Lys-Lys-.

CC :- COPACTOR: Binds 1 zinc ion per subunit (By similarity).

CC :- SUBCELLUTAR LOCATION: Attached to the membrane by a GPI-anchor.

CC :- SIMILARITY: Belongs to peptidase family M8.
      Query Match
Best Local Similarity
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SIGNAL 1
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PROSITE; PS00142; ZINC PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Eymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M80672; AAA29238.1; -.
EMBL; M28527; AAA29235.1; -.
PIR; A44951; A44951.
HSSP; P08148; ILML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006025; Pept M Zn BS. InterPro; IPR001577; Peptidase M8. Pfam; PF01457; Peptidase M8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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MEDLINE=90205976; PubMed=2320059;

Miller R.A., Reed S.G., Parsons M.;

"Leishmania gp63 molecule implicated in cellular adhesion lacks an Arg-Gly-Asp sequence.";

Arg-Gly-Asp sequence.";
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=44271;
[1]
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MEDLINE=92112918; PubMed=1370484;
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54.8%;
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ZINC (CATALYTIC) (BY SIMILARITY).

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similarity).
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EMAH!	EMAH	٥,
ALGFSVGFFEGAR	AGYGNGADVGQGADN 87	5; Mismatches
ILESI	VGQGA	8
SN 285	DN 87	8; Indels
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Search completed: March 11, 2004, 18:34:59
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Copyright (c) 1993 - 2004 Compugen Ltd
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sp_virus:*
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16
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Q7X237
Q7X237
Q54069
Q9S3J5
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Q92UUN9
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Q7X243
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                                         O8eih4 shewanella
Q8u6n9 agrobacteri
Q9zuu8 rhizobium m
Q7ucz1 shigella fl
Q8cw64 escherichia
Q83ru7 shigella fl
Q7x244 citrobacter
                                                                                                                                                                                                                                                                                            O33802 salmonella
Q7x243 citrobacter
Q7x240 citrobacter
Q8cw63 escherichia
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Q54069 salmonella
Q9s3j5 escherichia
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## ALIGNMENTS

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O3802;
O1-JAN-1998 (TrEMBLrel. 05, C
O1-JAN-1998 (TrEMBLrel. 05, L
O1-DEC-2001 (TrEMBLrel. 19, L
Agfa protein (Fragment).
                                                                                                                                                                               EMBL; AJO
NON TER
SEQUENCE
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                                                                                                                                                                                                                                                            Sukupolvi S.S., Lorentz R.G., Gordon J.I., Normark S.J., Rhen M.; "Expression of thin, aggregative fimbriae I
                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                  cells.";
Infect. Immun. 65:5320-5325(1997).
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                 MEDLINE=98053981; PubMed=9393832;
 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                               AJ000514; CAA04151.1; -.
ER 152 152
NCE 152 AA; 15401 MW;
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                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                              Conservative
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Pred. No. 2.8e-48;
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Q7X244

xanthomonas shewanella

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121

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RESULT 3
Q7X240
ID Y240
ID Y2740
AC Q7X2
AC Q7X2
DT 01-0
DT 01-0
DT 01-0
DT 01-0
CGLtx
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RP SEQU
RC STRA
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Matches 118
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01-OCT-2003
01-OCT-2003
                                                                                                                                                                                        Zogaj X., Bokranz W., Nimtz M., Romling U.; Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003).
                                                                                                                                                                       SEQUENCE
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01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                           STRAIN=Fec4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Citrobacter freundii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKSDTTIHQNGFGNGADVGQGSDNSTIDLTQNGFKNNATIDQWNGKNSDITVSQYGG
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                                                                                                                                                                   15260 MW;
                                                                                               68.0%;
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78.1%;
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                                                                   Score 532; DB
Pred. No. 5.7e-
17; Mismatches
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Pred. No. 6.3e-40;
0; Mismatches 22
                                                                                                                                                                946DD52017F648FD CRC64;
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RESULT 5
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Q7X237;
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01-MAR-2003
01-MAR-2003
                                                                                                           Enterobacter sakazakii.
Bacteria; Proteobacteria;
Enterobacteriaceae; Entero
  STRAIN=Fec39;
Zogaj X., Bob
                                                                                 NCBI_TaxID=28141;
                                                                                                                                                                                               Curlin-csgA
                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna I
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete
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152 AA;
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    Bokranz
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Enterobacter.
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Escherichia.
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Pred. No. 4.8e-34;
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                                                                                                                                                                                                                                                                                                          PRT;
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RESULT 7
Q9S3J5
ID Q9S3
AC Q9S3
AC Q9S3
AC Q9S3
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DE Curl
GN CSGA
OC Esct
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Q54069
ID Q540
AC Q540
AC Q540
DT 01-N
DT 01-D
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GN AGFPA
OS Salin
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Q9S3J5;
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01-MAY-2000
01-MAR-2001
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Q54069;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cox J.M., Eglezos S., Woolcock J.B.; "Virulence of Salmonella enteritidis in chickens correlates colony morphology and expression of SEF17 fimbriae."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel 01, 01-NOV-1996 (TrEMBLrel 01, 01-DEC-2001 (TrEMBLrel 19,
  Bacteria; Proteobacteria; Gamma
Enterobacteriaceae; Escherichia
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                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                            (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
ift monomer (Fragment).
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                        Gammaproteobacteria; Enterobacteriales;
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Pred. No. 1e-17;
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Best Local Similarity
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Q8EIH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          La Ragione R.M., Collighan R.J., woodward M.J.;
"Non-curliation of Escherichia coli 078:K80 isolates associated IS1 inserti on in csgB and reduced persistence in poultry infect FEMS Microbiol. Lett. 175:247-253(1999).
EMBL, AJ131756; CAB45380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete SEQUENCE 502 AA; 52441 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nat. Biotechnol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shewanella oneidensis.";
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349
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                                                NNAAL VNQTASDSSVMVRQVGFGN----NATAN
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NNELVAFATGEDNS I E I SQEGDANFAYVDATGN
                                                                                                    IQGDDNDITIKQKGDSNGAEFQVWGDSNDVDLKQRGDANFATFGAYGTDN
                                                                                                                                                     VVTHE----MAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                        GDNHTGFVYALAGSENDISMEQEGSNNTAYLSMTTGDDNTVDITQDGDSN-TVGDSLIAD
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No. 0.0022;
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D08CA23D6C46B62D CRC64;
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Q92UUB PREMILIE.

Q92UUB;
Q92UUB;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical glycine-rich protein SMb21548.
PR0989 OR SMB21548.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu4768.
ATU4768 OR ACR I 228.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group; Agrobacterium NCBI_TaxID=176299;
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Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefacions C58.";
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Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Alheida N.F., Jr.,
Okura V.K., Zhou Y., Chen J., Wood G.E., Alheida N.F., Jr.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon
Raymond S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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H98144; H98144.
                                                                                                                                                                                                                                                                            116
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AE009405; AAL45562.1; -.
AE008209; AAK88682.1; -.
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145 AA; 14984 MW;
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DEDC870E1713D51A CRC64;
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Q7UCZ1;
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01-0CT-2003
01-0CT-2003
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InterPro; IPR002016; Peroxidase.
InterPro; IPR002173; PfkB.
Pfam; PF03797; Autotransporter; 1.
PROSITE; PS00435; PEROXIDASE 1; 1.
PROSITE; PS00583; PFKB KINASES 1; 2.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 2174 AA; 203314 MW; 008EB68297B44182
"Complete genome sequence and comparative flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003).
EMBL; AE016981; AAP16542:1; -.
SEQUENCE 151 AA; 15868 MW; 5D5D266B964
                                                                                                                              Mau B., Perna N.T., Payne S.M., Runyen-Janecky Schwartz D.C., Blattner F.R.;
                                                                                                                                                                               STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=25590274; PubMed=12704152;
Wei J. Goldberg M.B., Burland V., Venkatesan M.M., D.
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gam
Enterobacteriaceae; Shigella.
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Finan T.M., Weidner S., Wong K., B
Vorhoelter F.J., Hernandez-Lucas I
Golding B., Puehler A.;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                    Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                               CSGB OR S1108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minor curlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0004601; F:peroxidase activity; IEA.
GO; GO:0006979; P:response to oxidative stress; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti."; Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
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Plasmid pSymB (megaplasmid 2).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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Gremblrel.
Gremblrel.
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27.0%;
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Last annotation update)
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01-JUN-2003
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MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roe:

Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J.

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete gen

of uropathogenic Escherichia coll.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

EMBL; AE016759; AAN79778.1; -.
     SEQUENCE FROM N.A.
STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., S
Yang J., Yang F., Zhang X., Zhang
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01-MAR-2003 (TrEMBLrel. 23,
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Shigella flexneri.
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01-MAR-2003
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Enterobacteriaceae; Shigel
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Pred. No. 0.12;
17; Mismatches
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Q8PD38;
Q1-OCT-2002
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Q7X244;
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"Production of Cellulose and Curli Fi
Enterobacteriaceae Isolated from the
Infect. Immun. 72:4151-4158 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Citrobacter sp. Fec2.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Shigella flexneri 2a: insights into through comparison with genomes of Escherichia coli K12 Nucleic Acids Res. 30:4432-4441(2002).
EMBL; AE015131; AAN42658.1; -.
NCBI_TaxID=340;
                             Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                       Ice nucleation XCC0507.
                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ515700; CAD56671.1; SEQUENCE 151 AA; 16158 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleation
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01-OCT-2003
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                Xanthomonadaceae;
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                                                                                                                                                                                                                                                          GIASATSYDLAHSEYNFAVNELSKSSFNQAAIIGQVGTNNSAKMRQEGSKLLSVVSQEGG
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RX MEDLINE-2002145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Gamargo L.E.A.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
RA Martins E.C., Meidanis J., Menck C.F. M., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Meidanis J., Menck C.F., M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Moreira L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Spinola L.A.F., Kitajima J.P.,
RA Spinola L.A.F., Silva G., de Souza R.F.,
RA Schubal J.C., Kitajima J.P.,
RA Spinola L.A.F., Silva G., de Souza R.F.,
RA Schubal J.C., Kitajima J.P.,
RA Schubal J.C., Kitajima J.P.,
RA Schubal J.C., Kitajima J.P.,
RA Schubal J.C., Kitajima J.P.,
ROSITE; PS00314; C.E. Mucleation, 68.
RHINTS; PR00327; ICenucleation, 68.
RHINTS; PR00327; ICENUCLEATIN.
DR EMBL, ABM39231; -L.
DR EMBL, SCO0314; ICE NUCLEATIN.
DR PROSITE; PS00314; ICENUCLEATIN.
DR EMBL, SCO03214; ICENUCLEATIN.
DR EMBL, SCO03214; ICENUCLEATIN.
DR EMBL, SCO03214; ICENUCLEATIN.
DR EMBL SCO03214; ICENUCLEATIN.
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DR EMBL SCO03214; ICENUCLEATIN.
DR EMBL SCO03214; ICENUCLEATIN.
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Best Local Similarity 26.3
Matches 46; Conservative
951 TÓTAGYESTLTAG-YGSTOTÁQEISWLTTGYGSTÓTÁGHGSILT--AGYGSNSTÁ 1002
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                                                                                                               904 QTAGYDSFLT-----AGYGS----TQTAQSSSWLITGYGSTSTASFQSSLIAGYGS
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                                                    -QWNAKNSDITVGQYGGNNAAL------VNQTASDSSVMVRQVGFGNNATA 148
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26.3%; Pred. No. 3;
vative 22; Mismatches
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Search completed: March 11, 2004, 18:40:46 Job time: 31.5 secs

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Result
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Maximum DB
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Maximum Match
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1: geneseqp1980s:*
2: geneseqp1990s:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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Aab36351 AgfA :equ
Aab36341 Salmonell
Aab363570 Salmonell
Aab36350 AgfA::PT3
Aab36353 AgfA::PT3
Aab36355 AgfA::PT3
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Abr82644
                                                                           Aar52664
Aar52663
                                                                                                                   Aar62761
                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                     Aaw23569
         664 Fibronect
663 FNB curli
163 Salmonell
118 Salmonell
128 Salmonell
22 Salmonell
23 Salmonell
                                                                                                   AgfA sequ
Salmonell
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. <u>4</u> .5	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30	29	28	27	26
87.5	87.5	87.5	87.5	87.5	87.5	89	89	89.5	90	91.5	92	94.5	96	96	96	102	109	109	109
11.3	11.3	11.3	11.3	11.3	11.3	11.5	11.5	11.5	11.6		11.9	12.2		12.4	12.4	13.2	14.1	14.1	14.1
1477	1419	842	468	447	249	354	24	151	24	502	1074	151	19	19	19	26	23	23.	23
U	υ	ທ	w	w	w	7	7	نیا	7	N	σ	w	ω	w	نبا	7	w	ω	w
ABP69841	ABP69842	ABP66189	AAG29727	AAG29728	AAY69523	AB023520	ABR82647	AAB36344	ABR82642	AAW32312	ABU22692	AAB36342	AAB36328	AAB36336	AAB36323	ABR82649	AAB36319	AAB36324	AAB36340
Abp69841 Human pol	Abp69842 Human pol		Aag29727 Arabidops	Aag29728 Arabidops	Aay69523 Anti-CD38	Abo23520 Mycobacte	Abr82647 E. coli c	Aab36344 Escherich	Abr82642 E. coli N	Aaw32312 Leishmani	Abu22692 Protein e	Aab36342 Salmonell	Aab36328 Salmonell	Aab36336 Salmonell	Aab36323 Salmonell	Abr82649 E. coli V	Aab36319 Salmonell	Aab36324 Salmonell	Aab36340 Salmonell

ALIGNMENTS

## RESULT 1 AAB36354 ID AAB3 WPI; 2000-672631/65. N-PSDB; AAC64630. White AP, 05-APR-1999; 05-APR-2000; 2000WO-CA000356 WO200060102-A2. Synthetic. Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; AgfA::PT3#9 amino acid sequence 26-FEB-2001 AAB36354; AAB36354 standard; (UYVI-) UNIV VICTORIA 12-OCT-2000. Escherichia Salmonella enteritidis. vaccine; immune response; Doran JL, coli. (first entry) 99US-0127888P protein; Collison immunogen 151 SK, 8 SEQ ID NO:28 Kay WW;

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombinant of a recombinant gene back into the chromosome of the homologous species, (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 138; 139pp; English.

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RESULT 2
AAB36351
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Best Local Similarity
Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                            N-PSDB; AAC64627.
                                                                                                                                                                                                                                                         WPI; 2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA::PT3#6 amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQMNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                             Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127888P
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Pred. No. 2.5e-67;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                  Kay WW
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밁 S 밁 Ş 밁 S

Disclosure; Page

137; 139pp;

English

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RESULT 3
AAR74625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively (2)
CC directing recombination of a recombinate gene into the chromosome of the homologous species; (3) directing recombination of a recombinate gene into the chromosome of the homologous species, replacing the native compositing species, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or an arity of a salmonella, and introducing the strength of the superession of recombinant AgfA protein which is useful for C superint for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation cystem the heterologous antigens are greened in high numbers (up to 100,000 copples/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong immunogens, which may be immortant for directing an armune response.
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Best Local S
Matches 144
                                                                                                                                                                                                                                   Salmonella
                                                                                                                                                                                                                                                                        Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
26-JUN-1995
                                                                           26-APR-1993;
                                                                                                                26-APR-1994;
                                                                                                                                                         10-NOV-1994
                                                                                                                                                                                            WO9425598-A2
                                                                                                                                                                                                                                                                                                               AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 AAR74625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR74625 standard; protein; i51 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segmente which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDARKSETTITQSGYGNGAD------YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,
                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                           93US-00054452
                                                                                                                94WO-IB000207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.9%;
91.1%;
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Pred. No. 3.3e-61;
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Best Local Similarity
Matches 136; Conserv
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
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N-PSDB; AAQ87467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-1999;
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                                                                                                           Disclosure; Page 135; 139pp; English
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DB; AAC64617.
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90.1%;
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(Updated
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC AgfA, CsgA and AgfA-homologue finbrin subunits, respectively; (2)
Cd directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombination of a recombinant gene combination of a recombinant gene combination of a recombinant gene composed into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino compression of a recombinant AgfA protein containing a replacement segment or segments of foreign amino compared in the sequence or sequences grown on a Salmonella, E. coli or conterobacteriaceae host cell, from the host cell and introducing the collymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation conjunction with a carrier of diluent. (I) is conjunction with a carrier of diluent. (I) is conjunction with a carrier of diluent. (I) is conjuncting an immune response in an animal. In a fimbrial presentation conjunction with a carrier of diluent. (I) is conjunction to the heterologous antigens are presented in high numbers (up to conjunction) and adhesion properties relevant for an efficient live conjunction, the hybrial subunit proteins are usually strong cimunogens, which may be important for directing an immune response constitute the inserted epitope, and hybrid fimbriae are easy and convergency and the exemplification of the present invention
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  Collinson SK,
                                                                                                                                                                03-JUN-1997
                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis
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29-SEP-1997
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                                                                                  26-APR-1993;
                                                                                                                        26-APR-1994;
                                                                                                                                                                                                         US5635617-A
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                                          (UYVI-) UNIV VICTORIA INNOVATION &
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Кау
                                                                                  93US-00054452
                                                                                                                        94US-00233788
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                               /note= "Encoded by GCC"
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Pred. No. 2.2e-58;
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                                          DEV CORP
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RESULT 6
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Best Local Sim
Matches 135;
Recombinant agfA gene which encodes foreign
                                          N-PSDB; AAC64626.
                                                       WPI; 2000-672631/65.
                                                                                  White AP,
                                                                                                                                     05-APR-1999;
                                                                                                                                                               05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99 of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                          12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36350 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                           (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                    WO200060102-A2
                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                       Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                              Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                         AgfA::PT3#5 amino
                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-309886/28.
N-PSDB; AAT74142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNPALVNOTASDSSVMVRQVGFGNNATANOV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                               Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 7; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents agfA encoded by the full agfA gene Salmonella enteritidis 27655-3b. The nucleic acid can
                                                                                                                                      99US-0127888P
                                                                                                                                                                                                                                                                                                  response;
                                                                                                                                                                                                                                                                                                             chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                         acid sequence SEQ ID NO:20
                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.5%;
            having a segment replaced by a foreign DNA sequence
                                                                                Collison
                                                                                                                                                                                                                                                                                                ımmunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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Pred. No. 6.6e-58;
                                                                                SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
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epitope

or

antigen,

expresses

recombinant

05-APR-2000; 2000WO-CA000356

12-OCT-2000

WO200060102-A2

Escherichia coli. Synthetic.

Salmonella enteritidis.

vaccine;

immune

response;

ımmunogen

Salmonella; agfA; chromosomal gene replacement;

amino acid sequence SEQ

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NO:26

fimbrin;

epitope,

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RESULT 7
AAB36353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC (1) use of thin aggregative finbriae (SEFI7/TAF) nucleation depended are: CC (1) use of thin aggregative finbriae (SEFI7/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CE Enterobacteriaceae for the production of fimbriae comprising recombinant CC Agfa, CsgA and Agfa-homologue fimbria subunits, respectively, (2) CC directing recombination of a recombination for the chromosome of the homologous species; (3) directing recombination for a recombination contact gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the cuseful for the expression of recombinant Agfa protein which is useful for cuseful for the expression of recombinant Agfa protein which is useful for System the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response consideration of the present invention of the exemplification of the present invention consideration of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SEF17/TAF) nucleation described are:

assembly system of strains of Salmonnaire.
                                                                                                                                                                                                                                                                        26-FEB-2001
                                                                                                                                                                                                                                                                                                          AAB36353;
                                                                                                                                                                                                                                                                                                                                           AAB36353 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                               106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 81.9
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA-----------
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                                                                                                                                                                                                                                                                                                                                                                                                                               WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.4%;
                                                                                                                                                                                                                                                                                                                                           151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
2.4e-56;
0;
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RESULT 8
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AC AAB3
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DT 26-F
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DE A9fA
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KW Salm
KW vacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgfA, CggA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene hack into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence for the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for sequence response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA seguence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                      AAB36355 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
    vaccine; immune
                                                          AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                        26-FEB-2001
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                                                                                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128; Conservative
                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA---
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                                                                                                                                                                                                                                                                                                                                        RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 138; 139pp; English
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127888P
response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.6%;
73.6%;
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Pred. No. 5.7e-52;
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                                                                                                                                                                                                                                                                                                                               Matches 129;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                  system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the present sequence is given in the present sequence is given in the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                             Sequence 151
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Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 139; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                   the exemplification
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DB; AAC64631.
119
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                                    99 NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                        MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                     SDARKSETTITQSGYGNGAD------
                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA--
                                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doran JL,
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                        of the
                                                                                                                                                                                                                                                                 79.1%;
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                                                                                                                                                                                                                                                                                                                                                                   present
                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                 Score 613; DB 3;
Pred. No. 1.4e-51;
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                        invention
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                                                                                                                     -----YDQLVTRVVTHEMAHAFR
                                                                                                                                                                                                                                                <u>,</u>
                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                Indels
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Gaps

86 60 60 N د

AAB36346 ID AAB

AAB36346 standard; protein; 151

8

AgfA::PT3#1 amino acid sequence SEQ ID

NO:12

26-FEB-2001 AAB36346;

(first entry

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                                  S
                                                                                                                                                      Query Match
Best Local
                                                                          Matches
                                                                                                                                                                                                                                                        back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SER17/TAF) nucleation dependence assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
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                                                                                                                                                                                      immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
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                      CC directing recombination of a recombinate gene into the chromosome of the CC directing recombination of a recombination of a recombinate gene into the chromosome of the CC homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native CC back into the chromosome of the homologous species, replacing the native CC comprising separating an anino acid polymer comprising a recombinant AgfA CC comprising separating an anino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                 sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CspA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of a recombination of a recombination of a recombinant gene homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing a species; replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid foreign amino acid segment or segments of foreign amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doran JL,
                                                                                                                                                                                                                                                                                                                            invention describes a recombinant agfA gene (I) wher the gene has been replaced by a segment of a foreign
                                                                                                                                                                                                                                                                                                                                                                                                                   Page 136; 139pp; English.
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grown on a
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Pred. No. 1.3e-50;
4; Mismatches 25
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgGA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live
                                                                                                                         WPI; 2000-672631/65.
N-PSDB; AAC64628.
                                                                                                                                                                                                                                        05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151
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                                                                                                                                                                                                                                                                                                                                                                   vaccine; immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36352 standard; protein;
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                                                                                                                                                             Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                        amino acid sequence SEQ ID NO:24.
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                                                                                                                                                                                                                                                                                                                                                                   response;
                                                                                                                                                                                                                                                                                                                                                                               chromosomal gene replacement;
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Pred.
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                                                                                                                                                             Кау
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                                                                                                                                                                                                                                                                                                                                                                                 fimbrin; epitope;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described

Recombinant agfA gene having a segment replaced by a which encodes foreign epitope or antigen, expresses r protein useful for eliciting immune response in anima

animal.

foreign

DNA sequence ant AgfA

Disclosure; Page 138; 139pp; English

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RESULT 13
AAB36348
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Best Local S
Matches 123
WPI; 2000-672631/65
                                                             White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis.
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                                                                                                                                                                                    05-APR-1999;
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                                                         Doran JL,
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81.5%;
                                                             Collison
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Pred. No. 2.5e-50;
3; Mismatches 25;
                                                         SK,
                                                         Kay WW;
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12-OCT-2000

WO200060102-A2 Escherichia coli

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RESULT 14
AAB36343
ID AAB36
AC AAB36
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Matches
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                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                             Escherichia coli CsgA amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                             26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                    AAB36343 standard; protein; 151 AA
                                                                                                                                                       vaccine; immune response;
                                                                                                                                                                                                                                                                                                                         AAB36343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                            immunogen
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Pred. No. 3.3e-47;
4; Mismatches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 103; Conserv
                  E. coli CsgA
                                                            04-DEC-2003
                                                                                                                                       ABR82651 standard;
                                                                                                    ABR82651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                   TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
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                                                                                                                                       protein; 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
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Pred. No. 1.8e-41;
5; Mismatches 33
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Bscherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmor or Shigella infections.
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                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                     TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
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GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
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ative 15; Mismatches 34
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Perfect score:
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  Issued Patents AA:*

[CGD2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfIles1.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-072-967-204

US-09-252-991A-3098

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               Sequence 59, Appl Sequence 774, Appl Sequence 204, Appl Sequence 111, App Sequence 111, App Sequence 101, Appl Sequence 101, Appl Sequence 101, Appl Sequence 11518, A Sequence 11518, A Sequence 11518, A Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 24, Appl Sequence 27, Appl Sequence 280, Appl Sequence 280, Appl Sequence 280, Appl Sequence 24, Appl Sequence 27, Appl Sequence 28, Appl Sequence 21, Appl Sequence 21, Appl Sequence 11, Appl Sequence 13, Appl Sequence 13, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence
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Sequence

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1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

US-08-233-788A-59

Query Match 87.5%; Best Local Similarity 89.4%; Matches 135; Conservative

Score 678; DB 1 Pred. No. 4e-61; 1; Mismatches

DB 1; Length 151; 15; Indels

0;

Gaps

60

RESULT 1  US-08-233-788A-59  (Sequence 59, Application US/08233788A  Patent No. 5635617  GENERAL INFORMATION:  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  ADDRESSEE: Seed and Berry  STREET: 6300 Columbia Center, 701 Fifth Avenue  CONTRY: U.S.A.  ZIP: 98104-7092  COMPUTER: LIBM PC Compatible  COMPUTER: READABLE FORM:  MEDIUM TYPE: Plopy disk  COMPUTER: IBM PC Compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOCTWARE: PAPELICATION DATA:  APPLICATION NUMBER: US/08/233,788A  FILING DATE: 26-APR-194  CLASSIFICATION UNMBER: 920043.403C2  TELECOMMUNICATION INFORMATION:  NAME: King, Joshua  REGISTRATION UNMBER: 35,570  REFERENCE/DOCKET NUMBER: 920043.403C2  TELECOMMUNICATION INFORMATION:  TELEPHONE: (206) 622-4900  TELEFAX: (206) 622-4900  TELEFAX: (206) 622-4900  TELEFAX: (206) 622-4901  TELES: 3723836 SEEDANBERRY  INFORMATION FOR SED ID NO: 59:  SEQUENCE CHARACTERISTICS:  LENGTH: 151 amino acids  TYPE: amino acid  TOPOLOGY: linear  MOLECULE TYPE: procein	ALIGNMENTS	4 75.5 9.7 461 2 5 75.5 9.7 461 2	.5 9.7 432 4 US-09-403-089A-1 Sequence	1 75.5 9.7 293 5 PCT-US94-05669A-4 Sequence	75.5 9.7 293 3 US-09-219-019-6 Sequence	9 75.5 9.7 293 3 US-09-219-019-4	8 75.5 9.7 293 3 US-08-438-745-6 Sequence	7 75.5 9.7 293 3 US-08-438-745-4 Sequence	6 75.5 9.7 266 4 US-09-495-880A-26 Sequence	5 75.5 9.7 244 2 US-U8-553-49/A-22 Sequence	5 75 5 9.7 244 2 IIS-08-553-497A-22 Sequence	4 75.5 9.7 238 4 US-09-495-880A-42 Sequence	3 75.5 9.7 211 5 PCI-0895-08/43-34 sequence	THE COLOR OF THE C	2 75.5 9.7 211 5 PCT-US93-08364-16 Sequence	1 /5.5 9.7 211 4 US-09-729-397-10 sequence	1 75 5 0 7 311 / ITS_00_730_507_16 Company	0 75.5 9.7 211 3 US-08-907-739-16 Sequence	9 75.5 9.7 211 2 US-08-383-619-16 Sequence	8 /3.5 9.7 ZII I W 06-099-3/3-34 Sequence	9 75 5 9 7 211 1 175-08-809-575-34 Semience					
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               Sequence 4764, Application US/09328352 Patent No. 6562958
GENERAL
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57, Application US/08233788A Patent No. 5635617
                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE DOCKET NUMBER: 921
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/OFILING DATE: 26-APR-1994
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INFORMATION:
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                                                                                                                                   DQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                       amino acids
                                                                                                              GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
                                                                                                                                                                            VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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William W.
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86.6%;
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Patent NO. 6001592
GENERAL INFORMATION:
APPLICANT: Kunio NAKASHIMA et al
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gary L. Breton et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                              APPLICATION NUMBER: US/08
FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-
FILING DATE: 15-July-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Microsof SOFTWARE: Word Perfect 6.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                            TELEPHONE: (212) 986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
TYPE: amino acid
                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                         REGISTRATION NUMBER:
                      LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: JAPAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354
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C. wmmner: 22,389
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MAKASHIMA et al.

MINION:

MOVEL POLYPEPTIDE GENE CDNA, VECTOR

VENTION:

MOVEL POLYPEPTIDE GENE CDNA, VECTOR

VENTION:

MOVEL POLYPEPTIDE CDNA, HOST CELLS TRANSFORMED WITH SAID

VENTION:

MOTO POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
                                                                            (212) 953-7733
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IBM Compatible
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Pred. No. 4.
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                                                                                                                                          Query Match
Best Local &
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GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/056,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acid
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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LOCATION: from 1 to 73
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 07-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
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LICANT: Dillon, Davin C.
LE OF INVENTION: COMPOUNDS AND METHODS
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                                                      464 GSGNIGVFNVGSGSLGNYNIGSGN------LGIYNIGFGNVG-------DYNV 503
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74 GYGNGADYDQLVTRVVTHEMAHAFRUNATIDQWNAKNSDITVGQYGGN-----
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l Similarity 35.5%;
27; Conservative
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                                                                                                                                          Similarity
                                                                                       GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
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from 1 to 738
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                                                                                                                                        10.8%; Score 84; DB 4; Length 943, 24.7%; Pred. No. 5.1;
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Pred. No. 3.3;
4; Mismatches 22;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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ZIP: 98104-7092
                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                   504 GFGNAGDFNQ-
                                                                  554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN
                                                                                                  122 --- NAALVNQTASDSSVM---- VRQVGFGNNATAN 149
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Houghton, Raymond
Vedvick, Thomas S.

2-14 Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                        943 amino acids
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                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (206) 682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reed, Steven
                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                      10.8%;
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                                                                                                                                                                                                                                                                                    Score 84;
Pred. No.
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                                                                                                                                   -GFANTGNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 553
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                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                    Length 943
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TITLE OF INVENTION: Myc
TITLE OF INVENTION: imm
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
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CURRENT FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08990823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR TITLE TO THE PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENERAL INFORMATION:
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ADDRESSEE: SEED and BERRY LLP
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                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
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5. 6592877
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VENTION: COMPOUNDS AND
VENTION: AND DIAGNOSIS
SQUENCES: 355
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Vedvick, Thomas S.
Twardzik, Daniel R.
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Dillon, Davin C.
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                                     US/09/072,967
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                                                                                        TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                               REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 79
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/968,685A FILING DATE: No. 6214981ember 12, CLASSIFICATION:
                   STRANDEDNESS:
                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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COPOLOGY:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                              (212) 869-8864
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   unknown
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LENGTH: 558
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Patent No. 6551795
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Best Local Similarity
Query Match
                                                                                                             SEQ ID NO 32096
                                                                                                                        PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 199-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPPUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                       ORGANISM: Pseudomonas
                                                                                           LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 VHHAGGRGLDPHLLLQRAATHAVARAER 301
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1998-02-18
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Pred. No. 4.5;
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Score 80;
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Length 339;
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RESULT 13
US-09-336-115C-6
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APPLICANT: Gary Br
                        SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 6
LENGTH: 745
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Weltzin,
APPLICANT: Guy, Br
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LENGTH: 1207
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Patent No. 6610836
                                                                                                                                                   APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infect:
FILE REFERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
FRIOR APPLICATION NUMBER: US 09/100,258
FRIOR FILING DATE: 1998-06-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                   NUMBER OF SEQ ID NOS: 24
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ORGANISM: Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 GPVMQSQPAYNHNQFSGAIANGAESMISTFSLGSTLASGVSSAQALQSQKSEAFQSTLGR 541
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                                                                                                                                                                                                                                                                                                                                                                        Richard A.
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Pred. No. 18;
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RESULT 15
US-09-841-786-4
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US-09-252-991A-26438
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                                                 Sequence 4, Application Patent No. 6669940 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26438
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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APPLICANT: NAGARAJA, T. G.
APPLICANT: STEWART, GEORGE C.
APPLICANT: NARAYANAN, SANJEEV K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: VARIANT
LOCATION: 721
OTHER INFORMATION: Xaa = Any Amino
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                                                                                                                                                                               1045
                                                                                                                                                                                                            122 NAALVNQTA-SDSSVMV-RQVG--FGNNATAN 149
                                                                                                                                                                                                                                                 989
                                                                                                                                                                                                                                                                                                                      930 ADFAISGQ-LKDHASHYGAGGLVGRNRGGLIRSSGSQGTLSLSGHGMNLGGLVGYSSAGG 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 DINGGVYQFCKAKNGSSSSSNGGNGSSTQTTATTTQDGVTITTTYNNNKAT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 AYQAVFLAINAAVGL---WNTIGYAVMCGNGNGTESGPGSVIFNDQPGQDSTQITCNRFE 158
                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                     10 AAIVVSGSALAGVVPQWGGGG--NHNGGG--NSSGPDSTLSIYQYGSANAALALQSDA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                                                                                            44;
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                                                                                                                                                                                                                                                                                  -RKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN- 121
                                                                                                                                                                           NAAINNASAHGDVSLQAGRYLGGLIGHNQAGN 1076
                                                                                                                                                                                                                                                 LADVSASVDVSGNGQRGLYGGLIGLNVNSGIAHATASGKV----RGTDAEALGGLIGRNL 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STGPGKSMSIDEFKKLNEAYQIIQQALKNQSGFPELG-GNGTK----VSVNYNYECRQTA 213
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 1999-02-18
IMBER: US 60/074,788
1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                         10.3%;
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20.5%; Pred. No. 11
                                                                                       US/09841786
                                                                                                                                                                                                                                                                                                                                                                                        17;
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Pred. No. 25;
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US-09-841-786-4
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SEQ ID NO 4
LENGTH: 714
TYPE: PRT
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                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/841,786
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/558,257
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                     Local
151
                                   103 IDQWNAKNSDITVGQY 118
                                                                       92 NANKFKVNALSGGTQVAAGAGLEAVKESG-GQGKSYLLGTSASINLVNNEVSAKSENNTV 150
                                                                                                                                             35 VTSSDSTFVGA---WGGSAALQWNHIGSGNSNISAGLAGAAAVNNIQSKTSALVKNSDIR 91
                                                                                                                                                                             12 IVVSGSALAGVVPQWGGGG----NHNGGGN---SSGPDSTLSIYQYGSANAALALQSDAR
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                                                                                                                                                                                                                              Similarity
AGESESQKMDVDVTAY
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                                                                                                                                                                                                                   Conservative
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22.8%; Pred. No. 13;
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                                                                                                           TTITQSGYGNGADY---DQLVTRVVTHEMAHAFRNNAT 102
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Search completed: March 11, 2004, 18:44:54 Job time : 13.4 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                 Score
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seq length: 2000000000
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/cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*

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       . 249
2495
2597
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                                                    US-09-793-306-146

US-09-880-748-905

US-09-96-634-131

US-09-997-182-131

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US-10-193-002-199

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US-09-730-374-3
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     US-10-369-493-9134
US-09-880-748-1847
US-09-880-748-1201
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Sequence 146, App
Sequence 131, App
Sequence 131, App
Sequence 131, App
Sequence 199, App
Sequence 204, App
Sequence 9, Appli
Sequence 4894, Ap
Sequence 9134, Ap
Sequence 1847, Ap
Sequence 1847, Ap
                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                     Sequence 21, Appl
Sequence 3, Appli
Sequence 20638, A
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9.9	9.9	٠	9.9		9.9		9.9		٠	9.9	٠	9.9	9.9	9.9	9.9	•	10.0	10.0	10.0	10.0	10.0	10.1	0	10.1	10.1	0	10.3	10.3	10.3
2732	1778	1088	873	809	251	1046	271	257	255	255	250	250	250	250	250	250	1626	1621	562	518	438	892	3241	714	486	65	745	278	253
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US-10-238-075-1119	US-10-238-075-749	US-10-421-654-72	9	US-10-156-761-13874	-09-880-748-	US-10-369-493-1547	-10-156-761-	US-09-880-748-1494	US-09-880-748-1862	US-09-880-748-1153	-10-360-828-2	US-10-360-828-21	US-10-071-866-29	US-10-071-866-21	-10-072-301-	10-072-301-	990-	US-10-185-990-10	US-10-156-761-13039	US-09-976-297-2	US-10-156-761-9343	US-09-952-267-5	US-09-841-786-1	US-09-841-786-4	US-10-369-493-20619	US-09-996-194-16	US-08-834-666A-6	US-09-810-264-28	US-09-880-748-2098
1119	J	72,	13,	138	21			1494,	1862,	1153	29,	21,		21,	e 29,	Sequence 21, Appl	11,	Sequence 10, Appl	Sequence 13039, A	2, App]	934	G G	1, 1	4.	O	16,		28, App	Sequence 2098, Ap

### ALIGNMENTS

RESULT 1
US-09-820-843A-21
Sequence 21, Application US/09820843A
Publication No. US20030039963A1
Publication No. US20030039963A1
Publication No. US20030039963A1
FERENCE OF INVENTION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118 Ś 밁 Ś 밁 Ś US-09-820-843A-21 SEQ ID NO 21 Matches Query Match LENGTH: 354
TYPE: PRT
ORGANISM: M. tuberculosis NAME/KEY: misc feature OTHER INFORMATION: PPE NAME/KEY: misc feature OTHER INFORMATION: gi|1781260 FEATURE: y Match 11.5%; Score 89; Local Similarity 24.1%; Pred. No. hes 38; Conservative 17; Mismatc 115 VGQYGGNNAALVNQTASDSSVMVRQV---GFGNNATAN 149 200 258 SGFGHNDPAGSGNSGIQNSGFGNS-------GYVNTSTTSMFGGNSGVLN 10 AAIVVSGSALAG-VVPQWGGGGNHNGGG-----AALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDIT 114 AGDVNSGVGNAGDVNTGLGNSGNINTGGFNPGTLNTGFFSAMTQAGPNS--GFFNAGTGN 17; Mismatches DB 10; Length 354; 63; -----NSSGPDSTLSIYQYGSAN Indels 40; Gaps 257 54

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TG-YG--NSGFYNAAVNNTGIFVTGVMSSGFFNFGTGN 335

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US-10-369-493-20638
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20638, Application US/10369493 Publication No. US20030233675A1
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APPLICANT: Lust, John A.
APPLICANT: Donovan, Kat
  Best Local Similarity
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                      Query Match
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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Patent No. US20010031261A1
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PRIOR APPLICATION NUMBER: 60/088,277
PRIOR FILING DATE: 1998-08-05
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CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: PCT/US99/12512
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TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES
TITLE OF INVENTION: TO CD38 TO TREAT MULTIPLE MYELOMA
FILE REFERENCE: 150.188US2
                                                                                   NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                     FEATURE:
                                                                                                                                                                       ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                LENGTH: 445
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGNHNGGGNSSGPD---
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11.3%;
26.3%;
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Pred. No. 0.95
9; Mismatches
Score 87.5;
Pred. No. 2;
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                      DB 15;
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                      Length 445;
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US-09-793-306-146
                                                                                                           Sequence 905, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 146
LENGTH: 597
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
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PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: Description of Artificial Sequence: mTTC#3-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy IITLE OF INVENTION: of Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                             450
                                                                                                                                                                                                                                                                                                                  407
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                                                                                                                                                                                                                                                                                                                                                                                                                             26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
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                                                                                                                                                                                                                                             NAGTLN
                                                                                                                                                                                                                                                                                                                   TRVVTHEMAHAFRNNATIDQ--WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                          FGNSGNNNIGFFNSG~NNNVGFFNSGNNNFGFGNAGD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
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Corixa Corporation
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                                                                                                                              Application US/09880748
o. US20030059937A1
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20020098200A1
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Pred. No. 3.2;
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FILING DATE: 2000-06-15

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US-09-996-634-131
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US-09-880-748-905
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Best Local Similarity 23.0
29; Conservative
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                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 131, Application US/09996634
Patent No. US2002017268411
                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 61260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Nano,
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APPLICATION NUMBER: 60/276,248
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/000,254
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                                                                571 GSGNIGVFNVGSGSLGNYNIGSGN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 TLSCRASQSIRSNYLAWYQQKSGQAPRLLIYDVSSRATGIPDRFSGSGSGTDFTLTISRL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 ILTGYYMGSAFDQWGRGTMVTVSSGGGGSGGGGGGGGGGALEIVMTQSPGTLSLSPGERA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                             74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN------
                                                                                             16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                                                  943
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                                                                                                                                38;
                                                                                                                                                                                                                                                                                                           LING DATE:
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23.0%;
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-GFANTGNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS
                                                                                                                                               Score 84;
Pred. No.
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Pred. No. 1.7
                                                                                                                                Mismatches
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11;
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                                                                                                                                                             Length 943
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 131, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                     SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
                                                                            PRIOR APPLICATION NUMBER: 60/000,254
PRIOR FILING DATE: 1995-06-15
                                                                                                                       PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/447,135
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/997,182
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nano,
                                                           NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/997,181
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                      FILE REFERENCE: 61257
                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nano,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 61258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/447,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
LENGTH: 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  611 GFGNAGDFNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 --- NAALVNQTASDSSVM---- VROVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     571 GSGNIGVFNVGSGSLGNYNIGSGN------LGIYNIGFGNVG-------DYNV 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 --- NAALVNQTASDSSVM--- VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN------ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              943
                                          PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09997181
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                                                                                                                                                                                                                                                                                                                                                                                        IS20030049269A1
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GFANTGNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   694
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Best Local Similarity

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SEQUENCE DESCRIPTION: SEQ ID NO: US-10-193-002-199
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US-10-193-002-199
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   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 199, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                 INFORMATION FOR SEQ ID NO: 199: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                               TYPE: amino acid
                                                                                                                                                                                                           NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 694
                                                                               STRANDEDNESS: <Unknown>
                                                                                                            LENGTH: 943 amino acids
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                                                                                                                                                                                TELEPHONE: (206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                 ELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF SEQUENCES:
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0. US20030135026A1
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Vedvick, Thomas S.
Twardzik, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hendrickson, Ronald C.

VENTION: COMPOUNDS AND METHODS

TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Twardzik, Daniel
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed, Steven G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6300 Columbia
                                                                                                                                                                 (206)
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   10.8%;
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                                                                                                                                                               682-6031
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Pred. No.
Score 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GFANTGNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                               210121.417C9
                                                 199:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 943;
DB 14;
                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
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Length 943;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 204: US-10-084-843-204
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US-10-084-843-204
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   Matches
                    Query Match
Best Local Similarity
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                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 204
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                   NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lodes, Michael J.

Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 587
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   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---NAALVNOTASDSSVM---VROVGFGNNATAN 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300
                                                                                                                                                             ENGTH: 943 amino acids
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o. US20030143243A1
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton, Kaymon...
Vedvick, Thomas S.
Wardzik, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seattle
                                                                                                                                              amino acid
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Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campos-Neto, Antonio
                                                                                                                                                                                                                   (206)
                                                                                                            linear
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00 Columbia Center,
                    10.8%;
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                                                                                                                                                                                                                   682-6031
   12;
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Score 84; DB 14; Length 943; Pred. No. 11; 2; Mismatches 54; Indels
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30
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 50;
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Gaps
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16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS 73

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; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-813-214A-9
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US-09-813-214A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tucker, Kenneth
APPLICANT: Plosila, Laura
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Patent No. US20020177200A1
                                             CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE PROTEIN-106 POLYPEPTIDE,
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REFERENCE: 7969-089-999
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                                                                                                                                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                               APPLICATION NUMBER: JP 00/280988
              FILING DATE:
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                          OZAKI, AKIO
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ANDO, SEIKO
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NOS:
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            2000-08-03
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25.8%; Pred. No.
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
ITILE OF INVENTION: DIANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                            RESULT 14
US-09-880-748-1847
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Sequence 1847, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: pF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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SEQ ID NO 9134
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LENGTH: 224
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
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Pred. No. 3
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Pred. No. 18;
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1201
ENGTH: 252
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; ORGANISM: Homo sapiens
US-09-880-748-1201
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US-09-880-748-1201
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US-09-880-748-1847
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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SEQ ID NO 1847
LENGTH: 246
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CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17
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PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/276,248 PRIOR FILING DATE: 2001-03-16
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Local Similarity 31.1%;
hes 28; Conservative
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FILING DATE: 2000-10-17
APPLICATION NUMBER: 60/276,248
FILING DATE: 2001-03-16
217 ITGLQGEDEADYYCQ-SFDTSLGVRVFGGGTQLT 249
                             115 -VGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                                              164 GSGSNIGAGYD
                                                                                                                                                                                        114 WGKGTLVTVSSGGGGGGGGGGGGG------GSAQAVLTQPSSVSGAPGQRVTISCT 163
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                                                                                                                                         74 GYGN--GADYDQLVTRVVTHEMAH-----AFRNN----ATIDQWNAKNSDIT---- 114
                                                                                                                                                                                                                                     26 WG-----GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD---ARKSETTITQS 73
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                                                                                            ---VHWYQHLPGTAPKLLIFGNNNRPSGVPDRFSGSKSGTSASLA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 80; DB 10; Length 246; Pred. No. 5.2; 6; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                               DB 10; Length 252;
                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Gaps
                                                                                                                                                                                                                                                                                  50; Gaps
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                                                                                                                                                                                                                                                                                    9;
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Search completed: March 11, 2004, 19:18:40 Job time : 25.6 secs

Copyright GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd

OM protein protein search, using sw model

March 11, 2004, 18:24:14 ; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec

US-09-543-407-28 775

Perfect score:

Sequence: 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB Maximum DB

seq length: 0
seq length: 2000000000

Post-processing:

summaries

Minimum Match 0% Maximum Match 100% Listing first 45 s

Database

4 W 2 H PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

#### SUMMARIES

Result

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	ហ	4	w	2	卢	No.
85.5	85.5	96	86.5	86.5	86.5	87	87.5	87.5	87.5	88	89	89.5	89.5	89.5	89.5	89.5	91	91	91.5	94	94.5	97	107	487.5	487.5	509	683	683	Score
11.0	11.0	11.1	11.2	11.2			11.3	11.3	11.3	11.4	11.5	11.5	11.5	11.5	11.5	11.5	11.7	11.7	11.8	12.1	12.2	12.5	13.8	62.9	62.9	65.7	88.1	88.1	Query
2204	1053	590	151	145	145	590	1258	1034	447	407	354	1567	1322	151	151	151	615	573	602	645	151	1748	2174	152	152	151	151	151	Length
Ŋ	N	Н	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	۳	N	N	N	N	N	N	N	N	N	BB
A70524	B70987	A45621	AH0635	H98144	AD3143	E70946	JQ0188	JC2143	G84687	T21956	B70663	S11672	S07053	G85665	C90806	S70787	E70663	C86266	PL0221	F70825	JC6040	S42136	E95965	H85665	D90806	S70788	AI0635		ID
PPE	PPE prote	leishmanolysin (EC	nucleation compone	hypothetical prote	λų	probable PPE prote		ice nucleation act		hypothetical prote	probable PPE prote	ice nucleation pro	ice nucleation pro	curlin minor chain		ıclea	probable PPE prote	F3F19.21 protein -	olys:	PPE pro	•	cnjB protein - Tet		hypothetical prote	9	curlin protein csg	n cha	rin protein a	Description

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

## ALIGNMENTS

C; Genetics:
A; Gene: agfA
C; Function: fimbrin protein agfA precursor - Salmonella enteritidis (;Species: Salmonella enteritidis (;Species: Salmonella enteritidis (;Species: Salmonella enteritidis C;Date: 31-Dec-1996 #sequence revision 31-Dec-1996 #text\_change 08-Oct-1999 C;Accession: JC6039; PC6015; Ā44898 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol. 178, 662-667, 1996 A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasmin C;Keywords: fimbria C;Keywords: fimbria F;1-20/Domain: signal sequence #status predicted <SIG> F;21-151/Product: fimbrin protein agfA #status experimental <MAT> A;Molecule type: protein
A;Residues: 21-52 <CO2>
A;Experimental source: strain 27655-3b
A;Rote: the authors translated the codon ACG for residue 44 as Ile
R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W.
J. Bacteriol. 173, 4773-4781, 1991
A;Title: Purification and characterization of thin, aggregative fimbriae from Salmonell.
A;Reference number: A44898; MUID:91310586; PMID:1677357
A;Contents: 27655 Ś 밁 밁 \$ A; Note: sequence extracted from NCBI backbone (NCBIP:45936) A; Molecule type: protein A; Residues: 21-33 < CO3 > A;Accession: A44898 A; Accession: PC6015 A;Cross-references: A;Molecule type: DNA A;Residues: 1-151 <C A; Accession: JC6039 Status: preliminary Matches 136; Query Match Best Local ( 61 61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120 ۲ 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ 1-151 <COL> Similarity SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ Conservative GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714 88.1%; 1; Score 683; DB 2; Pred. No. 1.4e-51; Mismatches 14; Indels Length 151; plasminogen activator 0; Gaps 60 60 0;

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A,Cross-references: EMBL:X90754; NID:gl147558; PIDN:CAA62282.1; PID:gl147564
A,Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augus
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Ri
A,; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002 C;Accession: S70788; G64846; S31202; S34560; S34559 R;Hammar, M; Arngvist, A.; Bian, Z.; Olsen, A.; Normark, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               curlin protein csgA precursor - Escherichia coli (strain K-12) N;Alternate names: csgA protein; major curlin protein C;Species: Escherichia coli
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A;Gene:
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A;Title: Complete genome sequence of a multiple drug resistant A;Title: Complete AB0502; MUID:21534947; PMID:11677608
          A;Residues: 1-151 <BLAT>
A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; PID:g1787279, A;Experimental source: strain K-12, substrain MG1655
R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S.
                                                                                                                                                                                                                                                                                                                                                                                                                              R; Hammar, M.; Arnqvist, A.; Bian, Mol. Microbiol. 18, 661-670, 1995 A; Title: Expression of two csg open
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                                                                                                    A; Molecule type: DNA
                                                                                                                       A;Status: nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic
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C;Accession: AI0635
R;Parkhill, J; Dougan, G; Jan
th T.: Connerton, P; Cronin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AI0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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A; Residues: 1-151 < PAR>
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A;Accession: AI0635
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Matches 136
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A.; Arnqvist, robiol. 7, 523
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                                                                                                                                                                                                                                                                                                                           1-151 <HAM>
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No. 1.4e-5
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                                                                                                                       translation
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ies, R.M.; Dowd
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Salmonella enterica
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, L.; White,
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Riley, M.;
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                                                                                                                                                                                                       A;Gene:
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A;Title: Complete genome sequence of
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QSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYG
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curlin major subunit CsgA [imported] - Escherichia
C;Species: Escherichia coli
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A; Residues: 21-42;44-50 <OLS2>
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A;Residues: 1-6,'V',8-151 <OLS1>
A;Cross-references: EMBL:L04979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: major component of wild-type curli; interaction between CsgA and CsgB A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli th and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers f;1-20/Domain: signal sequence #status predicted <SIG>
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A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:LO4979; NID:g290424;
A;Experimental source: strain K-12, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Olsen, A.N.; Arnqvist, A.M. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: S31202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression A;Reference number: S31202; MUID:93211294; PMID:8459772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S34559
                                                                    ;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change
                                                                                                                                                                                                                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITOSGYGNGADYDOLVTRVVTHEMAHAFRNNATIDOWNAKNSDITVGOYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                  TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
Makino, K.; Ohnishi,
Kasunaga, T.; Kuhara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 509; DB 2;
Pred. No. 1.1e-36
5; Mismatches 3:
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  Kurokawa, K.;
Shiba, T.; Hat
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W3110
  Hattori,
                                                                                                                      coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151
                           Ishii,
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; Yokoyama,
Shinagawa,
                                                                         18-Jul-2001
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A; Experimental source: C; Genetics
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A; Residues: 1-152 < HAY >
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                                                                                               Similarity
                                   MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
                                                                            Conservative
                                                                                                                                                                                                GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
Se: strain O157:H7, substrain RIMD 0509952
                                                                                             62.9%;
                                                                                                                                                                                                                                                                                                                 puence of enterohemorrhagic Escherichia coli 0157:H7
MUID:21156231; PMID:11258796
                                                                          Score 487.5; DB 2
Pred. No. 7.6e-35;
6; Mismatches 34
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                                                                            Indels
                                                                                                                 Length
                                                                            1:
                                                                            Gaps
60
                                       59
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2174 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid psymb
R;Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
R;Galibert, F; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                             R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: H85665
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein csgA [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                          A, Reference number: A96039; MUID: 21368234; PMID: 11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical glycine-rich protein [imported] - C; Species: Sinorhizobium meliloti
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                                                  Contents: annotation
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Gene: SMb21548
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Pred. No. 7.0
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Nucleic Acids Res. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and glycine-rich repeats A;Reference number: S42135; MUID:94051569; PMID:8233798
A;Molecule trace.....
                                                                                                                                                                                                                                                                              A;Gene: cnjB
A;Genetic code: SGC5
A;Introns: 85/3; 136/1; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 708/3; 777/3;
A;Introns: 85/3; 136/1; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 708/3; 777/3;
C;Reywords: zinc finger
C;1164-1450/Region: glycine-rich
F;1451-1464/Region: zinc finger CCHC motif
F;1478-1491/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1530-1543/Region: zinc finger CCHC motif
F;1555-1568/Region: zinc finger CCHC motif
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R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene
A;Reference number: S03650; MUID:88189811; PMID:3357771
A;Accession: S03650
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F;1602-1615/Region:
F;1626-1748/Region:
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A;Residues: 236-250,'I',252-255,'N',257-773
A;Cross-references: EMBL:X06462
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1164-1174; 1179-1198; 1233-1252; 1285-1293; 1297-1309; 1316-1326; 1331-1341; 1343-1
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A;Cross-references: EMBL:L03710; NID:g161751;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---K 65
                                                                                                                                                                    Similarity

    Tetrahymena thermophila

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                 DOLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGEVSVSLTDSAIRTGOGG
                                                                       QFGGGGNSNGGQSWGTSSGSDWN-----
                                                                                                             QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADY
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                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                            zinc
                                                                                                                                                                                                                          glycine-rich
                                                                                                                                                                                                                                              finger CCHC
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                                                                                                                                                                12.5%;
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                                                                                                                                                   20;
                                                                                                                                                                  Score 97;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 107; DB 2; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          October
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     821
DNQQQQNENTGGGGWGSSNS---
                                                                                                                                                                                                                                              motif
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                                                                                                                                                   Mismatches
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                                                                                                                                                                                      BB
                                                                       -----CQSNVQES-TTTSSGGWGSSGSG
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                                                                                                                                                                                  Length 1748
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C;Accession: JC6040
R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol. 178, 662-667, 1996
A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative A;Reference number: JC6039; MUID:96146512; PMID:8550497
                                                                                                                                                                                                                                                             Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                            A; Experimental source: C; Genetics:
                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-645 < COL>
                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                           R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                       probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jull-1998 #sequence_revision 17-Jul-1998 #text_change
C;Accession: F70825
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C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                       A; Gene:
                                                                                                                                                                                                                                               A; Accession: F70825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1-21/Domain: signal sequence #status predicted <SIG>F;22-151/Product: fimbrin protein agfB #status predicto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: minor component of thin aggregative A; Note: fimbriae bind to fibronectin, plasminogen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-151 < COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fimbrin protein agfB precursor - Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Date: 31_Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
                                                                                                                                ;Cross-references: GB:AL021958; GB;
;Experimental source: strain H37Rv
                    Query Match
Best Local
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Best Local
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                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARVROEGSKLLSVISO--EGGNNRAKVDQAGNYNFAYIEOTGNAN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WGSNNQAS
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    Conservative
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                    12.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.2%; Score 94.5;
26.9%; Pred. No. 0.
  14;
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Score 94; DB:
Pred. No. 2;
14; Mismatches
                                                                                                                                                       GB:AL123456; NID:g3261536; PIDN:CAA17522.1; PID:e12532
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  42;
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tissue plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                            #text_change 15-Sep-2003
                                         Length 645;
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  Indels
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50;
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Gaps
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7;
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C;Superfamily: leishmanolysin
C;Superfamily: leishmanolysin
C;Superfamily: leishmanolysin
C;Keywords: blocked carboxyl end; cell adhesion; glycoprotein; homodimer; hydrolase;
F;139/Domain: signal sequence #status predicted <SIG>
F;40-100/Domain: activation peptide #status predicted ANTP>
F;101-577/Product: leishmanolysin #status experimental <MATP>
F;101-577/Product: leishmanolysin #status experimental <MCTP>
F;701-577/Product: leishmanolysin #status experimental <MCTP>
F;578-602/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;40,264,268,334/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status F;100-101/Cleavage site: Val-Val (autolytic) #status experimental
F;125-142,191-230,314-386,393-455,406-425,415-489,466-510,515-565,535-558/Disulfide
F;264,268,334/Binding site: zinc, catalytic (His) (active) #status experimental
F;265/Active site: Glu #status predicted
F;265/Active site: Glu #status predicted
F;265/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Experimental source: strain LEMS13
R;Schlagenhauf, E.; Etges, R.; Metcalf, P.
submitted to the Brookhaven Protein Data Bank, March 1997
A;Reference number: A68135; PDB:ILML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Bouvier, J.; Bordier, C.; Vogel, H.; Reichelt, R.; Ett
Mol. Biochem. Parasitol. 37, 235-246, 1989
A;Title: Characterization of the promattigote surface p:
A;Reference number: A60648; MUID:90114330; PMID:2608099
                                                                                                           F;577/Modified site: GPI-anchor ethanolamine amidated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Description: catalyzes the hydrolysis of peptide bonds between two \hat{\mathbf{A}}_i, Note: the activated form can activate the proenzyme form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Contents: annotation; X-ray crystallography, 1.86 angstroms, A;Note: strain LRC-L119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 101, 'E', 103-118, 'SV', 121-123 <BOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Button, L.L.; McMaster, W.R.
J. Exp. Med. 167, 724-729, 1988
A;Title: Molecular cloning of the major surface antigen
A;Reference number: A27598; MUID:88154764; PMID:3346625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:Y00647; NID:g9554; PIDN:CAA68673.1; A;Note: this is a revision to the sequence from reference; R;Button, L.L.; McMaster, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: promastigote surface proteinase. C;Species: Leichmann.
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A;Residues: 1-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A27598
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                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complex: homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Leishmanīa major
                                                                                                                                            407/Binding site: carbohydrate (Asn) (covalent)
                             Local
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                          11.8%;
Score 91.5; DI
Pred. No. 3;
2; Mismatches
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81 YDQLVTRVVTHEMAHAF-

----RNNATIDOWNAKNSDITV-

-coyc

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YDQLVTRVVTHEMAHALGFSGPFFEDARIVANVPNVRGKNFDVPVINSSTAVAKAREQYG

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minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: C90806
C;Accession: C90806
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and

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RESULT 14 C90806	9	Query Match Best Local Matches 3	A;Gene: csgB A;Map position: C;Function: A;Description: A;Note: curli a and H-kininoge F;1-21/Domain: F;22-151/Produc	A; Status: nuclei A; Molecule type: A; Residues: 1-15: A; Cross-reference A; Experimental so	Science 2 A;Title: A;Referen	A; Residues: A; Cross-ref: A; Experiment A; Experiment A; Note: the R; Blattner, A: Rose.	A;Reference A;Reference A;Accession A;Status: r A;Status: r	C; Accessi C; Accessi R; Hammar, Mol. Micro	RESULT 13 S70787 curlin nu N;Alterna C;Species	B &	B. 8	Дb
	38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAF 97  ::      ;     ;     ;   ;     ;   ;   ;	Match 11.5%; Score 89.5; DB 2; Length 151; Local Similarity 28.1%; Pred. No. 0.92; es 32; Conservative 15; Mismatches 62; Indels 5; Gaps 2;	A;Gene: csgB A;Map position: 23.15 C;Punction: C;Punction: minor component of wild-type curli; interaction between CsgA and CsgB truA;Description: minor component of wild-type curli; interaction between CsgA and CsgB truA;Description: minor component of wild-type curli; interaction between CsgA and CsgB can self-assemble into polymers and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <sig> F;22-151/Product: minor curlin chain #status predicted <mat></mat></sig>	A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-151 - GBLAT> A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278, A;Experimental source: strain K-12, substrain MG1655	7, 1453-1462, 1997 he complete genome see e number: A64720; MUI	1-15 1-15 erence tal se tal se nucle	s number: 870783; MUID:96414468; PMID:8817489 1: S70787 1: S70787 1: S70787 1: S70787 1: S70787	; F64846 ist, A.; Bian, Z.; Olsen, A.; Normark, S. 661-670, 1995	tein csgB precursor - Escherichia coli (strain K-12sgB protein; curlin nucleation component; minor cur	132 DSSVMVRQVGFGNNATAN 149	75 YGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTAS 131	365 SGTGNIGFGNSGNNNIGFFNSG-DGNIGFFNSGDGNTG 401

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RESULT 15
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85665
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A;Accession: C90806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <HAY>
A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:913360879; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
Search completed: March 11, 2004, 18:42:12 Job time: 11.3 secs
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A;Residues: 1-151 <STO>
A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85665
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              86
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                                                                                                                                                                                                                77
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                                                                                                                                                                                                     SNRAKIDOTGDYNL-AYIDOAGSANDASISOGAYGNTAMIIOKGSGNKANITOY 129
                                                                                                                                                                                                                                                                                                              RNNATIDOWNAKNSDITVGOYGGNNAALVNOTASDSSVMYROVGFGNNATANOY 151
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28.1%; Pred. No. 0.92;
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Maximum DB seq length: 2000000000
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Perfect score:
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775
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entities requires a license agreement (See or send an email to license@isb-sib.ch).
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI, CURLI ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1357528;
Arnqvist A., Olsen A., Pfeifer J., Ri
"The Crl protein activates cryptic ge
fibronectin binding in Escherichia co
Mol. Microbiol. 6:2443-2452(1992).
SEQUENCE OF 21-31.
MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emmody L., Trust T.
"Purification and characterization"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kinura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sampei G., Seki Y., T
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A 718-kb DNA sequence of the I corresponding to the 12.7-28.0
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Hammar M., Arnqvist A., Bian Z., Olsen A.,
"Expression of two csg operons is required fibronectin- and congo red-binding curli po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olsen A., Arnqvist A., "The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding conscious coll.";

Mol. Microbiol. 7:523-536(1993).
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Enterobacteriaceae; Escherichia.
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Shao Y.;
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Q93U24;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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Perna N.T., Plunkett G. III, Burland V., Rose D.J., Mayhew G.F., Evans P.S., Grego Posfai G., Hackett J., Klink S., Boutin & Grotbeck E.J., Davis N.W., Lim A., Dimala Apodaca J., Anantharaman T.S., Lin J., Ye Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Es
                                                                                                                                                                                                                       STRAIN=0157:H7 / ATCC 43895;
MEDLINE=21218556; PubMed=11319125;
Whilch G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations expression in certain strains of Escherichia coli O157:H7."
Appl. Environ. Microbiol. 67:2367-2370(2001).
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                                                                                                                                              STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
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STRAIN=0157:H7 / E
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STRAIN=0157:H7 / A
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NCBI_TaxID=83334;
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, Gregor J., Kirkpatrick H.A.,
, Ountin A., Shao Y., Miller L.,
Dimalanta E.T., Potamousis K.,
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      Escherichia coli O157:H7.";
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Matches 101
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P55226;
01-OCT-1996
01-OCT-1996
28-FEB-2003
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                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                   SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Kurokawa C., Tanaka M., Tobe 1 Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Yasunag Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shimagawa H.;

Kuhara S., Shiba T., Hattori M., Shimagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark "Curli fibers are highly conserved between Salmonella ty Escherichia coli with respect to operon structure and re
                                       SPECIES=S.typhimurium; STRAIN=SR-11; MEDLINE=98117058; PubMed=9457880;
                                                                                                                                       Salmonella typhimurium, and Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR;
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / R
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                                                                  SEQUENCE FROM N.A.
                                                                                           NCBI_TaxID=602,
                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Salmonella.
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SIMILARITY: BELONGS
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Pred. No. 6e-
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Tobe T.,
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P08148; P15906;
01-AUG-1988 (Rel
01-APR-1990 (Rel
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             01-AUG-1988 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell
(Major surface glycoprotein) (GP63 protein) (1
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-- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-- COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY ATTEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONE
endopeptidase)
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EMBL; AE008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
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MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Bar
"Salmonella enteritidis agfBAC operon encoding
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MEDLINE=21534948; PubMed=11677609
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SIMILARITY: BELONGS
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Zymogen;
SIGNAL
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PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptidase M8.
Pfam; PF01457; Peptidase M8; 1.
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                                                                                                                                                                                                                                                                                                                                                                                      Structure
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Homans S.W., Bordier
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"Molecular cloning of the major
"Med. 167:724-729(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       μειβηπαπία major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                 MEROPS; M08.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91009116; PubMed=2145267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS)
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SIMILARITY: Belongs to peptidase family M8.
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Biol. Chem. 265:16955-16964(1990)
                                                                                                                                                                             PL0221; PL0221.
1LML; 17-SEP-97.
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                                                    Metalloprotease; Glyciqnal; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6:1035-1046(1998).
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171:589-589(1990)
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Bordier C.
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the major surface metalloproteinase from Leishmania
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                                                                     Glycoprotein; Metal-binding;
            ACTIVATION PEPTIDE LEISHMANOLYSIN.
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                                                       GPI-anchor;
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Matches 25
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SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
STRAIN-K12 / MG1657;
MEDLINE-91426617; PubMed-9278503;
Mellattner F.R., Plunkett G. III, Bloch C.A.,
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., F
Gregor J., Davis N.W., Kirkpatrick H.A., Gc
Mau B., Shao Y.;
"The complete genome sequence of Escherichi
                                                                                                               SEQUENCE FROM N.A.
STRAIN=K12 / MC4100;
STRAIN=96414468; PubMed=8817489;
MEDLINE=96414468; ubMed=8817489;
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                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
                                                                                                     Mol. Microbiol. 18:661-670(1995).
                                                                                                                                                                                                     NCBI_TaxID=562, 83334;
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                                                                                                                                                                                                                                                                                                                                                                                                               81
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Pred. No. 1.6;
2; Mismatches
    of Escherichia coli K-12.";
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                      C.A., Perna N.T., Burland V.D., Rode C.K., Mayhew G.F., A., Goeden M.A., Rose D.J.,
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MEDLINE=21156321; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka Iida T., Takami H., Honda T., Sasakawa C., Ogasawara Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escher O157:H7 and genomic comparison with a laboratory stra
                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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"Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coli can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";

Mol. Microbiol. 13:1021-1032(1994).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWT TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
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                          EcoGene, EG12621,
Fimbria, Signal, C
                                                             PIR; C90806; C90806.
PIR; G85665; G85665.
PIR; S70787; S70787.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A 718-kb DNA sequence of the E corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
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"A 718-kb
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                 SIGNAL
                                                                                                                                                                         EMBL; X90754; CAA62281.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=O157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=0157:H7
                                                                                                                                                                                                                                                                                                                                  - !- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
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, Itoh T.,
                             proteome
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Τ., Tanaka
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P20469;
                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000258; Ice nucleatn. Pfam; PF00818; Ice nucleation; 69. PRINTS; PR00327; ICENUCLEATN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abe K., Watabe S., Emori Y., Watanabe M., Arai S.;
"An ice nucleation active gene of Erwinia ananas. Sequence similarity
to those of Pseudomonas species and regions required for ice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pantoea ananas (Erwinia uredovora).
Bacteria, Proteobacteria, Gammaproteobacteria,
Enterobacteriaceae, Pantoea.
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PROSITE; PS00314; ICE_NUCLEATION; 49.
ICE nucleation; Repeat; Outer membrane.
DOMAIN 162 1281 OCTAPEFTIDE PERIODICITY.
DOMAIN 1322 AA; 131094 MW; 89B0EEZ4AA837039 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X17316; CAA35194.1; PIR; S07053; S07053.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleation activity.";
FEBS Lett. 258:297-300(1989)
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                                                                                                                                                                          Local Similarity
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SUBCELULIAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSEN
OCTAPEFTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
SIMILARITY: Belongs to the bacterial ice nucleation p
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(See http://www.isb-sib.ch/announce/
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-!- FUNCTION: Ice nucleation proteins enable bacteria to nucleat crystallization in supercooled water.

-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A RESIDUE AND A RESIDUE AND A RESIDUE PERIODICITY IS SUPERIMPOSED.

-!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEARING PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEARING PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEARING PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEARING PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEARING PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEARING PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEARING PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEARING PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE NUCLEARING PROTEIN DISPLAYS A SYMMETRY RELATED PROTEIN DISPLAYS A SYMMETRY RELATED PROTEIN DISPLAYS A SYMMETRY RELATED PROTEIN DISPLAYS A SYMMETRY RELATED PROTEIN DISPLAYS A SYMMETRY RELATED PROTEIN DISPLAYS A SYMMETRY RELATED PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00818, Ice nucleation, 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
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"Conserved repetition in the ice nucleation gene inaX from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xanthomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the bacterial ice nucleation
                                                    103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XANCT
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                                                                                                              264
                                                                                                                                                                  60
A----RKGSDITAG-YGSTGTAGSDSALIAGYGSTQTAGSESSLT--AGYGSTQTARK 374
                                                    IDQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                           STLTAGYGSTQTAQEGSRLTSGYGSTATSGSDSAVISGYGSTQTAGSESSLTAGYGSTQT
                                                                                                                                                                                                                       VYGSTLTGADQSRLVAGYGSTETAGDHSDLIAGYGSTGTAGSDSSI-LAGYGSTQTAAGR 263
                                                                                                                                                                                                                                                                           VSGSALAG-----VVPQWGG----GGNHN------GGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSQTARE 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNATANO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TQTGQENSDLTTG-YGSTSTAGYESSLIAGYGSTQTASFKSTLM--AGYG 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                1567 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 16, Created)
(Rel. 16, Last sequence up)
(Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                               SDARKSETTITQSGYG----NGAD-----YDQLVTRVVTHEMAHAFRNNAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonas
                                                                                                                                                                                                                                                                                                                                                         11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                152548 MW;
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                                                                                                                                                                                                                                                                                                                               Score 89.5; D
Pred. No. 7.2;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                C8B451D959ECAD63 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1567;
                                                                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleate
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RESULT 9
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Best Local (
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- DOMAIN: CONTAINS IMPERFECT REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RES
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                      PROSITE; PS00314; ICE NUCLEATION; 34.
Ice nucleation; Repeat; Outer membrane.
DOMAIN 162 993 OCTAPEPTII
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000258; Ice_nucleatn. Pfam; PF00818; Ice_nucleation; 51. PRINTS; PR00327; ICENUCLEATN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PERIODICITY IS SUPERIMPOSED.

-!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF IC-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94264407; PubMed=7764866; Michigami Y., Watabe S., Abe K., Obata H., An "Cloning and sequencing of an ice nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICEN PANAN
Q47879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pantoea ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; JC2143; JC2143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D14992; BAA03636.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uredovora."
                                                                                                                                                                                                                                                          Local Similarity
                                                244
                                                                                                                                                                                                                                                                                                                                                                                                                      P06620; 1INA.
                                                                                                                                                                                                          12 IVVSGSALAGVVPQW--GGGGNHNGGGNSS-----GPDSTLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biotechnol. Biochem.
                                                                                                                                          ALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pean Bioinformatics Institute. There are no restrictions on non-profit institutions as long as its content is in no
                                                YGSTGTAGDDSSLIAGYGSTQTAGEDSSLT--AGYGSTQTAQK 284
                                                                              YG----
                                                                                                            -----GEESSQMAGYGS-----
                                                                                                                                                                            IATYGSTLSGTHQSQLIAGYGSTETAGDSSTLIAGYGSTGTAGSDSTL-VAGYGSTQTA-
                                                                                                                                                                                                                                                                                                         1034 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                           Conservative
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                                                                            GNNAALV-----NOTASDSSVMVRQVGFGNNATANO 150
                                                                                                                                                                                                                                                         11.3%;
                                                                                                                                                                                                                                                                                                         103378 MW; FA222523D333EADD CRC64;
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                                                                                                                                                                                                                                                         Score 87.5; D
Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                          OCTAPEPTIDE PERIODICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Erwinia
                                                                                                                                                                                                                                           63;
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STANDARD;

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CSGB_SA
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Best Local S
Matches 41
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Q8Z7M3;
28-FEB-2003
28-FEB-2003
10-OCT-2003
                                                                                SALTI
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                 Ice nucle
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M26382; AAA24823.1;
PIR; JQ0188; JQ0188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The consensus sequence of ice nucleation proteins herbicola, Pseudomonas fluorescens and Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Warren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90152370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
Enterobacteriaceae; Panto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erwinia herbicola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTYSTABLIZATION IN SUPERFOOLED WATER.
SUBCELLULAR LOCATION: OUTER membrane.
DOMAIN: CONTAINS 126 IMPERFECT REPEATS OF A CON
A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A
PERIODICITY IS SUPERIMPOSED.
MISCELLANBOUS: A STRUCTURAL MODEL IS SUGGESTED
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED
SIMILARITY: Belongs to the bacterial ice nuclea
family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Ice nucleation proteins enable
                                                                                                                                                    118
                                                                                                                              244
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                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                      41;
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                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                   IATYGŚTLSGTHQSQLIAGYGSTETAGDSSTLIAGYGSTGTAGADSTL-VAGYGSTQTA-
                                                                                                                                                                                                                                            IVVSGSALAGVVPOW--GGGGNHNGGGNSS----
                                                                                                                         YGSTGTAGDDSSLIAGYGSTQTAGEDSSLT--AGYGSTQTAQK
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                                                                                                                                                                                                                                                                    Conservative
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(Rel. 14,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corotto
                                                                  STANDARD;
                                                                                                                                              -GNNAALV-----NOTASDSSVMVRQVGFGNNATANQ
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                                                                                                                                                                          -GEESSQMAGYGS----
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tto L.V.;
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25.2%;
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                                                                                                                                                                                                                                                                    18;
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annotation updat
                                                                                                                                                                                                                                                                  Score 87.5; D
Pred. No. 8.2;
L8; Mismatches
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                                                                  PRT;
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                                                                 151
                   update)
                                                                                                                                                                                                                                                                             8.2;
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                                                                                                                                                                                                                                                                                        DB 1;
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                                                                                                                                                                                                                                                                                       Length 1258;
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D A REGIONAL 48-RESIDU
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                CRC64;
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                                                                                                                                                                                                                                                                 63;
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RESULT 12
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ID GP63_LI
AC P23223,
DT 01-NOV-
DT 01-NOV-
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Best Local S
Matches 34
     P23223;
01-NOV-1991
01-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fimbria; Signal; Complete proteome.
SIGNAL 1 21 POTENTIAL.
CHAIN 22 151 MINOR CURLIN SUBUNIT.
SEQUENCE 151 AA; 16254 MW; 161C54326E573495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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-!- FUNCTION: CURLII IS THE STRUCTURAL SUBUNIT OF THE CURLI. CUCILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT CETEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL627269; CAD08267.1; -. EMBL; AE016840; AAO69400.1; -.
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmoneila enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
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STRAIN=TY2 / ATCC 700931;
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner
"Comparative genomics of Salmonella enterica serova
and CT18.";
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Enterobacteriaceae; Salmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhi
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SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                    LEIDO
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                                                                                                                                                                                                                  QSHMAIRVTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                            ARVRQEGSKLLSVISQ--EGENNRAKVDQAGNYNFAYIEQTGNAN
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  (Rel.
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                                                                                 STANDARD;
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Salmonella.
Created)
Last sequence
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Pred. No. 0.89;
17; Mismatches
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F.R.;
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Typhi strains
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Matches 21
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-I. FUNCTION: Has an integral role during the inferint in the mammalian host.

-I. CATALYTIC ACTIVITY: Preference for hydrophobic pl' and basic residues at p2 and p3'. A model cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.

-I. COPACTOR: Binds 1 zinc ion per subunit (By sim.)

-I. SUBCELLULAR LOCATION: Attached to the membrane.

-I. SIMILARITY: Belongs to peptidase family M8.
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Leishmanolysin |
(Major surface of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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InterPro; IPR001577; PeptIdase M8,
Pfam; PF01157; PeptIdase M8, 1.
PRINTS; PR00782; LSHMANOLYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Webb J.R., Button L.L., McMaster k.m.
"Heterogeneity of the genes encoding
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NCBI_TaxID=5661;
                                                                                                                               SEQUENCE
                                                                                                                                                                 TIPID
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Hydrolase; Metalloprotease; Glycoprotein; Metal-binding;
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P08148; 1LML.
                                                                              Similarity
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YDOLVTRVVTHEMAHALGFSVVFFRDARILESISNVRHKDFDV
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precursor (EC 3.4.24.36) (Cell
glycoprotein) (GP63 protein) (
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L.L., McMaster R.W.;
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                                                                           11.1%;
48.8%;
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Medina-Acosta E., Karess R.E., Russell D.G.;
"Structurally distinct genes for the surface protease
"Structurally distinct genes for the surface protease
mexicana are developmentally regulated.";
Mol. Blochem. Parasitol. 57:31-46(1993).
-!- FUNCTION: Has an integral role during the infection the mammallan host.
-!- CATALYTIC ACTIVITY: Preference for hydrophobic repring and basic residues at P2 and P3'. A model non cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
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SIGNAL
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X64394; CAA45733.1;
PIR; S19916; S19916.
HSSP; P08148; 1LML.
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Eukaryota; Euglenozo
NCBI_TaxID=5665;
                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
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(Major surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to peptidase family M8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metalloprotease;
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1. 32, Last sequence update,
al. 42, Last annotation update)
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     tease; Glycoprotein; Metal-binding;
adhesion; Multigene family.
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L outstation -
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Best Local S
Matches 23
                                                  EMBL; M80672; AAA29238.1;
EMBL; M28527; AAA29235.1;
PIR; A44951; A44951.
                                                                                                     entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                       expressed during development of Leishmania donovani chagasi promastigutes to an infectious form.";

J. Biol. Chem. 267:1888-1895(1992).
                              MEROPS; M08.001;
                                                                                                                               use by non-profit institumodified and this statement
                                                                                                                                                the European
use by non.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92112918; PubMed=1370484;
Ramamoorthy R., Donelson J.E., Pa
Wilson M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=9020596; PubMed=2320059;

Miller R.A., Reed S.G., Parsons M.;

"Leishmania gp63 molecule implicated in cellular

"Arg-Gly-Asp sequence.";
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NCBI_TaxID=44271;
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Eukaryota; Euglenoz
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P15706;
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                                                                                                                                                                                                      CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and basic residues at P2 and P3'. A model nonapeptide cleaved at -Ala-Tyr-|-Leu-Lys-Lys-COFACTOR: Binds 1 zinc ion per subunit (By similarity). SUBCELLULAR LOCATION: Attached to the membrane by a GPI-ar SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                            in the mammalian host. CATALYTIC ACTIVITY: Pr
                                                                                                                                                                                                                                                                                                FUNCTION: Has an integral role during
                                          P08148;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem.
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    IPR006025;
IPR001577;
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646 AA;
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Bioinformatics Institute. There are ...
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(Rel. 14, Last sequence update)
(Rel. 42, Last annotation update)
sin precursor (EC 3.4.24.36) (Cell
ace glycoprotein) (GP63 protein) (I
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Peptidase_M8
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Pred. No. 6
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(Promastigote surfa
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                                                                                J. Bacteriol. 170:3177-3188(1988).
-!- FUNCTION: Bacterial hemolysins are cell membranes and cause cell ruptu
            This
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                                                                                                             marcescens.";
                                                                                                                  MEDIINE-88257037; PubMed=3290200;
Poole K., Schiebel E., Braun V.;
"Molecular characterization of the hemolysin determinant
                                                                                                                                                 STRAIN=SN8
                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                               01-APR-1990 (Rel. 01-NOV-1990 (Rel.
                                                                                                                                                                                  Bacteria; Proteobacteria;
Enterobacteriaceae; Serrat
                                                                                                                                                                                                    Serratia marcescens.
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                        REQUIRES SHLB FUNCTION.
SUBCELLULAR LOCATION: Outer membrane.
SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                      ERYTHROCYTES BY INTERACTION
                                                               FUNCTION: CELL-BOUND HEMOLYSIN,
SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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Hemolysis; Toxin; Outer membrane; Signal.
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07X243
07X243
07X237
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Q7x237 enterobacte
Q54069 salmonella
Q983j5 escherichia
Q89j14 bradyrhizob
Q8y106 ralstonia s
Q8x3d6 ralstonia s
Q8x3d6 ralstonia s
Q8x6d13 shewanella
Q8eih3 shewanella
Q92uu8 rhizobium m
Q8eih4 shewanella
Q92us rhizobium m
Q8eih4 shewanella
Q89j13 bradyrhizob
Q7u5x6 synechococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7x243 citrobacter
Q7x240 citrobacter
Q8cw63 escherichia
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Q25275 leishmania Q7x241 citrobacter Q9saf2 arabidopsis Q7tyr8 mycobacteri P95249 mycobacteri Q8e833 shewanella Q841y5 campylobact Q7x238 enterobacte Q7x238 enterobacte Q7x238 enterobacte Q7x238 enterobacte Q7x38 enterobacte Q89ji6 bradyrhiob Q83ru7 shigella fl Q80d38 xanthomonas					)	
8761 <sub>66</sub> 03687		16	2411	11.5	89.5	44
767 6 2 9 8 2 7 1		ĭ	1333	11.5	89.5	Ü
9 2 9 9 9 9 7 7		16	160	11.5	89.5	2
+ a C 2 0 8 2 C L		1	153	11.5	89.5	Ξ
a c w o o o c _	6 Q7UCZ1	16	151	11.5	89.5	ô
$a^{\omega}$	Q7X238	N	151	11.5		ø
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۳ ک <sub>د</sub> ه		1	615	11.7	91	ō
∾ ດ ∟		16	614	11.7	91	Ű
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	o	ຫ	598	11.9	92	32
v		16	1765	11.9	92.5	3
O43994 leishmania	0	ഗ	644	11.9	92.5	ö
O93397 cyprinus ca		13	348	11.9	92.5	29
		1	157	12.0	93	83
Q8mny9 leishmania	O	ທ	644	12.1	93.5	7
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Q8ewd6 mycoplasma		16	368		95	20
Q94821 tetrahymena	0	υ	1748	12.5	97	ø
Q89ji5 bradyrhizob	6 Q89JI5	1	154	12.6	97.5	8
O33801 salmonella	033801	N	179	12.6	98	7

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O33802;
O3-JAN-1998 (TrEMBLrel. 05
f 01-JAN-1998 (TrEMBLrel. 05
T 01-DEC-2001 (TrEMBLrel. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJO
NON TER
SEQUENCE
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z.,
Normark S.J., Rhen M.;
"Expression of thin, aggregative fimbriae promotes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells.";
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       NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSAVAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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ilarity 88.7%;
Conservative :
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Last annotation update)
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Q7X240
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Q7X243
ID 207X2
AC Q7X2
AC Q7X2
DT 01-C
DT 01-C
DT 01-C
DT 01-C
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01-OCT-2003
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                    Zogaj X., Bokranz W., Nimtz M., Romling U.; "Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
                                                                                                                                                                                                                                                                                        STRAIN=Fec4;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=546;
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"Production of Cellulose and Curli Fimbriae by Members of th
Enterobacteriaceae Isolated from the Human Gastrointestinal
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515700; CAD56672.1;
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Bacteria; Proteobacteria; Gammar
Enterobacteriaceae; Citrobacter.
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                                                                        108;
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71.5%;
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Pred. No. 6.5e
10; Mismatches
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Last annotation update)
                                                                 Score 530; DB 2;
Pred. No. 6.3e-36;
6; Mismatches 25
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Q7X237;
01-OCT-2003
STRAIN=Fec39;
Zogaj X., Bok
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                                          SEQUENCE FROM
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Enterobacteriaceae;
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01-OCT-2003
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                                                                                NCBI_TaxID=28141;
                                                                                                                                                      Enterobacter sakazakii.
                                                                                                                                                                                              Curlin-csgA
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Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna I
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
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01-MAR-2003
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    Bokranz
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Escherichia.
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01-MAY-2000
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EMBL; AJ515702; CAD56678.1; -.
SEQUENCE 150 AA; 15112 MW; 5D8BBZD872DF15F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COX J.M., Eglezos S., Woolcock J.B.;
"Virilence of Salmonella enteritidis in chickens correlates
colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TremBLrel.
01-DEC-2001 (TremBLrel.
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                                                    Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNGALVDQTASNSTVNVTQIGFGNHATAHQY 150
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L; Mismatches
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Matches 26
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DNA Res. 9:189-197(2002).
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MEDLINE=22484998; PubMed=12597275;
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MEDLINS=99314153; PubMed=10386375;

La Ragione R.M., Collighan R.J., Woodward M.J.;

"Non-curliation of Escherichia coli 078;K80 isolates associated "Non-curliation of Escherichia coli 078;K80 isolates associated ES1 inserti on in csg8 and reduced persistence in poultry infect FEMS Microbiol. Lett. 175;247-253(1999).

EMBL; AJ131756; CAB45380.1; -.
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Bacteria, Proteobacteria,
Bradyrhizobiaceae, Bradyrh
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01-JUN-2003
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Pred. No. 0.08
28; Mismatches
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Matches 41
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GO; GO:0004519; F:endonuclease activity; IE

GO; GO:0003676; F:nucleic acid binding; IEA

InterPro; IPR001604; Endonuclease

InterPro; IPR008619; Fil haemagg.

InterPro; IPR008619; Haemagg act.

Pfam; PF05894; Fil haemagg; ZO.

Pfam; PF05896; Haemagg act; 1.

PROSITE; PS01070; NUCLEASE NON SPEC; 1.
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum."
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01-MAR-2002 (TrEMBLrel. 20, Last sequen
01-CCT-2003 (TrEMBLrel. 25, Last annota
Probable hemaggiutinin-related protein.
                                                                                                                                                                                                                                                                    MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid megaplasmid
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"Genome sequence of the plant pathogen Ralstonia solan Nature 415:497-502(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable hemagglutinin-related protein.
RSC0887 OR RS06116.
Ralstonia solanacearum (Pseudomonas solanacearum).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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29.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Pseudomonas solanacearum)
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Pred. No. 5.
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                                                                                                                          , Demange N.,
Schiex T.,
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Schiex T.,
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Best Local :
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01-MAR-2003
01-MAR-2003
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                                                                                                                                                                                                                               MEDLINE-22297686; PubMed=12368813;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen JA., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Meyer T., Todson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Meboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., DeBoy R.T., Dodson R.J., Umayam L.A., White O., Wolf A.M., Vanathevan J., Weddman J., Imparaim M., Lee K., Berry K., Lee C., Wueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Meller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., "Genome sequence of the dissimilatory metal ion-reducing bacterium had a sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                  SEQUENCE
                                                                                                                                                                                           Nat. Biotechnol. 20:1118-11:
EMBL; AE015532; AAN53942.1;
                                                                                                                                                               Complete
                                                                                                                                                                                TIGR;
                                                                                                                                                                                                                            Shewanella
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MR-1
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shewanella oneidensis.
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Pfam; PF05860; Haemagg_act; 1.
PROSITE; PS01070; NUCLEASE_NON_SPEC;
Plasmid; Complete proteome.
SEQUENCE 3552 AA; 352934 MW; C54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR001604; Endonuclease.
InterPro; IPR008619; Fil haemagg.
InterPro; IPR008638; Haemagg_act.
Pfam; PP05594; Fil haemagg; 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 415:497-502(2002).
EMBL; AL646079; CAD17691.1; -.
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                               41
                                                                                                                                                                                S00866; -
 99
                                                           39
                                                                                       l Similarity
30; Conser
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                                                                                                                                                               proteome.
NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGN 144
                            SGRDNLIDLVQQGTANQGIVFQSGSDNS-AYVTQAGNDN----ISLVTQIGT
                                                        SGPDSTLSIYOYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGSHFSTAGPSWGDLGRNVGGGPNSSG----VGLAPYGSAHSADNAAGNSSRQNASVVIG
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larity 28.3%;
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                                                                                                                                                  AA,
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                                                                                                                                                 14811 MW; 41EC1CFA76957920 CRC64;
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                                                                                     Score 110; DB 16;
Pred. No. 0.13;
9; Mismatches 33;
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Last annotation updat
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Pred. No. 5.
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RESULT 13

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AC Q92UU
AC Q92UU
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DT 01-DE
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DE HYPOCL
GN RBD98
OS Rh1zc
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Nat. Biotechnol. 20:1118-1123 (2002).
                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical glycine-rich protein SMb21548.
R80989 OR SMB21548.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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01-DEC-2001
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01-OCT-2003
                              SEQUENCE FROM N.A
                                                                        NCBI_TaxID=382;
                                                                                                               Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000437; Prok_lipoprot_S.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22297686; PubMed=12368813;
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Alteromonadaceae; Shewanella.
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                                                                                                             Sinorhizobium/Ensifer
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Last annotation update)
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                 2174
                                                                                                          group; Sinorhizobium
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RESULT 14
Q8EIH4
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Matches 37
Query Match
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Q8EIH4;
01-MAR-2003
                                                                                                                     MEDLINE=22297686; PubMed=12368813;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Galdos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Seott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., DeBoy R.T., Deterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium of the control of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worhoexed.
Golding B., Puehler A.;
Golding B., Puehler A.;
"The complete sequence of the 1,683-kb pSymB megar
fixing endosymbiont Sinorhizobium meliloti.";
fixing endosymbiont Sinorhizobium meliloti.";
Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03797; Autotransporter; 1.
PROSITE; PS00435; PEROXIDASE 1; 2.
PROSITE; PS00583; PFKB_KINASES 1; 2.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 2174 AA; 203314 MW; 008EB66297B44182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; E95965; E95965.

GO; GO:0046821; C:extrachromosomal DNA; IEA.

GO; GO:0006601; F:peroxidase activity; IEA.

GO; GO:0006979; P:response to oxidative stre
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=70863;
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01-MAR-2003
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Vorhoelter F.J., Hernandez-Lucas I.,
                                                                                                            Shewanella oneidensis."
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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InterPro; IPR002173; PfkB.
Pfam; PF03797; Autotransporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., B
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                                                                                             Biotechnol.
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                                                                                Niotechnol. 20:1118-1123(2002)
AE015532; AAN53941.1; -.
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37; Conservative
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                                       nl protein; Complete proteome.
502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                                                                                                                                                                                                                                                                         oneidensis.
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13.7%;
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I., Becker A.,
106.5;
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              Length 502;
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Similarity

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Search completed: March 11, 2004, 18:40:47 Job time: 31.5 secs
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Q89JI3
ID Q89JI
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                                                                                                                                                                                                                                                                                       Query Match 12.8%; Score 99.5; DB 16; Best Local Similarity 24.7%; Pred. No. 1.2; Matches 39; Conservative 26; Mismatches 56;
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Q89JI3;
Q89JI3;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; APO05954; BAC50565.1; --
Complete proteome.
SEQUENCE 171 AA; 17448 MW; 995DB08C01498381 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-USDA 110;
STRAIN-USDA 110;
MEDLINE=22484998; PubMed=12597275;
MEDLINE=27484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bardyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
                                                                        131
                                                                                     120 GNNAALVNOTA-----SDSSVMVROVGFG-NNATANO 150
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                                                                                                                                                                                                                                               1 MKLĻKVĀAFĀAIVVSGSĀLĀGVVPQWGGGGNHNGGGNSSGPDSTLSIVQYGSĀNĀALALQ 60
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                                                                  GNNGSAITQNSFGPPALQNNSASVGQLSFGINTSTVSQ 168
                                                                                                                                                                                                                     MRKLFFASVAVLALSSAAQAA------
                                                                                                                                          NGLTNDSSSTTQIGILNGASTMQGTS-----SPSLNNVSTVNQAGVQNS-ATTGQVAF 130
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Database
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Listing first 45 summaries
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seq length: 0
seq length: 2000000000
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768
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1: geneseqp1980s:*
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100.0
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Aar74625 AgfA sequ
Aab36341 Salmonel1
Aaw23570 Salmonel1
Aaw23570 Salmonel1
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Aar52663
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RESULT 1
AAB36355
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26-FEB-2001 AAB36355;

(first entry)

AAB36355 standard;

protein; 151

B

Result No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
92.5	92.5	92.5	92.5	93.5	94	94.5	95	95.5	96	96	96	98	99.5	101.5	102	104.5	109	109	109
12.0	12.0	12.0	12.0	12.2	12.2	12.3	12.4	12.4	12.5	12.5	12.5	12.8	13.0	13.2	13.3	13.6	14.2	14.2	14.2
1721	1028	850	738	2204	354	908	718	908	19	19	19	26	151	520	26	151	23	23	23
Q	4	4	N	σ	7	4	w	4	w	ω	w	7	w	σ	7	w	w	w	W
ABU34624	ABB62708	ABB65764	AAW56163	ABU36440	AB023520	ABB62355	AAY78364	ABB65007	AAB36328	AAB36336	AAB36323	ABR82645	AAB36342	AA016497	ABR82649	AAB36344	AAB36319	AAB36324	AAB36340
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Abu34624	Abb62708	Abb65764	Aaw56163	Abu36440	Abo23520	Abb62355	Aay78364	Abb65007	Aab36328	Aab36336	Aab36323	Abr82645	Aab36342	Aao16497	Abr82649	Aab36344	Aab36319	Aab36324	Aab36340
Protein e	Drosophil	Drosophil	New DNA s	Protein e	Mycobacte	Drosophil	H. pylori	Drosophil	Salmonell	Salmonell	Salmonell	E. coli c	Salmonell	Argiope t	E. coli V	Escherich	Salmonell	Salmonell	Salmonell

# ALIGNMENTS

WPI; 2000-672631/65. N-PSDB; AAC64631. White AP, Doran JL, 05-APR-1999; WO200060102-A2 Synthetic. Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; 05-APR-2000; 2000WO-CA000356 12-OCT-2000 Escherichia coli. Salmonella enteritidis. vaccine; immune AgfA::PT3#10 amino acid sequence SEQ ID NO:30 (UYVI-) UNIV VICTORIA 99US-0127888P response; immunogen Collison SX, Kay WW;

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 139; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native

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RESULT 2
AAB36352
ID AAB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Best Local
Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                WPI; 2000-672631/65.
N-PSDB; AAC64628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                               05-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis.
                                                                                                                                                                                                                                         (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                              05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia colì.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                            2000WO-CA000356
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                                                                                                                                                                                                                                                                                            99US-0127888P
                                                                                                                                                                                         JĽ,
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                                                                                                                                                                                      Collison SK,
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Pred. No. 1.7e-66;
Pred. No. 1.7e-66;
                                                                                                                                                                                      Kay WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
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Disclosure; Page 138; 139pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directing recombination of a recombinant gene into the chromosome of the Chomologous species; (3) directing recombinant gene back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the CC ummunogenicity and adhesion properties relevant for an efficient live CC vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are easy and cc inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                26-APR-1994;
                                                                                                                                                       10-NOV-1994
                                                                                                                                                                                                                                  Salmonella
                                                                                                                                                                                                                                                                     Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
26-JUN-1995
                                                                         26-APR-1993;
                                                                                                                                                                                           WO9425598-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR74625 standard; protein; 151 AA
                (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J.
                                                                                                                                                                                                                                                                                                          AgfA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                            AAR74625;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEMAHA-----NOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,
                                                                         93US-00054452
                                                                                                                94WO-IB000207
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Pred. No. 6.8e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
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RESULT 4
AAB36341
ID AAB3
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Best Local Simi
Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune respons Salmonella in animals (e.g. food producing animals) and humans. (Upo on 25-MAR-2003 to correct PN field.)
                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                                                                                   WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36341 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-358275/44.
N-PSDB; AAQ87467.
                                                     Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                               05-APR-1999;
                                                                                                                                                                                                                                                                                    12-OCT-2000
                                                                                                                                                                                                                                                                                                              WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                              Salmonella;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MK1LKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIXQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collinson
                                                                                                                                                                          Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig
                                                                                                                                                                                                                                                                                                                                                                              agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.7%;
                                                                                                                                                                            Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                  immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
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Pred. No. 4.7e-58;
2; Mismatches 12;
                                                                                                                                                                            SK,
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                                                                                                                                                                          Kay WW;
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ns. (Updated
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, B. coli or acid sequence or sequences grown on a Salmonella, B. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation gystem the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sessesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response capainst the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the present incomplete the properties of the present sequence is given in the present incomplete the present sequence is given in the present incomplete the present sequence is given in the present sequence is given in the present incomplete the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the
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Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                    Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 151 AA;
Collinson SK,
                                                                                                                                             26-APR-1994;
                                                                                                                                                                                            03-JUN-1997
                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW23570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW23570 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the exemplification of the present invention
                                               (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                              26-APR-1993;
                                                                                                                                                                                                                                         US5635617-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATYDOLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNENGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                    enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enteritidis 27655-3b agfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
Kay WW,
                                                                                              93US-00054452
                                                                                                                                             94US-00233788
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                     /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.7%;
90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 681; DB 3;
Pred. No. 4.7e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 6
AAB36347
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Best Local Simi
Matches 136;
Recombinant agfA gene which encodes foreign
                                        WPI; 2000-672631/65.
N-PSDB; AAC64623.
                                                                              White AP,
                                                                                                                                   05-APR-1999;
                                                                                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                             05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                WO200060102-A2
                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                    Salmonella enteritidis
                                                                                                         (UYVI-) UNIV VICTORIA
                                                                                                                                                                                        12-OCT-2000
                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                               vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                            AAB36347;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36347 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated Salmonella gene agfa - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-309886/28.
N-PSDB; AAT74142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNPALVNOTASDSSVMVRQVGFGNNATANOV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Fig 7; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                             Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                 99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.0%;
                                                                              Collison
                                                                                                                                                                                                                                                                                              immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 676;
Pred. No. 1
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                                                                             Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
.4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
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having a segment replaced by a foreign DNA sequence epitope or antigen, expresses recombinant AgfA

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RESULT 7
AAB36351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live cracine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are easy and CC inexpensive to purify in large amount. The present sequence is given in two very
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
         05-APR-2000; 2000WO-CA000356
                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                    12-OCT-2000
                                                                                                                       Synthetic
                                                                                                                                         Escherichia coli
                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                     AgfA::PT3#6
                                                                                                                                                                                                                                                                                        26-FEB-2001
                                                                                                                                                                                                                                                                                                                              AAB36351;
                                                                                                                                                                                                                                                                                                                                                             AAB36351 standard; protein; 151
                                                                                    WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 81.9
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVTRVVTHEMAHA----
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                                                                                                                                                                                                                                                     amino
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                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ã,
                                                                                                                                                                                             response; immunogen
                                                                                                                                                                                                                                                 acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 659; DB 3;
Pred. No. 6.4e-56;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                 NO:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
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Also described are:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 8
AAB36354
ID AAB:
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AC AAB:
XX
DT 26-1
XX
DE Agfi
XX
KW Sall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directing recombination of a recombination of the chromosome of the chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrian protein possesses both the immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are usually strong the segment of the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                            AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
                                                                                                       26-FEB-2001
                                                                                                                                                                                     AAB36354 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-672631/65.
                                                                                                                                                                                                                                                                                                                                  119
                                                                                                                                                                                                                                                                                           106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CagA and AgfA-homologue fimbrin subunits, respectively;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136;
                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                               μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                    SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 AA;
                                                                                                                                                                                                                                                                                         WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.5%;
                                                                                                                                                                                                                                                                                                            -GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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Pred. No. le-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 30;
                                                                                                                                                                                                                                                                                                                                                                           YDQLVTRVVTHEMAHADQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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                                                                                                                                                                                                                                                                                                                                                                                                                    118
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                                                                                                                                                                                                                                                                                                                                                                                                                  cc copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for cellciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the cimunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and contains the inserted epitope, and hybrid fimbriae are easy and contains the inserted epitope, and hybrid fimbriae are easy and contains the inserted epitope, and hybrid fimbriae are easy and contains the inserted epitope, and hybrid fimbriae are easy and contains the inserted epitope, and hybrid fimbriae are easy and contains the inserted epitope, and hybrid fimbriae are easy and contains the inserted epitope, and hybrid fimbriae are easy and contains the inserted epitope, and hybrid fimbriae are easy and contains the inserted epitope, and hybrid fimbriae are easy and contains the present easy and contains the present sequence is given in the present sequence in the present invention.
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Best Local Sin
Matches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-672631/65.
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1999;
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  99
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                                                                                                                                           61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA--
                                                                                                                                                                                                                                                         \vdash
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doran JL,
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127888P
                                                                                                                                                                                                                                                                                                                               79.8%;
74.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collison SK,
                                                                                                                                                                                                                                                                                                            <u>,</u>
                                                                                                                                                                                                                                                                                                                                  Score 613; DB 3; Length 151; Pred. No. 1.9e-51;
                                                   GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                            Indels
                                                                                                        TRVVTHEMAHAFR
                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                            Gaps
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60 60

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                                                                                                      Matches
                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                           immunogens, which may be important for directing an immune responsive the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is
                                                                                                                                                                                                                                                                                                             system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 135; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella;
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                                                                                                                                                                                                                                   exemplification of the
                                                                                                   122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-672631/65.
                                                                                                                      Similarity
MKILKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSTYQYGSANAALALQ
                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                           151
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                                                                                              78.5%;
larity 80.8%;
Conservative
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                                                                                          Score 603; DB
Pred. No. 1.7e
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segment replaced by a foreign DNA sequence or antigen, expresses recombinant AgfA mmune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SK,
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                                                                                                                                                                                                                                 invention
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                                                                                       DB 3; L
1.7e-50;
hes 23;
                                                                                                                                       Length 151;
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                                                                                                                                                                                                                                                    is given in
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given

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CC back into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, cc comprising separating an amino acid polymer comprising a recombinant Agfa comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or contact the animal in conjunction with a carrier or diluent (1) is cuseful for the expression of recombinant Agfa protein which is useful for cuseful for the expression of recombinant Agfa protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 100,000 copies/cell), the hybrid fimbrin protein possesses both the cimmunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong cimmunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and internative to consider the inserted epitope.
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AAB36353
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(1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrian subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which encodes foreign epitope or antigen, protein useful for eliciting immune respon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA;
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AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant on f a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                   Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                           White AP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis.
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DB; AAC64625.
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81.5%;
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Pred. No. 3.4e-50;
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Best Local Sim
Matches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151
                                                                                                                                          WPI; 2000-672631/65.
                                                                                                                                                                      White AP,
                                                                                                                                                                                                                           05-APR-1999;
                                                                                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
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Pred. No. 4.2e-50;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described

are:

Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.

DNA sequence AgfĀ

N-PSDB; AAC64626.

Disclosure; Page 137; 139pp; English

N-PSDB; AAC64624.

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CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
CC directing recombination of a recombinant gene into the chromosome of the CC homologous species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC acid sequence host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (1) is CC useful for the expression of recombinant AgfA protein which is useful for cell-ting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC 100,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong which may he important for directing an immune response
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WPI; 2000-672631/65
                                                          White AP, Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; immune response; immunogen
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                                                                                                                           (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                             Collison
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Pred. No. 6.6e
5; Mismatches
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26-FEB-2001 AAB36343;

(first entry)

AAB36343 standard; protein; 151 AA

Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;

Escherichia coli CsgA amino acid sequence SEQ ID NO:7.

vaccine; immune response; immunogen

Escherichia coli.

12-OCT-2000

WO200060102-A2

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for a limburg an immune response in an animal. In a fimbrial presentation expression are presented in the bacteriation.
                                                                                                                                                                                                                                                                                                                                                                                                                                              system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogenis, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given inexpensive to purify in large amount.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                              Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                           exemplification of the present invention
121
                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                     122;
                                                                                           61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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NNAALVNOTASDSSVMVROVGFGNNATANOY
                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
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                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 6.7e-47;
                                                                                                                                                                                                                                                                                       Mismatches
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151
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                                                                                                                                                                                                                                                                                                                               Length 151;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising separating an amino acid polymer comprising a recombinant AgfA corotain containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbria protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and the carrier of the present invention of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) the homologous species; (3) directing recombinantion of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, and comprising a parameter of the homologous species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                    E. coli CsgA subunit 15 kDa protein.
                                                          04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                   ABR82651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-1999;
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                                                                                                                                                                                                                                                          121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105;
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                   standard; protein;
                                                                                                                                                                                                                                    GNGAAVDOTASNSSVNVTOVGFGNNATAHOY 151
                                                                                                                                                                                                                                                                                                            TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 517; DB 3;
Pred. No. 3.8e-42;
7; Mismatches 29;
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Best Local S
Matches 104
                                                                                                                                                                                                                                                               The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR02642, ABR026449. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli 15 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated peptide capable of binding a mammalian plasma pruseful in the manufacture of a medicament for the prevention treatment of a bacterial infection, such as Escherichia coli,
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               or Shigella infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2002; 2002GB-00002275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasma protein; immune response; antibacterial; vaccine; gene therapy
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121
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                        NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                            MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                      SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATYDOLVTRVVTHEMAHAGG
                                                                                                                    MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                          TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
                                                                                                                                                                            66.7%;
ilarity 68.9%;
Conservative 1:
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                                                                                                                                                                             17;
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Pred. No. 1.2e
17; Mismatches
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                              151
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.2e-41;
 151
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on and/or
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Search completed: March Job time : 45.9 secs 11, 2004, 18:33:46

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Result
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Maximum Match 10
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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Perfect score:
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Match Length DB
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768
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/cgn2 6/ptcdata/2/iaa/BCTUS COMB.pep:*
/cgn2 6/ptcdata/2/iaa/backfles1.pep:*
    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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US-09-196-387-8

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US-09-196-387-2

US-09-841-835-2

US-09-115A-8

US-09-336-115C-6

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US-09-252-991A-28148 US-09-403-089A-1	US-09-489-847-322	US-09-495-880A-42	US-09-177-650-91	US-08-968-685A-10	US-08-169-927-2	US-09-445-472-6	US-08-894-818B-8	US-08-750-532-9	US-09-336-447A-9	US-09-336-447A-7	US-09-543-681A-5434	US-08-804-227C-3	US-09-595-684B-39	US-09-252-991A-26658
Sequence Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
28148, 1, Appl	322, A	42, App	91, App	10, App.	2, Appli	6, Appl	8, Appl	9, Appl	9, Appl	7, Appli	5434, F	<ol> <li>Appli</li> </ol>	39, Appl	26658,

## ALIGNMENTS

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RESULT 1
US-08-233-788A-59
; Sequence 59, Application U
; Patent No. 5635617
; Patent INFORMATION:
                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 95,570.
REFERENCE/DOCKET NUMBER: 9200.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 622-6031
TELEEX: 3723836 SEEDAMBERRY
INFORMATION FOR SEQ ID NO: 59:
Query Match
Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                      STREET: 6300 Columbia Center, 701 Fifth Averone CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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                   Similarity
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6300 Columbia Center,
88.0%; ilarity 90.1%; Conservative
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                   Score 676; DB 1;
Pred. No. 2.7e-61;
  Mismatches
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    13;
                                    Length 151;
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RESULT 3
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US-08-233-788A-57
Sequence 3, Application Patent No. 6001592 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:

NAME: King, Joshua

REGISTRATION UNMBER: 35,570

REFERENCE/DOCKET NUMBER: 9200

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Doran,
APPLICANT: Kay, W
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                          GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
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Clouthier, Sharon C.
ENTION: METHODS AND COMPOSITIONS FOR DETECTION
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N: 435
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                             US/08864038A
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Pred. No. 4e-43;
2; Mismatches
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RESULT 4
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Best Local :
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JF 8-184459
FILING DATE: 15-Vuly-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: 2-5610
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 953-773
INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                              123
                                                                 509
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                                                                                                                                                              63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNN 122
                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                              3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
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                                                                                                                                                                                                                                                                                Similarity
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                                                               AAAAAAAAAASGGGGRALRRALRRQMRGGGSAAA 543
                                                                                              AALVNQTASDSS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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(212)953-7733
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VENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
VENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JAPAN
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                                                                                                                                                                                                                                                                              Score 92.5;
Pred. No. 0.
                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                              Length 738;
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                                                                                                                                                                                               460
                                                                                                                               508
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GENERAL INFORMATION:
APPLICANT: de Lange,
APPLICANT: Smith, Su
TITLE OF INVENTION:
TITLE OF INVENTION:

de Lange, Titia Smith, Susan

A PROTEIN THAT BINDS TO TRF1 AND METHODS OF USE THEREOF

Sequence 8, Application US/09196387 Patent No. 6277613

NUMBER OF SEQUENCES: 1

ADDRESSEE:

STREET: 411 Hack CITY: Hackensack

411 Hackensack Avenue,

4th Floor

Klauber & Jackson

New

Jersey

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                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09841835 Patent No. 6506587
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Best Local Similarity
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 673 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                            APPLICANT: de Lange, Titia
APPLICANT: SMith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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APPLICATION NUMBER:
                                                              COUNTRY:
ZIP: 076
                                                                                                                                         STREET:
                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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TELEFAX: 201-343-1684
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                                                                                                                       Hackensack
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                                                                                                   New Jersey
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                                                                                                                                           4th Floor
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US-09-196-387-10
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Best Local Similarity
                               CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 09/
APPLICATION NUMBER: 10, 1
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                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                             ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LENGTH: 673 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                  FILING DATE: June 10, 19 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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                                                                                                          APPLICATION NUMBER: FILING DATE:
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o. 6277613
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Jackson Esq., David A
                                                                                                                                                                                                                                                                                        New Jersey
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Smith, Susan
                                                                                                                                                                                                                   Floppy disk
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                                                        09/095,225
                                                                                                                             US/09/196,387
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                                                                                                                                                                Version
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                             REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS TITLE OF INVENTION: OF USE THEREOF NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 201-487-5800
LENGTH: 949 amino acids
                                                                                                                                 NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 TELEFAX:
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 949 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 Hackensack Avenue, 4th Floor
                                                                 201-343-1684
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Smith, Susan
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29.4%; Pred. No. 0.8;
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                                                                                                                                26,742
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US-09-196-387-2
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   Query Match
Best Local Similarity
Matches 42; Conserv
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GENERAL INFORMATION:
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Best Local
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/095,22:
APPLICATION NUMBER: 01, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                     TOPOLOGY: 1 MOLECULE TYPE:
                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 201-487-5800
                                                                                      HYPOTHETICAL:
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Klauber & Jackson
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTE
TITLE OF INVENTION: OF USE
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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6277613
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 Conservative
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linear
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11.9%; Score 91.5; DB 3; 29.4%; Pred. No. 1.3; ative 17; Mismatches 65;
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29.4%; Pred. No. 0.8;
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                               Length 1327;
 Indels 19; Gaps
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US-09-841-835-2
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US-09-841-835-2
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Patent No. 6506587
                                                                                                                                                                                                                                Query Match
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
COPPRATING SYSTEM: PC-DOS/MS-DOS
COPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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APPLICANT: Smith, Susan
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                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
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207
                               121 NNAALVNQTASDSSVMVRQVGFG 143
                                                                158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD-----VSRV--KRLVDAAN 206
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                                                                                               KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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VNAK--DMAGRKSSPLHFAAGFG 227
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411 Hackensack Avenue,
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Pred. No. 1.
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TYPE: PRT
                                              NAME/KEY: VARIANT LOCATION: 721
                                                                                                                                FEATURE:
                                                                                                                                                                               LENGTH: 745
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) OTHER INFORMATION: Xaa = Any Amino Acid US-09-336-115C-6
                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 6
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APPLICANT: Weltzin, Richard A.
APPLICANT: Guy, Bruno
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Patent No. 6576244
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                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/336,115C CURRENT FILING DATE: 1999-06-18 PRIOR APPLICATION NUMBER: US 09/100,258 PRIOR FILING DATE: 1998-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06132/055002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2000-04-10
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APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Piatyszek A.
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CURRENT FILING DATE: 2001-10-05
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                                                                                                                      NAME/KEY: SIGNAL LOCATION: (1)...(20)
                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSPTSS-SSSSPSSPGSSLAESPEAA
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            SOFTWARE: PatentIn
SEQ ID NO 5130
LENGTH: 1216
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                                                                                                                                                                                                                                         Sequence 5130, Application US/09134000C Patent No. 6617156
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LENGTH: 2736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                             CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local :
                                                                                                                                                              APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: ENTEROCOCCUS FARCALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                       FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                             56 ALALQSDARKSETTITQSGYGNGADV-GQGADNSTIELTQNG-----FRNNATYDQLVTR 109
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                                                                                                                                                                                                                                                                                                                                              VVT----DPAGNASPPAQVTAPDTT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSAGTALLVGAAAIGAGVAISNSSGGGG---GGGSSVPPDTTPPKAASGLKIAPDGSSIS 205
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
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Pred. No.
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Pred. No. 1
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US-09-134-000C-5130
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. MICCEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
                                                                                                                           Sequence 2676, Application US/09540236 Patent No. 6673910
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LENGTH: 589
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TITLE OF INVENTION: NOTITLE OF INVENTION: POTENCE: 2709.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 10.6%;
Local Similarity 24.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                         29 GGNHNGGGNSSGPDSTLSIYQYGS-----ANAALALQSDARKSETTITQSGYGNGA- 79
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                                                                                                                                                                                                                                                                                                                                                                        GGLDRNGANANGOTDTFGIYAFDTLTLTERIEINGGLRLDNYHTKYDSATACGGSGRGAI 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gary Breton et. al
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PNEUMONIAE FOR DIAGNOSTICS A
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Pred. No. 4.
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Pred. No. 8.2;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2676
; LENGTH: 867
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2676
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Search completed: March 11, 2004, 18:44:55 Job time: 13.4 secs
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                                                                              203 VAQ 205
                                                                                                                   148 ANQ 150
                                                                                                                                                          143 RGNQATGAGSFAAGVGNQATGAGSFAAGVGNQANADNAVAVGNKNSITGKDSVAIGSNNT 202
                                                                                                                                                                                98 R-NNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMV-----RQVGFGNNAT 147
                                                                                                                                                                                                                                                                           44 TLSIYQYGSANAALALQSDARKSETTITQSGY----GNGADVGQGADNST--IELTQNGF 97
                                                                                                                                                                                                                                                                                                                  93 TIA----GGRN-----NQATKENSTVGGGKFNQAKGRNSTVAGGYNNEATGIDSTIAGG 142
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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-6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
                                                                                                                                                 10 US-09-972-115A-8

14 US-10-199-937-4

14 US-10-199-937-4

14 US-10-311-406-2

15 US-09-793-306-146

15 US-08-834-66A-6
                                                                                                                                                                                                                                                                                                               15 US-10-369-493-20638

10 US-09-820-843A-21

US-09-841-835-8

US-09-841-835-2

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                                                                                       US-10-374-780A-590
US-10-021-811-26
                                                         US-10-238-075-749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                Sequence 20638, A
Sequence 21, Appl
Sequence 8, Appl
Sequence 10, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 146, Appl
Sequence 146, Appl
Sequence 6, Appli
Sequence 590, Appl
Sequence 26, Appl
Sequence 274, Appl
Sequence 749, Appl
Sequence 749, Appl
Sequence 24, Appl
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GENERAL INFORMATION:

Sequence 20638, Application US/10369493 Publication No. US20030233675A1

### ALIGNMENTS

```
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
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                                                                                                                                                         Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                  PEATURE: PEATURE: LOCATION: (1)...(445)
OTHER INFORMATION: unsure at all Xaa locations
51 GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNA-----TY 103
                                                                     19
                                                                                                                                                       44;
                                                            AFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS 77
                                                                                                               AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY 50
                                                                                                                                                            Conservative
                                                                                                                                                         13.4%; Score 103; DB 15; Length 445; 26.3%; Pred. No. 0.046; ive 27; Mismatches 62; Indels 3
                                                                                                                                                       27;
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                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09841835 Patent No. US20020076795A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 21, Application US/09820843A Publication No. US200300390292277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Council of Scientific and Industrial Research TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES FILE REFERENCE: Q63915
                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
OTHER INFORMATION: PPE
NAME/KEY: misc feature
OTHER INFORMATION: gi | 1781260
                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 354
TYPE: PRT
ORGANISM: M. tuberculosis
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                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                              CITY: Hackensack
                                                                                                                                                                                                             STREET:
                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 WNGGSTNTGLANAGAGNTGFFDAGNYNFGSLNAGNINSSFGNSGDGNSGFLNAGDVNSGV 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 GNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG------GNNAALVNQT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 WGGGGNHNGGGNSSGPDS---TLSIYQYGSANAALALQSDARKSETTI-----TQSGY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
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                                                                                                                                                                                                          411 Hackensack Avenue, 4th Floor
                                                                                                                                                            USA
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25.0%; Pred. No.
           US/09/841,835
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                                             Version #1.30
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US-09-841-835-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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APPLICANT: de Lan
APPLICANT: Smith,
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INFORMATION FOR SEQ ID NO:
           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                  ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRE1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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LENGTH: 673 amino acids
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 TELEPHONE:
                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
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                                                                                                                                                                                                                                                                                                                     07601
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201-487-5800
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ER: 600-1-230 CIP1
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Pred. No. 1.
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                                   CIP1
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                                                                                                                                               APPLIANCE ARTE:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TOTAL PHONE: 201-487-5800
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Best Local S
Matches 42
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Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO
TITLE OF INVENTION: OF USE THEREOF
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   NFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               TOPOLOGY: 1:
                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 HYPOTHETICAL:
                                                                                                                                     TELEFAX: 133521
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les 42; Conservative
                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                   ss: single
linear
protein
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GENERAL INFORMATION:

APPLICANT: Christenson, Erik
APPLICANT: Christenson, Erik
APPLICANT: Genaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
APPLICANT: McElligott, David L.
APPLICAT: McElligott, David L.
TITLE OF INVENTION: TANKYRASEZ MATERIALS AND
FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
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US-10-199-937-4
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                       Sequence 4, Application US/10199937 Publication No. US20030190739A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Piaty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 64
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                    VNAK--DMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSETTIT----OSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNAK--DMAGRKSSPLHFAAGFG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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llarity 29.4%;
Conservative 17
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Pred. No. 2.6;
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Pred. No. 2.6;
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                                                                                        AND METHODS
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                                                                                      RESULT 9
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US-10-311-406-2
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US-10-311-406-2
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Sequence 146, Application US/09793306 Patent No. US20020098200A1 GENERAL INFORMATION:
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Best Local Similarity
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SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sasaki, Masahiro
APPLICANT: Yamada, Hideyuki
APPLICANT: Osada, Katsue
APPLICANT: Osada, Katsue
APPLICANT: Terada, Satoshi
TITLE OF INVENTION: MEDIUM SUPPLEMENT AND ANIMAL CELL CULTURE MEDIUM
FILE REFERENCE: U 014351-5
CURRENT APPLICATION NUMBER: US/10/311,406
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: PCT/JP02/03836
PRIOR FILING DATE: 2002-04-17
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PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                            101 ATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                715 AGSSTSGGTSTYGYSSRHRGGSVSSTGSSSNTDSSTKNAGSRTSGGTSTYGYSSSHRGGS
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                                                                                                                                                                                                                                                        59 LQSDARKSET------TIT---QSGYGNGADVGQGADNSTIELTQN-GFRNN 100
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Similarity 29.4%;
                                                                                                                                      GG----TSTYGYSSSHRGGSVSSTGSSSNTDSS--TKNAGSSTSGGSSTY 878
                                                                                                                                                                                                                  VSSTGSSSNTDSSTKNAGSRTSGGTSTYGYSSSHRGGSVSSTGSSSNTDSSTKNAGSRTS
                                                                                                                                                                                                                                                                                                                                      SGSALAGVVPQWGGGGNHNGG-----GNSSGPDST-----LSIYQYGSANAALA 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAAFAAI-VYSGSALAGVVPQWGGGGNHNGGGNSGGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                              11.5%; Score 88.5; DB 14; ilarity 22.2%; Pred. No. 4.6; Conservative 29; Mismatches 63;
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Pred. No. 2.6;
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US-08-834-666A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08834666A Publication No. US20020044949A1 GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: of Tuberculosis
FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR PRIOR PRIOR OF SEQ ID NOS: 164
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                       COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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APPLICANT:
APPLICANT:
                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,666A
FILING DATE: 01-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Campos-Neto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 597
TYPE: PRT
ORGANIAM: Artificial Sequence
FEATURE:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: 76 kDa Helicobacter Polypeptides and TITLE OF INVENTION: Corresponding Polynucleotide Molecules
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Miller, Charles
APPLICANT: Al-Garawi, Amal
                                        CLASSIFICATION: 424
                                                                                                                                                                                                                                                                CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 DNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNN 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kleanthous, Harold
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                                                                                                                                                                                  Diskette
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                                                                   TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REPERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR PRIOR APPLICATION NUMBER: 60/310,847
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR APPLICATION NUMBER: 09/936,049
                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sherman, Bradley K
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 745 amino acids
TYPE: amino acid
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TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,175
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POPOLOGY:
                                   FILING DATE: 2001-11-19
APPLICATION NUMBER: 60/338,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 INGGVYQFCKAKNGSSSSSNGGNGSSTQTTATTTQDGVTITTTYNNNKAT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 AYQAVFLAINAAVGL---WNTIGYAVMCGNGNGTESGPGSVIFNDQPGQDSTQITCNRFE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             590, Application US/10374780A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 RNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STGPGKSMSIDEFKKLNEAYQIIQQALKNQSGFPELG-GNGTKV---SVNYNYECRQTAD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riechmann, Jose Luis
Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
                                                                                                                                                                                                                                                                                       Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                    Pilgrim, Marsha L
Dubell III, Arnold T
Pineda, Omaira
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Keddie, James
                                                                                                                                                                                                                                                                                                                                                                Broun,
                                                                                                                                                                                                                                                                                                                                                                                                                     Adam, Luc J
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NUMBER: 10/171,468
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                     2001-12-11
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20.0%; Pred. No. 4;
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US-10-021-811-26
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RESULT 13
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US-10-021-811-26
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SEQ ID NO 590
LENGTH: 321
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LENGTH: 323
                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Fang, Yiwen
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BBL194 US NA
CURRENT APPLICATION NUMBER: US/10/021,811
CURRENT FILING DATE: 2001-12-14
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
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PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                    Local
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                                                                                                                           199 AAYASSADNIARLLQGWMRPGGG---
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                                                                                       67 ETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                               10 AAIVVSGSALAGVVPQW----GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKS
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                                                                                                                                                                                                                  11.1%;
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                                                     - GEGAASASASASQSGAAAAATAQTPECSTETSKMATGGG
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                                                                                                                                                                                                                  Score 85;
Pred. No.
                                                                                                                                                                                                   Mismatches
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; Sequence 749, Application publication No. US20030141 ; GENERAL INFORMATION: APPLICANT: I.N.S.E.R.M.; TITLE OF INVENTION: Polyr; TITLE OF INVENTION: E.cc.

Polynucleotides which are of nature B2/D+ A-E.coli, and biological uses of these polynuc

polynucleotides

and which are

US-10-238-075-749

Application US/10238075

US20030148324A1

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US-09-905-176-24
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                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 24
LENGTH: 322
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APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/905,176
CURRENT FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHOD FOR DETERMINING THREE-DIMENSIONAL PROTEIN STRUCTURE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
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CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
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TYPE: PRT
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                              186 ANSKRIDDONOLLIGEGDHAETYTGGLKYDANNIYLATOYTOTYNATRAGSLGFANKAON 245
                                                                            105
                                                                                                        126 SDFFGLVGLNFALQYQGKNGSVSGEGATNNGRGALKQNGDGFGTSVTYDIFDGISAGFAY 185
147 -- TANQY 151
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                                                                                                                                                      72 QSGYG-----
                                                                                                                                                                                                                        12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT
                                                                                                                                                                                          88 VVYDVTSWTDVLPEFGGD----
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                                                                                                                                                                                                                                                                      Conservative
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                                                                      OLVTRVVTHEMAHAGG-----NNAALVNQ-TASDSSVMVRQVGFGNNA-- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALQSDARKSETTITQSGYGNG----ADVGQGADNSTIELTQNGFRNNATY 103
                                                                                                                                                                                                                                                                                  11.0%; Score 84.5; DI 23.0%; Pred. No. 2.2;
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                                                                                                                                                  ----NGADVGQGADNS---TIELTQNGFRNNATYD------
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PRIOR APPLICATION NUMBER: 60/250,073
PRIOR FILLING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/253,878
PRIOR APPLICATION NUMBER: 60/253,878
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,338
PRIOR FILING DATE: 2000-11-30
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LENGTH: 65
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Best Local S
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16,
                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/996,194
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/250,348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 35800/240590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bandaru, Rajasehkar
TITLE OF INVENTION: 84242, 8035, 55304, 52999, and 21999,
TITLE OF INVENTION: No. US20020151696Alel Human Proteins
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
34 RNH--YDOLVTRVVTHEIAHALGFSVGL 59
                                     98 RNNATYDOLVTRVVTHEMAHAGGNNAAL 125
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                                                                               l Similarity
19; Conserv
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                                                                             Conservative
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                                                                           Score 84; DB
Pred. No. 0.33
3; Mismatches
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                                                                                                                Length 65;
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Search completed: March 11, Job time: 25.6 secs 2004, 19:18:41

1,

Title: Perfect score: Sequence: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Scoring table: Run on: OM protein - protein search, using sw model Database : Searched: PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-543-407-30
768
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 March 11, 2004, 18:24:14; Search time 10.3 Seconds (without alignments) 1410.186 Million cell updates/sec 283366 seqs, 96191526 residues GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 283366

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	s	4	ω	2	۳ ا	No.	Regult	
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Q	р <b>Q</b>	ου ος .	Query Match Best Local Similarity Matches 137; Conser	C;Function: A;Description: major component of thin A;Note: fimbriae bind to fibronectin, I C;Keywords: fimbria F;1-20/Domain: signal sequence #status F;21-151/Product: fimbrin procein agfA	A; Accession: A4898 A; Status: preliminary A; Molecule type: protei A; Residues: 21-33 < CO3> A; Note: sequence extrac C; Genetics: A: Gare: agfA	R;Collinson, S.K.; Emody, L.; Muller, K.H.; J. Bacteriol. 173, 4773-4781, 1991 A;Title: Purification and characterization ( A;Reference number: A44898; MUID:91310586; I A;Contents: 27655	A; Accession: PC6015 A; Molecule type: protein A; Residues: 21-52 <co2> A; Experimental source: strain 27655-3b A; Note: the authors translated the cod</co2>	A; Receive number: A; Accession: UC6039 A; Molecule type: DNA A; Residues: 1-151 <c a;="" cross-references:<="" td=""><td>RESULT 1  JC6039  fimbrin protein agfA precursor - Sa fimbrin protein agfA precursor - Sa fimbrin protein agfA precursor - Sa fimbrin protein agfA precursor - Sa C;Species: Salmonella enteritidis C;Accession: JC6039; PC6015; A44998 C;Accession: JC6039; PC6015; A44998 C;Accession: JC6039; PC6015; A44998 C;Accession: JC6039; PC6016; SC; J. Bacteriol. 178; 662-667; 1996 A;Title: Salmonella enteritidis agf</td><td>ייסי</td></c>	RESULT 1  JC6039  fimbrin protein agfA precursor - Sa fimbrin protein agfA precursor - Sa fimbrin protein agfA precursor - Sa fimbrin protein agfA precursor - Sa C;Species: Salmonella enteritidis C;Accession: JC6039; PC6015; A44998 C;Accession: JC6039; PC6015; A44998 C;Accession: JC6039; PC6015; A44998 C;Accession: JC6039; PC6016; SC; J. Bacteriol. 178; 662-667; 1996 A;Title: Salmonella enteritidis agf	ייסי
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MVRQV	GAGAD	GSALA        SSALA		t of onect	om NC	Mull 1991 racte UID:9	2765 d the	, NID	revi Fevi S.C. 996	и и О т
NNAALVNQTASDSSVMVRQVGFGNNATANQY 151	SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 	MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 	Score 681; DB 2; Le Pred. No. 3.3e-49; 2; Mismatches 12;	Function: Description: major component of thin aggregative fimbriae Description: major component of thin aggregative fimbriae Note: fimbriae bind to fibronectin, plasminogen, tissue plasmin Keywords: fimbria 1-20/Domain: signal sequence #status predicted <sig> 21-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>	inary iprotein 3 <co3> extracted from NCBI backbone (NCBIP:45936)</co3>	R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W. J. Bacteriol. 173, 4773-4781, 1991 A;Title: Purification and characterization of thin, aggregative fimbriae A;Reference number: A44898; MUID:91310586; PMID:1677357 A;Contents: 27655	A;Accession: PC6015 A;Molecule type: protein A;Residues: 21-52 <co2> A;Experimental source: strain 27655-3b A;Experimental source: strain 27655-3b</co2>	A;Reterence number: OC0039 A;Accession: UC6039 A;Accession: UC6039 A;Molecule type: DNA A;Residues: 1-151 <col/> A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1;	RESULT 1  JC6039  JC60	C42049  ALIGNMENTS
	TYDQLVTRVVTHEMAHAGG 120 	DSTLSIYQYGSANAALALQ 60                    DSTLSIYQYGSANAALALQ 60	Length 151; Indels 0; Gaps 0;	C;Function: A;Description: major component of thin aggregative fimbriae A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C;Keywords: fimbria C;Keywords: fimbria F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>	936)	; Kay, W.W. regative fimbriae from Salmonella	e 44 as Ile	599.1; PID:91184714	t_change 08-Oct-1999 , P.A.; Kay, W.W. thin, aggregative fimbriae.	leishmanolysin (EC

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Cirtum Procession Solvession 20-Feb-1998 #text_change C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change C;Date: 12-Feb-1998; G64846; S31202; S34560; S34559
C;Accession: S70788; G64846; S31202; S34560; S34559
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
Mol. Microbiol. 18, 661-670, 1995
Mol. Microbiol. 19, 661-670 operons is required for production of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process o
                                                                                                                                                                                                                                                                                                                       A;Experimental source: strain K12, substrain W3110

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64846
                                       A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S.
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Ayîtle: Complete genome sequence of a multiple drug resistant
A;Title: Complete genome sequence of a party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party of the party o
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A;Residues: 1-151 <BLAT>
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A;Molecule type: DNA
A;Residues: 1-151 <PAR>
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
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Matches 137
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Decies has also been called Salmonella typhi
-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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in, A.;
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Pred. No. 3.3e-49;
2; Mismatches 12
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Best Local
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ECs1420

104;

Conservative

18;

Score 502.5; DB 2 Pred. No. 1.6e-34; 8; Mismatches 29

Indels Length

1;

Gaps

DB 2;

152;

Similarity

68.4%;

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MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL

QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG MKILKVAAIAAIVFSGSALAGVVPQYGGGGGHHGGGGNNSGPNSELNIYQYGGGNSALAL

119 60 59

60

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curlin major subunit CsgA [imported] -
c;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision
C;Accession: D90806
C;Accession: T; Makino, K.; Ohnishi, M.;
gasawara, N.; Vasunaga, T.; Kuhara, S.;
DNA Res. 8, 11-22, 2001
                                                                                                         A; Title: Complete genome sequence of enterohemorrhagic Escherichia A; Reference number: A99629; MUID:21156231; PMID:11258796 A; Accession: D90806
                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;ACCEBSIONA
A;ROSECTIONA
A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424;
A;Cross-references: strain K-12, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: major component of wild-type curli; interaction between CsgA and A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia cc and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-20/Domain: signal sequence #status predicted <SIG>
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A; Accession: S34559
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A; Residues: 21-4:
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;Function:
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                                                                                                                                                                                Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii
Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
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Pred. No. 1e-35;
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N;Alternate names: csgB p
C;Species: Escherichia co
C;Species: Escherichia co
C;Datc: 12-Feb-1998 #sept
C;Accession: S70787; F648
R;Hammar, M.; Arnqvist, A
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A.Recession: $70787
A.Recession: $70787
A.Recession: $70787
                                                                                A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62281.1; PID:g1147563 A;Experimental source: strain K12, substrain W3110 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Augum R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: F64846
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85665
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <STO>
A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GNOO: A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            curlin nucleator protein cagB precursor - Escherichia coli (strain K-12) N;Alternate names: cagB protein; curlin nucleation component; minor curl C;Species: Escherichia coli
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                       A; Molecule type: DNA
A; Residues: 1-151 <BI
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A; Residues: 1-151 <H
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Matches 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change: Accession: S70787; F64846
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                                                                                                                                                                                                                                                                                         1-151 <HAM>
                       1-151 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QADARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKDSHMTVKQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKILKVAAFAAIVVSGSALAGVVPOW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNNAALVNOTASDSSVMVROVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                acid sequence
  GB: AE000205;
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                                                                     not
  GB:U00096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 502.5; DB 2;
Pred. No. 1.6e-34;
B; Mismatches 29;
                                                                     shown;
                                                                     translation not
  NID:g1787265;
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  PIDN: AAC74125
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V.; Riley,
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PID:g1787278
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K.; Aj
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curlin minor chain precursor, CsgA homolog [importe C,Species: Bscherichia coli C,Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 C,Accession: G85665 R,Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, IIIer, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Di Nature 409, 529-533, 2001

A,Title: Genome sequence of enterohemorrhagic Esche A,Title: Genome sequence of enterohemorrhagic Esche

[imported]

Escherichia coli (strain

0157:H

A; Molecule type: DNA
A; Residues: 1-151 < S'
A; Cross-references: '

1-151 <STO>

GB:AE005174;

NID:g12514573;

PIDN: AAG55787

Ë

GSPDB:GN00145;

UWGP: 216

A;Accession: G85665 A;Status: prelimina

preliminary

A, Reference number:

A85480;

of enterohemorrhagic Escherichia 90; MUID:21074935; PMID:11206551

; Mau, ь., A.; Dimalanta,

B.; Glasner, imalanta, E.;

J.D.; Rose, Potamousis,

D.J.; Mayhew K.; Apodaca,

coli

0157:H7

#text\_change 14-Sep-200:

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A; Gene: csgB
A; Map position:
C; Function:
G85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               minor curlin subunit precursor CsgB [imported] - Esc;Species: Escherichia coli
C;Species: Bodul-2001 #sequence_revision 18-Jul-2001
C;Accession: C90806
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: minor component of wild-type curli; interaction between CsgA and CsgB tria, Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <SIG>F;22-151/Product: minor curlin chain #status predicted <MAT>
                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: C90806
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A; Residues: 1-151 <HAY>
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DNA Res. 8, 11-22, 2001
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                                                                                                                                                                                                                                                                                                        A;Gene:
                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                          Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
Experimental source: strain O157:H7, substrain RIMD 0509952
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Best Local Similarity
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                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS 76
                                                                          SNRAKIDQ----TGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                RNNATYDOLVTRVVTHEMAH---AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                     AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                                                                                                      SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
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T.; Kuhara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain
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                                                                                                                                                                                                                                               13.6%;
29.1%;
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                                                                                                                                                                                                                                               Score 104.5;
Pred. No. 0.0
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                                                                                                                                                                                                                                Mismatches
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Shiba, T.; Hat
                                                                                                                                                                                                                                                 .087;
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                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishii,
                                                                                                                                                                                                                                Indels
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C;Keywords: zinc finger
F;1164-1450/Region: zinc finger CCHC motif
F;1451-1464/Region: zinc finger CCHC motif
F;1478-1491/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1530-1543/Region: zinc finger CCHC motif
F;1530-1543/Region: zinc finger CCHC motif
F;1579-1592/Region: zinc finger CCHC motif
F;1579-1592/Region: zinc finger CCHC motif
F;1602-1615/Region: zinc finger CCHC motif
F;1602-1615/Region: zinc finger CCHC motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A;Reference number: S03650; MUID:88189811; PMID:3357771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-1748 <TAY>
A;Residues: 1-1748 <TAY>
A;Cross-references: EMBL:L03710; NID:g161751; PID:g161752
A;Cross-references: EMBL:L03710; NID:g161751; PID:g161752
R;Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and glycine-rich repeats
A;Reference number: $42135; MUID:94051569; EMID:8233798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Taylor, F.M.; Martindale, J.m.
submitted to the EMBL Data Library, October 1992
A:Reference number: S42136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Genetic code: SGC5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: cnjB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773
A;Cross-references: EMBL:X06462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-
A;Cross-references: EMBL::037.0
R;Martindale, D.W.; Taylor, F.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cnjB protein - Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Date: 19-Mar-1997 #sequence revision 18-Jul-1997
C;Accession: S42136; S42135; S03650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: S03650
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                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                        ;1626-1748/Region: glycine-rich
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Best Local
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                                                                                                                                                                                                             Similarity
                                                                                                                                       QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                           GQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNRAKIDO----TGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
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                                                                                                                                                                                                           13.2%;
29.7%;
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                                                                                                                                                                                                      Score 101;
Pred. No. 2.
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                                                                                                                                                                                     Mismatches
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                       ----QNENTGGGGWGSSNSNQTNNESS-----
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                                                                                                                                                                                                                                DB
                                                                                                       ----CQSNVQES-TTTSSGGWGS----
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                                                                                                                                                                                     32;
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A; Molecule type: DNA
A; Residues: 1-151 < P
                                                                                                                                                                                                                                                                                                                                                              A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A;Title: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleation component of curlin monomers [imported] - Salmonella (;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AH0635
                                                                                                                                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Parkhill, J.; Dougan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413, 848-852, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: fimbria
F;1-21/Domain: signal sequence #status
F;22-151/Product: fimbrin protein agfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: minor component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Salmonella enteritidis agfBAC operon encoding A;Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fimbrin protein agfB precursor - Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #tex
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A;Cross-references: GB:U43280; NID:g1184712;
A;Experimental source: strain 276755-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: JC6040
R;Collinson, S.K.; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h, T.; Connerton, P.; Crc
S.; Moule, S.; O'Gaora,
                                                                                                                                          Matches
                                                                                                                                                                                     Query Match
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Bacteriol. 178, 662-667, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST----IELTQ
                                                                                                                                                                Similarity
NGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                               -151 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                          GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ 73
                                                                                         GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST----IELTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGGNNRAKVDQAGNYNFAY-IEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
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                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Igan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
                                                                                                                                                                                                                                                                     GB:AL513382; PIDN:CAD08267:1; PID:g16502314; GSPDB:GN00176
                                                                                                                                                           13.0%;
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28.2%; Pred. No. 0.
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                                                                                                                                        16;
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                                                                                                                                                      Score 99.5; DB Pred. No. 0.22;
                                                                                                                                   Mismatches
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#status predicted <MAT>
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                                                                                                                                                                              Length
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Salmonella enterica s
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C;Accession: AD3143
C;Accession: AD3143
C;Accession: AD3143
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; R;Wood, D.W.; Setubal, C.; Guenthner, D.; F erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; F ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GS
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Amp
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.
A;Title: The composite genome of the legume symbiont Sinorhizobium
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
AD3143
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                   202
                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein Atu4768 [imported] C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2003
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A;Title: The Complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Finan,
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Best Local S
Matches 32
                                                          ;Molecule type: DNA;Residues: 1-145 KUR>;Residues: 1-145 KUR>;Cross-references: GB:AE008689; PIDN:AAL45562.1; PID:g17743277; GSPDB:GN00187;Experimental source: strain C58 (Dupont)
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Residues: 1-2174 <KUR>
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/Species: Sinorhizobium meliloti
/bate: 24-Aug-2001 #sequence_revision
                                       Genetics:
                                                                                                                                           Status: preliminary
                                                                                                                                                                 Accession: AD3143
                                                                                                                                                                                  Reference number:
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                   Atu4768
                                                                                                                                                                                  The Genome of the Natural Genetic number: AB2577; MUID:21608550;
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linear chromosome
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Pred. No. 4.
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                                                                                                                                                                                                                                                P.; Jung, M.; Krespan,
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                                                                                                                                                                                     Engineer Agrobacterium PMID:11743193
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Kutyavin,
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T.; Levy, R.; Li, M.;
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hypothetical protein AGR_L_228 [imported] -
C;Species: Agrobacterium tumefaciens
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Science 294, 2323-2328, 2001
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Q-VGRGCSANVSQGGNDNVA 138
                               QLVTRVVTHEMAHAGGNNAA
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Pred.
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RESULT

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, A;Title: Deciphering the biology of Mycobacterium tuberculosis from the cc A;Reference number: A70500; MUID:98295987; PMID:9634230 probable PPE protein - Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 C;Accession: F70825 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; A; Reference number: A70500; A; Accession: F70825 A; Status: preliminary; nucl A; Molecule type: DNA A; Residues: 1-645 <C F70825 <C0L> AL021958; nucleic acid sequence not shown; translation not shown GB:AL123456; NID:g3261536; PIDN:CAA17522.1; PID:e125329 T.; Churcher, C.; Harris, D T.; Gentles, S.; Hamlin, N.; , K.; Skelton, S.; Squares, (strain H37RV) #text\_change 15-Sep-2003 the complete B.G . . Holroyd, genome

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A;Experimental source: strain H37RV
C;Genetics:
A;Genetics:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 11, 2004, 18:14:48; Search time 6.3 Seconds (without alignments) 1248.031 Million cell updates/sec

Title: Perfect score: Sequence: US-09-543-407-30 768 1 MKLLKVAAPAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151

Scoring table: Searched: BLOSUM62 Gapop 10.0 , Gapext 0.5 141681 seqs, 52070155 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

141681

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| 3 3 C                    | 30         | 29         | 2 2                | 20           | 25         | 24         | 23           | 22           | 21         | 20         | 19         | 18         | 17         | 16         | 15         | 14         | 13         | 12        | 11         | 10         | 9          | 80         | 7                 | თ                 | <sub>5</sub> | 4                  | ω                  | N          | <b>_</b>          | Result<br>No.  |
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| 165<br>1845              | 347        | 172        | 7 4<br>7 0 1       | 1148         | 576        | 363        | 1469         | 1196         | 760        | 678        | 1655       | 850        | 602        | 599        | 1567       | 646        | 590        | 262       | 1778       | 959        | 1656       | 1327       | 1028              | 151               | 151          | 151                | 152                | 151        | 151               | Length I       |
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| GRP1 ORYSA<br>Z236 HUMAN | MSA2 PLAF2 | CH18 DROME | CEA CITER          | ICEK_PSESX   | DEAF_DROME | OMPC_KLEPN | BCL9 DROME   | ICEV PSESX   | YBIL ECOLI | YF48 MYCTU | OMPB_RICCN | PRSN PIERA | GP63_LEIMA | GP63_LEICH | ICEN_XANCT | GP63_LEIME | GP63_LEIDO | VG38_BPT2 | N189_SCHPO | N100_YEAST | OMPB_RICJA | TNKI HUMAN | OVO DROME         | CSGB_SALTY        | CSGB_SALTI   | CSGB_ECOLI         | CSGA_ECO57         | CSGA_ECOLI | CSGA_SALTY        | ID             |
| 4 oryza                  | лφ         | drosophila | P34291 caenornabd1 | 1 pseudomona |            |            | 9 drosophila | 9 pseudomona | escherichi | ₹          | r outer    | 4          | œ          | σ          | 7          |            |            | -         |            | 9 8        |            | _          | P51521 drosophila | P55226 salmonella | w            | P39828 escherichia | Q93u24 escherichia | 7<br>e     | P55225 salmonella | cription       |

| 45         | 44                 | 43         | 42        | 41                 | 40         | 39         | 38         | 37         | 36         | 35         | 34         |
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| 79.5       | 79.5               | 80         | 80        | 80                 | 80         | 80         | 80.5       | 80.5       | 80.5       | 80.5       | 80.5       |
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| 663        | 163                | 5560       | 1571      | 850                | 491        | 380        | 1258       | 1210       | 880        | 874        | 534        |
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| DUS8_MOUSE | HCY_NATPH          | SPEN DROME | C3G_DROME | PRSN PIEBR         | YK98 MYCTU | PLYA_COLGL | ICEN ERWHE | ICEN_PSEFL | GUN4_THEFU | ALE6_AZOVI | GCR2_YEAST |
|            | P39442 natronomona |            |           | Q9gv36 pieris bras |            |            |            |            |            |            |            |

# ALIGNMENTS

| RA           | R.               | 2 X                                | מ<br>מ<br>מ | RN | RL | RT                             | RT | R.A                         | R.A                                                             | R.A                                                              | R.A                                                  | ₽.           | Ŗ,                                                              | R.A                                                                  | R.A                                                      | RX. | RC :      | ָ<br>ק | R F                       | 1 2     | RAT | R.A | RA | R.A | R.A. | R.A | 쭚                                  | RC | R.P | 2 2 | 2 Z                                                                                            | 0 X                                                                 | 2 2                                                         | 2 5                               | RC | RP | RN | õ | 8                               | റ്റ | 20         | က္က | တ္တ | 2 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |           | 37                              | ΤC                  | AC      | ij                                | ES E     |
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| V., Kodoyian | II, Mayhew G.F., | MEDITIE=22511467 - 01hMcd=1264504: | -           |    |    | enterica serovar Typhi CT18."; |    | Whitehead S., Barrell B.G.; | Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., | Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C | Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd | Cronin A., D | Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., | Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., | Parkhill J., Dougan G., James K.D., Thomson N.R., Pickaı |     | SPECIES=S |        | Nacure 413:002-836(2001). | LIZ. ", |     |     |    |     |      |     | MEDLINE=21534948; PubMed=11677609; |    |     | [2] | T Barteria Cott with respect to operon enturine and regularity. T Barterial 180-729-731 (1998) | " Curit tipers are nightly conserved between sammonetia cyphimurium | Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.; | MEDILNE=98117058; PubMed=9457880; |    |    |    |   | Enterobacteriaceae; Salmonella. |     | Salmonella |     |     | MAJOE CULTIE DESCRIPTION OF STATIST OF ELLIPSE OF SERVICE OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION | (Ret. 42, | (Rel. 34, Last sequence update) | 1996 (Rel. 34, Crea | P55225; | CSGA SALTY STANDARD; PRT: 151 AA. | RESULT 1 |

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  StyGene;
Fimbria;
   EMBL; AJ002301; CAA05317.1; --
EMBL; AE008749; AAL20074.1; --
EMBL; AL627269; CAD08268.1; --
EMBL; AE016840; AA069399.1; --
   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
   SEQUENCE OF 21-33.

SPECIES-S.enteritidis; STRAIN=27655-3B;

MEDLINE=91310586; PubMed=1677357;

Collinson S.K., Emoedy L., Mueller K.-M., T;

Collinson S.K., Emoedy L., Mueller K.-M., T;
   SEQUENCE
  CONFLICT
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  This
  J. Bacteriol. 173:4773-4781(1991).
-i- FUNCTION: COTLIN IS THE STRUCTURAL SUBUNIT OF
-COILED SURFACE STRUCTURES THAT ASSEMBLE PREFER
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI
  Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D. Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W., "DNA-based diagnostic tests for Salmonella species targeting the structural gene for thin, aggregative fimbriae.", Clin. Microbiol. 31:2263-2273(1993).
   SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=94013373; PubMed=8104955; Doran J.L., Collinson S.K., Burian J.,
   MEDLINE=96146512; PubMed=8550497; Collinson S.K., Clouthier S.C., E "Salmonella enteritidis agfBAC op
  and
  Salmonella enteritidis."
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   "Comparative and CT18.";
  s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
   Bacteriol.
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SIMILARITY: BELONGS
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   5039; csg...
;; SG10608; csg...
a; Signal; Complete p
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21 151
174 151
  U43280; AAC43599.1; -.
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  Similarity
                   NNAALVNQTASDSSVMVRQVGFGNNATANQY
NNAALVNOTASDSSVMVRQVGFGNNATANQY
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   OF 21-151 FROM N.A.
   151
  Conservative
  genomics
  AA,
  178:662-667(1996).
   185:2330-2337(2003).
  15305 MW;
  88.7%;
90.7%;
  Ġ,
  TO THE CSGA/CSGB FAMILY.
   STRAIN=27655-3B;
   agfBAC operon
   proteome
  Salmonella
  Score 681; DB Pred. No. 1.8e 2; Mismatches
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  MAJOR CURLIN SUBUNIT.
SVMVRQVGFGNNATANQY ->
REF. 6).
   B7DAC0D16B621359
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  enterica serovar Typhi strains
   J.L., Banser P.A:, Kay W.W.; encoding thin, aggregative
  There are no restrictions ong as its content is in
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   Trust T.J., Kay W.W.;
n, aggregative fimbriae
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.
Riley M., Collado-Vides J., Glasner J.D.
Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
"The complete genome sequence of Escheri
Science 277:1453-1474(1997).
  MEDLINE=93023873; PubMed=1357528;
Arnqvist A., Olsen A., Pfeifer J.,
"The Crl protein activates cryptic
fibronectin binding in Bscherichia
Mol. Microbiol. 6:2443-2452(1992).
  Oshima T., Aiba H., Baba T., Fu
Ikemoto K., Inada T., Itoh T.,
Kimura S., Kitagawa M., Makino
Mori H., Motomura K., Nakamura
Sampei G., Seki Y., Tagami H.,
  MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emcedy L., Trust T. "Purification and characterization Salmonella enteritidis.";
  Morı...
Sampei G., Sexı...
M., Horiuchi T.;
   J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN IS THE STRUCTURAL
  SEQUENCE OF 21-40.
STRAIN=K12 / YMEL;
MEDLINE=93023873;
   "A 718-kb DNA sequence of the E corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
   SEQUENCE
   MEDITNE-96414468; PubMed=8817489;

Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.,

"Expression of two csg operons is required for production fibronectin and congo red-binding curli polymers in Esche
   MEDLINE=97061202;
  SEQUENCE FROM
   STRAIN=K12
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   Major curlin s
CSGA OR B1042
   CSGA_EC
   repression of csgA,
Escherichia coli.";
   STRAIN=K12
  Escherichia
   28-FEB-2003
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01-OCT-1996
   "The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding o
   STRAIN=K12 / W3110;
MEDLINE=93211294; P
   Enterobacteriaceae;
   Bacteria; Proteobacteria;
   SEQUENCE FROM N.A.
   sen A., Arnqvist A.;
    TEMPERATURES FIBRONECTIN.
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  t G. III, Bloch C.A., Perna N.T., s J., Glasner J.D., Rode C.K., May Kirkpatrick H.A., Goeden M.A., R
  Created)
   a T., Fujita K., Hayashi K., Honjo A., toh T., Kajihara M., Kanai K., Kashimoto K., Makino K., Masuda S., Miki T., Mizobuchi K., akamura Y., Nashimoto H., Nishio Y., Saito N. ami H., Takemoto K., Wada C., Yamamoto Y.,
                      DEGREES
  Gammaproteobacteria; Enterobacteriales;
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   Escherichia coli K-12.";
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            STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glas

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpa

Posfai G., Hackett J., Klink S., Boutin A., Shao Y.,

Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Pc

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwar

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia co
   SEQUENCE FROM N.A.
STRAIN-0157:H7 / ATCC 43895;
MEDLINE-21218556; PubMed=11319125;
MILICH G.A., Keen J.E., Elder R.O.;
Multations in the csgD promoter associated with variations expression in certain strains of Escherichia coli 0157:H7."
Appl. Environ. Microbiol. 67:2367-2370(2001).
   SEQUENCE
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   EMBL;
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   Major curlin subunit precursor. CSGA OR Z1676 OR ECS1420. Escherichia coli O157:H7.
   SEQUENCE FROM N.A. STRAIN=0157:H7 / H
  28-FEB-2003
28-FEB-2003
  Fimbria; Signal; Complete SIGNAL 20
  NCBI_TaxID=83334;
  Enterobacteriaceae;
   Bacteria; Proteobacteria;
   EcoGene; EG11489; csgA.
  EMBL;
   BL; L04979; AAA23616.1; -.
BL; X90754; CRA62282.1; -.
BL; AE000205; AAC74126.1; -.
BL; D90741; BAA35832.1; -.
BL; D90742; BAA35840.1; -.
R; S70788; S70788.
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   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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409:529-533 (2001).
   Similarity
  GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
   NNAALVNOTASDSSVMVROVGEGNNATANOY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
   TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
   MKLLKVAAIAAI VFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNI YQYGGGNSALALQ
   151 AA;
   (Rel. 41, Created)
(Rel. 41, Last sequence up)
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   Gammaproteobacteria; Enterobacteriales;
   proteome
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  Score 517; DB 1; Pred. No. 9.7e-37;
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  MAJOR CURLIN SUBUNIT.
   PRT;
   C003470D208D395F CRC64;
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28-FEB-2003
   01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
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SEQUENCE FROM N.A.
STRAIN=K12 / MC4100;
STRAIN=K12 / MC4100;
MEDILINE=96414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production fibronectin- and congo red-binding curli polymers in Esche
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334;
   CHAIN
   PIR;
  PIR;
   EMBL; AF275733; AAK53212.1; -.
EMBL; AE005315; AAG55788.1; -.
EMBL; AP002554; BAB34843.1; -.
  O157:H7 and genomic comparison with a laboratory strain K-:
DNA Res. 8:11-22(2001).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLICOLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND:
   STRAIN=0157:H7 / RIMD 0509952;

MEDL.INE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Y
Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., T
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., T
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Ya
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia
   Escherichia coli, and Escherichia coli 0157:H7.
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SEQUENCE FROM N.A.
  CSGB ECOLI
   NCBI_TaxID=562,
   Fimbria;
  FIBRONECTIN. SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
  H85665; H85665.
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   GNNAALVNQTASDSSVMVRQVGFGNNATANQY
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   STANDARD;
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Sampei G., Seki Y., Ta
Sampei G., Seki Y., Ta
Sampei G., Seki Y., Ta
                      This SWISS-PROT entry is copyright. It is produced through a centre of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institution. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.
   Arnqvist A., Olsen A., Normark S.;
"Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coli can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-!- FUNCTION: CURLIN IS THE STRUCTURE UBBUNIT OF THE CURLI. CURLI AI COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
   MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya
Hayashi T., Makino E., Ohakayama K., Murata T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
DIA Res. 8:11-22(2001).
  Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kitugawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
   MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhaw G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Posfai G., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
   "A 718-kb DNA sequence of the I corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
   MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I Mau B., Shao Y.;
  MEDLINE=95157246;
  SEQUENCE FROM N.A.
STRAIN=0157:H7 / R
   SEQUENCE FROM N.A.
STRAIN=0157:H7 / E
  SEQUENCE FROM
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   Nature 409:529-533(2001).
   MEDLINE=97061202;
  Science
  "The
send an email to license@isb-sib.ch).
   CURLIN MONOMERS.
SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
   complete genome sequence 
nce 277:1453-1474(1997).
  Microbiol.
   sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
   OF 1-21 FROM N.A.
  MG1655;
  18:661-670(1995)
  RIMD 0509952;
   EDL933 / ATCC
   PubMed=7854117;
   PubMed=8905232;
  the Escherichia coli
-28.0 min region on tl
   of Escherichia coli K-12.";
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  EMBL; AR000205; AAC74125.1; -
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EMBL; AB005315; AAG55787.1; -
EMBL; AP002554; BAB34842.1; -
PIR; C90806; C90806.
PIR; G85665; G85665.
PIR; S70787; S70787.
  Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamiln N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.", Nature 413:848-852(2001).
   0827M3;
28-FEB-2003 (Rel. 41, Createa)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
Minor curlin subunit precursor.
CCCR OR STY1180 OR T1777.
  CSGB SAI
  LT 5
_SALTI
  J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNCOLLED SURFACE STRUCTURES THAT ASSEMBLE TEMPERATURES BELOW 37 DEGREES CELSIUS. CELSIUS. THE MINOR SUBUNIT IS THE NU
   SEQUENCE FROM N.A.
STRALNE-TY2 / ATCC 700931;
MEDLINE=22531367, PubMed=12644504;
MEDLINE=22531367, PubMed=t G. III, Mayhew G.F., Rose D.J.,
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi st
and CT18.";
  SEQUENCE FROM N.A.
  Enterobacteriaceae;
   MEDLINE=21534947; PubMed=11677608;
  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
   SEQUENCE
  SIGNAL
   Fimbria;
   CURLIN MONOMERS.
SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
   SALTI
  77
   86
  38
  21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
   34;
  ; EGi2621; csgB.
; Signal; Complete p
1 21
22 151
   Similarity
   RNNATYDQLVTRVVTHEMAH---AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
  SNRAKIDO----TGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY
   151 AA;
   13.6%;
ilarity 29.1%;
Conservative 1
   STANDARD;
  Salmonella
   15882
   protecome.
poTENTIAL.
MINOR CURLIN SUBUNIT.
MW; B18D266B964014B8 CRC64;
   15;
   Score 104.5;
Pred. No. 0.
   PRT;
   Mismatches
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RESULT 6
  Query Match
Best Local S
Matches 33
  P55226;
01-OCT-1996
01-OCT-1996
28-FEB-2003
   SPECIES=S typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21334948; PubMed=11677609; MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Lat. Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulv. Leonard S. Nguyen C., Scott K., Holmes A., Grewal N., Mulv. Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan Materston R., Wilson R.K.;
  EMBL;
  SPECIES-S. enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
COllinson S.K., Clouthier S.C., Doran J.L., Banser P.A.,
"Salmonella enteritidis agfBAC operon encoding thin, aggr
  Romling U., Bian Z., Hammar M., Sierralta W.D., Normark "Curli fibers are highly conserved between Salmonella ty Bscherichia coli with respect to operon structure and re J. Bacteriol. 180:722-731(1998).
  Minor curlin subunit pre
CSGB OR AGFB OR STM1143.
   SEQUENCE FROM N.A.
SPECIES=S.typhimurium; STRAIN=SR-
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., S
  SIGNAL
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  Enterobacteriaceae;
   Bacteria; Proteobacteria;
  Salmonella enteritidis
   Salmonella typhimurium, and
  SEQUENCE
   Fimbria;
  or send
   entities
  modified
  Nature 413:852-856(2001).
  "Complete
                                 Bacteriol. 178:662-667(1996).
FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
 FIBRONECTIN. THE MINOR SUBUNIT IS CURLIN MONOMERS.
  SALTY
  AL627269; CAD08267.1; -. AE016840; AA069400.1; -.
  74
  95
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  33,
   Similarity
  an email to license@isb-sib.ch).
   Signal; Complete proteome.

1 21 POTENTIAL.

22 151 MINOR CURLIN SUBUNIT.
  GSANAALALQSDARKSE-----TTITQSGYGNGADVGQ-GADNST-----IELTQ
   requires
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  EGENNRAKVDQAGNYNFAY-IEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY
  NGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
  genome
MONOMERS
  151 AA;
  (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
  Conservative
  STANDARD;
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   a license
  teria; Gammaproteobacteria;
Salmonella.
  16254 MW;
   precursor
   13.0%;
  STRAIN=SR-11;
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  is not
  Salmonella enterica serovar Typhimurium
   Pred.
  Score 99.5;
   (Fimbrin SEF17
  161C54326E573495
  Mismatches
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  removed.
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  P51521; Q9XZ
01-OCT-1996
01-OCT-1996
  DROME
  STRAIN=Oregon-R;
MEDLINE=9129102; PubMed=1712294;
Mevel-Ninio M.T.M., Terracol R., Kaf
"The ovo gene of Drosophila encodes
for female germ line development.";
EMBO J. 10:2259-2266 (1991).
  CHAIN
SEQUENCE
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  Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavenbaby-ovo gene r melanogaster: relationship to genetic complexity. Mol. Cell. Biol. 14:6809-6818(1994).
   Ovo protein (Shaven baby OVO OR SVB.
  OVO
  PIR;
   TISSUE=Ovary;
MEDLINE=95021209; PubMed=7935398;
Liang Y.,
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
   StyGene; SG10609; csgB.
Fimbria; Signal; Complete proteome
   EMBL; AJ002301; CAA05316.1; -. EMBL; AE008749; AAL20073.1; -.
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  Ephydroidea;
  Eukaryota;
   Drosophila melanogaster (Fruit fly)
   SIGNAL
  or send an email to license@isb-sib.ch).
   NCBI_TaxID=7227;
  10-OCT-2003
  FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF I LINE CELLS: PLAYS A ROLE IN GERM LINE SEX DETERMINATION SUBCELLULAR IOCATION: Nuclear (potential).

DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING COGENESIS. STORED IN THE TIS APPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTIL PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.

SIMILARITY: Contains 4 C2H2-type zinc fingers.
  DROME
  JC6040; JC6040
                        SWISS-PROT entry
  74
  95 NGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   14 GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
  51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST--
   ω
•
   Q9XZU4;
   Similarity
  EGGNNRAKVDQAGNYNFAY-IEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
  151 AA;
  (Rel. 34, Last sequence update) (Rel. 42, Last annotation updat
   (Rel.
   Conservative
  AAC43598.1; -.
  STANDARD;
   34, Created)
  16182 MW;
   13.0%;
                      is copyright.
  protein).
   16;
  Drosophila
  MINOR
   Pred.
   Score
   POTENTIAL.
  PRT;
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095271; 0952
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   PROSITE; PS00028; ZĪNC FİNGER C2H2 1; 3.
PROSITE; PS50157; ZĪNC FĪNGER C2H2 2; 3.
Zīnc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
  EMBL;
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   FlyBase; FBgn0003028; ov
InterPro; IPR007087; Znf
Pfam; PF00096; zf-C2H2;
SMART; SM00355; ZnF_C2H2
  Transcription
   or send an email to license@isb-sib.ch).
   TRANSFAC; T00669;
  European Bioinformatics Institute. The by non-profit institutions as long
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  ; U11383; AAB60216.1;
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A56038; A56038.
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                          095272
   LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
  AALVNQTASDSSVMVRQVGFGNNATA 148
   ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNN
   non-profit institutions as acceptance and this statement is not removed. Usage by and recent and the statement (See http://www.isb-sib.
   LQNAAAAAYIMSAGSG----
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  -NNNNGGQTSMMGHPFYGGNPSA
  -----GGNGYINCGGVG-GPNNSLDGNNLLNFASVSNYNESNSKFHNHHHHHQHNNN
  Conservative
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   regulation.
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  12.0%;
   C2H2; 4.
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  ; ALT_SEQ.
   C2H2.
 annotation
        sequence update)
  15;
  MW;
  Score 92.5; I
Pred. No. 2.9;
5; Mismatches
  POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-ALA.
POLY-ALA.
POLY-ALA.
POLY-ALA.
POLY-ALA.
POLY-GLN.
POLY-GLN.
CZHZ-TYPE 3.
CZHZ-TYPE 3.
CZHZ-TYPE 3.
CZHZ-TYPE 4.
  POLY-GLY.
POLY-ASN.
POLY-GLN.
POLY-GLN.
   POLY-ALA.
  POLY-GLY
  -----GGGCTGNGGGGASGPGGGPSANSGGGGGGG-----
   > R (IN REF. 2).
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entities requires a license agreement (some send an email to license@isb-sib.ch).
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  MEDLINE-2055628; PubMed=10988299;
Chi N.-W., Lodish H.F.;
"Tankyrase is a Golgi-associated mitogen-activated protein kinase substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444 (2000).
  FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291 MEDLINE=21602874; PubMed=11739745; Cook B.D., Dynek J.N., Chang W., Shostak G., Smith
   Cook B.D., Dynek J.N., Chang W., Shost "Role for the related poly(ADP-Ribose)
  FUNCTION,
   to nuclear pore
   Smith S., de Lange T., "Cell cycle dependent localization of the telomeric PARP, tankyrase,
   MEDLINE=99454782; PubMed=10523501;
   SUBCELLULAR LOCATION
   Smith S., Giriat I., Schmitt A., de Lange "Tankyrase, a poly(ADP-ribose) polymerase Science 282:1484-1487(1998).
   MEDLINE=99040105; PubMed=9822378;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Tankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase interacting ankyrin-related ADP-ribose polymeTNKS OR TINKS1 OR TIN1 OR TINF1 OR PARPL. Homo sapiens (Human).
   Smith S., Giriat
   SEQUENCE FROM N.A. (ISOFORMS 1 AND TISSUE=Testis;
  NCBI_TaxID=9606;
   human telomeres.";
  PTM: Upon insulin-stimulation, phosphorylated on serine by MAPK kinases.
PTM: ADP-ribosvlated '.
  IsoId=095271-2; Sequence=VSP 004538, VSP 004539;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Ubiquitous; highest levels in
PTM: Upon insulin-stimulation
   SIMILARITY: Belongs to the PARP family.
SIMILARITY: Contains 15 ANK repeats.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
   Cell Sci.
  . Cell. Biol. 22:332-342(2002).
FUNCTION: May regulate vesicle trafficking and modulate the subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP subcellular distribution of successions and thereby contribute to the
   with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TNKS is found in the nucleus, associated with TRF1.

ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=2;
  Name=1
  IsoId=095271-1;
  AND PHOSPHORYLATION
  ore complexes and centrosomes."; 112:3649-3656(1999).
  Sequence=Displayed;
   It is produced through
  2)
   There are no
  polymerases
   polymerase)
            http://www.isb-sib.ch/announce,
  T.; at human telomeres.";
   Usage
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Matches 42
   Nuclear protein; Repeat; ANK repeat; ADP-ribosylation;
Phosphorylation; Alternative splicing.
REPEAT 215 247 ANK 1.
REPEAT 248 280 ANK 2.
REPEAT 368 400 ANK 3.
REPEAT 401 433 ANK 5.
REPEAT 434 466 ANK 6.
REPEAT 557 589 ANK 7.
REPEAT 557 589 ANK 9.
REPEAT 683 715 ANK 10.
REPEAT 683 715 ANK 11.
REPEAT 749 781 ANK 12.
REPEAT 749 781 ANK 13.
REPEAT 869 901 ANK 13.
REPEAT 869 901 ANK 14.
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REPEAT 902 934 ANK 15.
  DOMAIN
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   SEQUENCE
   PRINTS; PRO1415; ANKYRIN.
SMART; SM00248; ANK; 17.
SMART; SM00454; SAM; 1.
   GO; GO:0000781; C:chromosome, telomeric region; IDA. GO; GO:000350; F:NAD ADP-ribosyltransferase activity; IDA. GO; GO:0005515; F:protein binding; IPI. GO; GO:0007004; P:telomerase-dependent telomere maintenance;
  EMBL;
EMBL;
   PROSITE; PS50088; ANK_REPEAT; 15.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50105; SAM_DOMĀIN; 1.
Transferase; Glycosyltransferase; NAD; Golgi stack; Telomere;
   Pfam; PF00023; ank; 19. Pfam; PF00536; SAM; 1.
  Genew; HGNC:11941; TNKS. MIM; 603303; -.
   MUTAGEN
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   InterPro; IPR002110; ANK. InterPro; IPR001660; SAM.
  DOMAIN
207
  158
   121 NNAALVNOTASDSSVMVRQVGFG
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   000420;
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  AP082557;
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  Similarity
  GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD----
  KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
  VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS
   VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
  1327
  Conservative
   644
  137
  AAC79842.1;
AAC79843.1;
AAC79844.1;
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   11.9%;
29.4%;
  142010
   17;
   Ξ
Ξ
  . . .
   Score 91.5;
Pred. No. 4
  PARP.
POLY-HIS.
POLY-PRO.
POLY-SER.
   /FTId=VSP 004538.
Missing (In isoform 2).
/FTId=VSP 004539.
H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
   POLY-SER.
EST -> GH
   E->A: LOSS OF ACTIVITY; WHEN WITH A-1184.
   WITH A-1291.
  Mismatches
   143
   E14DE985C710B957
  GHS (in isoform
  밁
   1;
   65;
   Length 1327;
  -SSSSPSSPGSSLAESPEAA
   CRC64;
  Indels
   2
  -VSRV--KRLVDAAN
   ASSOCIATED
   19;
   NAS
   Gaps
  157
  206
  120
  64
```

RESULT 9
OMPB\_RICJA

sequence

update)

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RESULT 10

N100_YEAST

ID N100_YEAST

AC Q02629;

DT 01-JUL-1993

DT 01-JUL-1993
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   Ś
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  Query Match
Best Local S
Matches 40
   CHAIN .
  use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
  This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
  (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered layer with hexagonal symmetry.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
  Submitted (MAY-1997) to the RMBL/GenBank/DDBJ databases.
-- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR-STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
  Rickettsia japonica.
Rickettsia, Proteobacteria, Alphaproteobacteria,
Bacteria, Proteobacteria, Alphaproteobacteria,
  Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB) (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide]
  OMPB_RICJA STANDARD; PRT; 1656 AA

006653;

30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)
   SEQUENCE
   CHAIN
  TIGRFAMs;
   Pfam;
  EMBL; AB003681; BAA20138.1;
  STRAIN-YH
   Antigen;
  InterPro;
   -!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE
   Uchiyama T.;
  SEQUENCE FROM N.A.
  NCBI_TaxID=35790;
   OMPB.
  [nterPro;
   "Sequencing of japonica.";
   similarity).
   105
   548
  509
   PF03797; Autotransporter; 1.
AMs; TIGR01414; autotrans_barl; 2.
en; S-layer; Cell wall.
  66
  40;
  6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK
   Similarity
  NAQTLTISGTIGIIGANNTTLGQFNIGSSKTTLNGGNVAINELVIGNNGS
   QLVTRVVTHEMAHAGGNNAAL-----VNQTASDSSVMVRQVGFGNNAT 147
   ---TLTLGGANIISANGGTINFQANGGTIKLTSTQNNIVVDCDLAIATDQTGVVDASSLT
  SETTITOSG----YGNGADVGQGADNSTIELT---
  VLAAGAITLDGSATI-----TGDIGNGGG-----
  IPR006315; Autotransport. IPR005546; Autotransporter.
  528 5
1656 AA;
  1339
   (Rel.
  Conservative
  the gene encoding the protein rOmp
   STANDARD;
   26,
26,
   1338
  1656
   533
 , Created)
, Last seq
  11.7%;
23.5%;
   168097 MW;
   21;
  Score
Pred.
   POLY-
   120 kDa SURFACE-EXPOSED PROTEIN 32 kDa BETA PEPTIDE.
   PRT;
  Mismatches
   kDa BETA PEPTIDE.
  3132A69C9DD5999F CRC64;
  No.
   959
   update)
   8
   DB 1;
   ₽
  B
  57;
   Length 1656;
   Rickettsiales,
  Indels
  W
  ę,
  -GAALOSITLANDATK
   Rickettsia
  QNGFRNNATYD
  52;
   654
  collaboration
L outstation -
  .ch/announce/
  ANCHOR
   by a S-
   Gaps
  commercia
  ខ
   604
  104
  547
   65
  0
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8
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   밁
   Query Match
Best Local
  Matches
   SEQUENCE
  SGD; S0001551; NUP100.
GO; GO:0005643; C:nuclear pore; IDA.
InterPro; IPR007230; Nucleoporin 7:
InterPro; IPR004325; Nucleoporin FG.
Pfam; PF04096; Nucleoporin 7: 1.
Pfam; PF03093; Nucleoporin FG; 25.
Nucleoporin FG; 25.
   "A new family J. Cell Biol. [2]
   EMBL; Z15035; CAA78753.1; --
EMBL; X75780; CAA53406.1; --
EMBL; Z28068; CAA61905.1; --
PIR; B44402; B44402.
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   This
   "Sequence of a 20.7 kb region of yeast chromosome XI includes the NUP100 gene, an open reading frame (ORF) possibly representing a nucleoside diphosphate kinase gene, tRNAs for His, Val and Trp in addition to seven ORFs with weak or no significant similarity to
  MEDLINE=93054906; PubMed=1385442; Wente S.R., Rout M.P., Blobel G.; "A new family of yeast nuclear pore J. Cell Biol. 119:705-723(1992).
  Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
   Yeast
  Rasmussen S
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCBI_TaxID=4932;
   NUP100 OR NSP100
   - rUNCTION: Essential component of nuclear pore complex. Nucleoporins may be involved in both binding and transl the proteins during nucleocytoplasmic transport.

SUBCELLULAR LOCATION: Nuclear pore complex.

DOMAIN: Contains G-L-F-G repeats.

SIMILARITY: Belongs to the GLFG family of nucleoporins.
  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                 131
   294 MNSST--
  243
   183
  80
   27
  proteins.";
10:S69-S74(1994).
  35;
  .ine; 139824; -.
  protein; Transport; Repeat.

33 571 29 X 6 AA APPROXIMATE REPEATS

G-L-F-G.
   Similarity
                               SDSSVMVRQVGFGNN 145
   SFGSKPVGSGSLFGQSNNTLGNTTN--NRNGLFGQM
   DVGQ-
   GNGSNIFGAGNNSQSNTTGSLFGNQQSSAFGTNNQQGSLFGQQSQNTNNAFGNQNQLGGS
   GGGGNHNGGGNSSGPDSTLSIY--QYGSANAALALQSDARKSETTITQSGYGN-----GA
  959 AA;
   11.6%;
ilarity 25.9%;
Conservative 2
   NUP100/NSP100 (Nuclear pore protein NUP100/NSP100)
SP100 OR YKL068W OR YKL336.
   (Rel. 43, Last annotation update)
QGVFGQN 305
  99988 MW;
   -GADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTA 130
   20;
  Score 89; DB 1
Pred. No. 5.3;
20; Mismatches
  D3985F9901BBAA51 CRC64;
  complex proteins.";
  There are no restrictions ong as its content is in
   ۲.
   52;
   Length 959;
   Indels
   --NSSNQGSSNSGLFGQNS
  complex.
and translocation
   28;
  얶
  Gaps
  no
no
   0f
  293
   242
  79
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RESULT

11

AL133357;

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RA SQUARY, GWALLIAM K., KaJanukram M.A., Lyhie M., Lyhie K., Dewan S., RA SQUARS J., Baker S., Basham D., Bowman S., RA SQUARS J., Baker S., Basham D., Bowman S., RA SQUARS K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Collins M., Commor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holroyd S., Simmonds M., Earther S., McDeanl J., Odell C., RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch B., RA Rutherford K., Rutter S., Squares R., Squares S., Stevens K., Sharp S., Stelton J., Simmonds M., Squares R., Squares S., Stevens K., Rab Faylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., RA Welljens I., Vonstreels E., Rieger M., Schaefer M., Mueller-Auer S., RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Thode G., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Daga R.R., Robert M., Gaillardin C., Fallada V.A., Garzon A., Thode G., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Spakovski G.V., Useery D., Barrell B.G., Nurse P., RA Shakovski G.V., Usery D., Barrell B.G., Nurse P., RA Cruztat 415:871-880(2002).
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   MEDLINE=22263608; PubMed=12376568;
Tange Y., Hirata A., Niwa O.;
"An evolutionarily conserved fission yeast protein, Ned in normal nuclear morphology and chromosome stability, Dis3, Pim1/RCC1 and an essential nucleoporin.";
J. Cell Sci. 115:4375-4385 (2002).
-!- SUBUNIT: Monomer. Interacts with ned1.
-!- SUBCELLULAR LOCATION: Nuclear pore complex (By simi
  entities requires a license agreement (s or send an email to license@isb-sib.ch).
   -!- DOMAIN: Contains G-L-F-G repeats.
-!- SIMILARITY: Belongs to the GLFG family of nucleoporins.
   MEDLINE=98162722;
Yoshioka S., Kato
   STRAIN-PR745
   SEQUENCE OF 1428-1778 FROM N.A.
  SCHPO
N189_s
  "Identification
  Nucleoporin nup189 (Nuclear pore protein nup189).
NUP189 OR SPAC1486.05.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
   DENTIFICATION, AND SUBUNIT
   SEQUENCE FROM N.A.
  Schizosaccharomycetales; Schizosaccharomycetaceae;
  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
   MEDLINE=21848401; PubMed=11859360;
  SCHPO
  4:363-369(1997).
   Gwilliam
  e
H
   STANDARD;
   PubMed=9501991;
   K., Nakai K.,
   R., Rajandream M.A.,
  open
   akai K., Okayama H., Nojima H.;
reading frames in Schizosaccharomyces
   1778
  update)
  Lyne M., Lyne R., Stewart
   B
  http://www.isb-sib
  similarity)
  Ned1, implicated
  restrictions
  and
  EMBL
  a collaboration
  .ch/announce/
   outstation
  with
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  ita
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RESULT
VG38_BP
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   S
  SOUR PLANTS
  Query Match
Best Local (
  Matches
  P07875;
01-AUG-1988
01-AUG-1988
01-AUG-1990
   SEQUENCE FROM N.A.

MEDILINE-87283911; PubMed=3302276;

Riede I., Drexler K., Eschbach M.L., Henning U.;

Riede I., Drexler K., Eschbach M.L., Henning U.;

"DNA sequence of genes 38 encoding a receptor-recognizing bacteriophages T2, K3 and of K3 host range mutants.";

J. Mol. Biol. 194:31-39(1987).

-I-FUNCTION: V938 is at the tip of the long tail fibers the phage recognition site for the cellular receptor.

-I-MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS
  HSSP; P22629; ISWF.
GeneDB_Spombe; SPAC1486.05; -.
GO; GO:0016020; C:membrane; ISS.
GO; GO:0005643; C:nuclear pore; ISS.
GO; GO:0005643; C:nuclear pore; ISS.
InterPro; IPR007330; Nucleoporin2.
InterPro; IPR004325; Nucleoporin_FG.
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  BPT2
InterPro; IPR007932; Tail_fibre_GP38. Pfam; PF05268; GP38; 1. Fiber protein; Phage recognition. SEQUENCE 262 AA; 25801 MW; 056736
   Nuclear protein;
   EMBL; X05312; CAA28935.1; PIR; S00275; S00275.
  or send an
  NCBI_TaxID=10664;
   Viruses; dsDNA viruses, T4-like viruses.
   Bacteriophage
   VG38
   DOMAIN
   AS RECEPTORS.
  ; D89145; BARL.
T50074; T50074.
   BPT2
   457
   400
   PF03093; Nucleoporin_FG; 24.
  15
  70
   Similarity
  requires a license agreement (S an email to license@isb-sib.ch).
  GTGGSL-----FGNANTA
  SGSALAGVVPQWGGGGNHNGGGNSSGPDSTL----SIYQYGSANAALALQSDARKSETT
  recognizing
  ASDSSVMVRQVGFGNNATA
   TTPA--SGGFSFGQNANNA----PKPAFGSTATTAPKPAGTGLFGGLGAGANTNTATNAT
  ITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQT
  (Rel.
(Rel.
   Conservative
  BAA13807.1;
   STANDARD;
   $
  Transport; Repeat.
625 GLY-RICH.
596 THR-RICH.
  08, Last
15, Last
   08, Created)
   442
   - FGFGANNNTANNNTAPTSTFGGNNSSNFSFGANNNAATKPSGFGFGSTT
   Last sequence update)
, Last annotation update)
protein (Protein Gp38)
  11.5%;
27.3%;
  189575
  5
   16;
  RNA stage; Caudovirales; Myoviridae;
  W.
  523
  148
  Score 88; DB
Pred. No. 13;
   ASN-RICH
   PRT;
 0567366918F6C745 CRC64;
   Mismatches
  1D2AED57D927ADC6 CRC64;
   Henning U.;
receptor-recognizing
range mutants.";
   262
   (See
  There are no restrictions
   ₿
   http://www.isb-sib.ch/announce/
  ۲:
   65;
   Length 1778;
  receptor.
E PROTEINS
   Indels
  and
  and
   EMBL
   OMPE
   protein
  þ
   20;
  for
   collaboration
  Berves
   DINA
   Gaps
   commercial
  8
  9
  129
   456
  69
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   á
   Query Match
Best Local S
Matches 26
DISULFID
DISULFID
DISULFID
DISULFID
DISULFID
  CHAIN
PROPEP
METAL
ACT_SITE
   Zymogen;
SIGNAL
PROPEP
   METAL
   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
   -|- CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and basic residues at P2 and P3'. A model nonapeptide cleaved at -Ala-Tyr-|-Leu-Lys-|Lys-. |
-|- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-an-
-|- SIMILARITY: Belongs to peptidase family M8.
  of Leishmania donovani.";
Mol. Biochem. Parasitol. 48:173-184(1991).
-i- FUNCTION: Has an integral role during in the mammalian host.
-i- CATALYTIC ACTIVITY: Preference for hyd.
   "Heterogeneity of the genes encoding to f Leishmania donovani.";
   GP63_LEIDO
P23223;
  EMBL; M60048; AAA29244.1;
HSSP; P08148; 1LML.
   entities requires a license agreement (S or send an email to license@isb-sib.ch).
  Eukaryota; Euglenozoa;
NCBI_TaxID=5661;
   01-NOV-1991
10-OCT-2003
   LEIDO
  Pfam; PF01457; Peptidase_M8; 1
PRINTS; PR00782; LSHMANOLYSIN
   SEQUENCE FROM N.A.
STRAIN=LV9;
   Leishmania
Eukaryota;
  01-NOV-1991
  Hydrolase;
   PROSITE; PS00142; ZINC PROTEASE; 1.
   InterPro;
   InterPro;
  MEROPS; M08.001;
   This
  MEDLINE=92107220;
  Leishmanolysin
  (Major surface
  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
   175
   27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQG 84
  26;
   Similarity
   Signal;
  GGGGRPFGVGGKIGSDSILS----GSNASL---TDAGTGGTTF-QYGAGNGGNVGAG
   IPR006025; Pept M Zn BS.
IPR001577; Peptidase M8.
   (Rel. 20, Create
(Rel. 20, Last a
(Rel. 42, Last
  Metalloprotease;
   donovani.
  40
88
566
251
252
252
253
253
253
112
112
112
112
301
301
301
301
   Conservative
  el. 20, Last sequence update)
el. 42, Last annotation update)
precursor (EC 3.4.24.36) (Cell
glycoprotein) (GP63 protein) (F
   STANDARD;
   Cell
   PubMed=1762629;
   11.3%;
  tease; Glycoprotein; Metal-binding; adhesion; GPI-anchor; Lipoprotein.
   Created)
   Kinetoplastida;
  .
ZINC (CATALYTIC)
BY SIMILARITY.
ZINC (CATALYTIC)
ZINC (CATALYTIC)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
   4.
  Score 86.5;
Pred. No. 2;
  REMOVED IN MATURE
  ACTIVATION
   LEISHMANOLYSIN
   PRT;
  Mismatches
   the major
  590
  (See http://www.isb-sib.ch/announce/
   Trypanosomatidae; Leishmania.
   There are no rest
   PEPTIDE.
   the
  В
   ll surface protease)
(Promastigote surfa
   Usage
  19;
  1;
  infection
  (BY SI
  ХВ)
ХВ)
  surface glycoprotein
  Length
   SIMILARITY)
SIMILARITY)
   SIMILARITY)
  Indels
   (BY SIMILARITY).
  restrictions
  262;
  GPI-anchor
   of macrophages
   and
   EMBL
   Zinc;
  þ
  at
  9;
   HOR
   collaboration
   outstation
   31
  Gaps
   9 9
  223
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   밁
  Query Match
Best Local S
Matches 24
                                       Zymogen;
SIGNAL
   use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (Secons send an email to license@isb-sib.ch).
  MEDIINE-33149206; PubMed-8426614;
Medina-Acosta E., Karess R.E., Russell D.G.;
Medina-Acosta E. Karess R.E., Russell D.G.;
"Structurally distinct genes for the surface protease of Leishmania maxicana are developmentally regulated.";
Mol. Biochem. Parasitol. 57:31-46(1993).

-I-FUNCTION: Has an integral role during the infection of macrophagin the mammalian host.

-I-CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 are constant and p3'. A model nonapeptide is p1' and basic residues at P2 and P3'. A model nonapeptide is
  PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PROTEAS
Hydrolase; Metalloprotease; Gl
  GlycoSuiteDB; P43150; --
InterPro; IPRO016025; Pept M Zn BS.
InterPro; IPRO01577; Peptidase MB.
Pfam; PF01457; Peptidase MB; 1.
   This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and
   _LEIME
GP63_LEIME
   DISULFID
DISULFID
DISULFID
CARBOHYD
  MEROPS; M08.001; -
   EMBL; X64394; CAA45733.1;
PIR; S19916; S19916.
   the
  PRINTS;
   STRAIN=MNYC/BZ/62/M379;
  Leishmania mexicana.
Eukaryota; Euglenozoa;
   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin C1 precursor (EC 3.4.24.36) (C)
(Major surface glycoprotein) (GP63 protein)
   SEQUENCE FROM N.A.
   P43150;
  SEQUENCE
  NCBI_TaxID=5665;
   TIPID
   cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
COFACTOR: Binds 1 zinc ion per subunit (By similarity).

amastigote forms.
SIMILARITY. ----
  SIMILARITY: Belongs to peptidase family M8.
  European Bioinformatics Institute.
  P08148; 1LML.
   PR00782;
  Signal;
   Similarity
   YDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVM-VRQVGFG----NNATA
  YDOLVTRVVTHEMAHALGFSVVFFRDARILESISNVRHKDFDVPVINSSTA
  103
266
  590
  Conservative
   503
523
587
  STANDARD;
   AA,
   Cell
  39
102
646
266
  institutions as long as its content atement is not removed. Usage by an
  553
546
565
   11.3%;
47.1%;
   62950
   adhesion;
  PROTEASE; 1.
   Kinetoplastida;
   ₩,
   Glycoprotein;
ion; Multigene
  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
VALUED (GLCNAC...
GPI-anchor amidated a similarity).
   Score 86.5; D
Pred. No. 4.9;
4; Mismatches
 POTENTIAL.
ACTIVATION PEPTIDE (POTENTIAL).
LEISHMANDLYSIN CL.
ZINC (CATALYTIC) (BY SIMILARITY
   4.
  PRT;
   0FB315D299659F58
   (See http://www.isb-sib.
   646
   Trypanosomatidae; Leishmania
  rmatics and the EMBL outs
There are no restrictions
  .9;
   A
   Metal-binding;
family.
   (Cell surface protease)
(Promastigote surface
(BY SIMILARITY)
   18;
  1;
  infection of macrophages
  CRC64;
  Length
  asparagine
   through a c
   (POTENTIAL)
  Zinc;
  590;
   a collaboration -
  for
  5
  (Ву
  291
   148
   ch/announce/
   in no way
  the
  Gaps
  and
  엺
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   Xanthomonas campestris pv. translucens Mol. Gen. Genet. 223:163-166(1990).
-!- FUNCTION: Ice nucleation proteins
   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonadaceae; Xanthomonas.
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   Local
   CYPSTAILIZATION IN SUPERFOOLED WATER:
SUBCELLULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
SIMILARITY: Belongs to the bacterial ice nucleation protein
family.
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  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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Best Local Similarity 26.4%; Pred. No. 18;
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  InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
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PROSITE; PS00314; ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
  1165 GYGSTQTAGYNSILT--TGYGSTQTAQE 1190
  1055 GSTGTAGADSTL-IAGYGSTQTA------GSDSSLT-AGYGSTQTARQGSDITAGYGS 1104
   1105 TGTAGADSSLIAGYGSTQTAGYDSNLTAGYGSTQTAREDSSLTAGYGSTSTAGHDSSLIA 1164
  127 ----NQTASDSSVMVRQVGFGNNATANQ 150
  82 --GQGADNSTIE---LTQN-GFRNNATYDQLVTRVVTHEMA------HAGGNNAALV- 126
  34 GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGN------GADV-----
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   SUMMARIES
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O33802 salmonella
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Q7x240 citrobacter
Q8cw63 escherichia
Q7x237 enterobacte
Q8eih63 salmonella
Q8eih3 shewanella
Q9sij5 escherichia
Q8eih3 shewanella
Q9sij4 bradyrhizob
Q89ji4 bradyrhizob
Q89ji4 bradyrhizob
Q7ucz1 shigella f1
Q8cw64 escherichia
Q83ru7 shigella f1
Q88hg0 pseudomonas
Q98ln6 rhizobium l
  Description
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| 94.5               | 94.5              | 94.5              | 94.5   | 95     | 95                 | 95.5   | 95.5   | 95.5   | 95.5               | 96.5               | 96.5   | 97     | 97.5   | 97.5   | 97.5   | 97.5   | 97.5               | 98     | 98.5              | 98.5   | 99                 | 99     | 99.5   | 99.5   | 101    | 101                | 101.5  | ZOT    |
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| 1712               | 909               | 908               | 153    | 196    | 151                | 908    | 346    | 154    | 151                | 313                | 191    | 1410   | 646    | 645    | 586    | 477    | 91                 | 145    | 624               | 348    | 441                | 362    | 2174   | 1209   | 7716   | 1748               | 531    | 1422   |
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| ORTGET             | Q8T4E0            | Q9VBC4            | Q89JI6 | 022638 | Q7X238             | Q9VM71 | Q95RS5 | Q89JI5 | Q7X244             | Q9SYZ5             | Q7XDR3 | Q8CMJ0 | 053818 | Q7U1C5 | Q8EXJ2 | Q7X4S5 | Q9S3J8             | Q8U6N9 | QBNIV1            | 093397 | 087327             | Q89D03 | Q92UU8 | Q89CK5 | Q7UWZ8 | Q94821             | QBAWAB | CHARRO |
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| Q8tgel saccharomyc | Q8t4e0 drosophila | Q9vbc4 drosophila | Q89ji6 | 022638 | Q7x238 enterobacte |        |        | Q89ji5 | Q7x244 citrobacter | Q9syz5 arabidopsis | Q7xdr3 | Q8cmj0 | 053818 | Q7u1c5 |        |        | Q9s3j8 escherichia |        | Q8niv1 neurospora | 7      | 087327 pseudomonas | Q89d03 | Q92uu8 | Q89ck5 | Q7uwz8 | Q94821 tetrahymena | æ      | Cheins |

# ALIGNMENTS

|                                                                  |                                                                                                                                                                   |         |                 |                                      |                                                                                                                                       |                        |                                                                                                         |               |                        |                                 |                                                                   |                               |                          |             |                 | _ |                           |                    |
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| 1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 | <pre>/ Match 87.5%; Score 672; DB 2; Length 152;<br/>Local Similarity 89.4%; Pred. No. 3e-46;<br/>les 135; Conservative 3; Mismatches 13; Indels 0; Gaps 0;</pre> | 152 AA; | J000514;<br>152 | .";<br>c. Immun. 65:5320-5325(1997). | "Expression of thin, aggregative rimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithelial | Normark S.J., Rhen M.; | MEDILINE=98053981; PUDMEC=9393632;<br>Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D., | NCE FROM N.A. | NCBI_TaxID=602;<br>[1] | Enterobacteriaceae; Salmonella. | Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; | Ref A. Calmonella typhimirium | AgfA protein (Fragment). | (TrEMBLrel. | (Tremblical OS, |   | PRELIMINARY; PRT; 152 AA. |                    |

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EMBL; AJ515701; CAD56675.1; -. SEQUENCE 149 AA; 15260 MW; 946DD52017F64
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01-OCT-2003
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01-OCT-2003
   Zogaj X., Bokranz W., Nimtz M., Romling U.; "Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003).
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NCBI_TaxID=213763;
  Citrobacter sp. Fec2.
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  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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   Welch R.A., Burland V., Plunkett G. III, Redford P., Ro Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna Nobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete ge of uropathogenic Escherichia coli."; Proc. Natl Acad Sci. U.S.A. 99:17020-17024(2002). EMBL; AE016759; AAN79779.1; -. Complete proteome.
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  COx J.M., Eglezos S., Woolcock J.B.; "Virulence of Salmonella enteritidis in chickens correlates colony morphology and expression of SEF17 fimbriae."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Medupu R., Peterson J.D., Umayam L.A., White O., Welf A.M., Vamathevan J., Weldman J., Impraim M., Lee K., Berry K., Lee C., Vamathevan J., Weldman J., Utterback T.R., McDonald L.A., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."
  01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
Curlin subunit monomer (Frag
   NON TER
  La Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli 078:K80 isolates associated
IS1 inserti on in csgB and reduced persistence in poultry infect
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL, AJ131756; CAB45380.1; -.
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  Kaneko T., Nakamura Y., Sato S., Minamisawa
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., I
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Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., S. Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
  STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darl
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01-WAR-2003 (TrEMBLrel. 23, Last annotation updat
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   "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003). EMBL; AE016981; AAP16542.1; --
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InterPro; IPR000437; Prok_lipoprot_S.
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Complete proteome.
SEQUENCE 157 AA; 16175 MW. Clerco.
   "Complete genome sequence and comparative metabolically versatile Pseudomonas putida Environ. Microbiol. 4:799-808(2002).
  "Genome sequence of Shigella flexneri 2a: insights into through comparison with genomes of Escherichia coli K12 Nucleic Acids Res. 30:4432-4441 (2002).
EMBL; AE015131; AAN42658.1; -.
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Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang Yang J., Yang G., Wu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wer
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  CSGB OR SF1035.
Shigella flexneri.
  MEDLINE=22423060; PubMed=12534463;
  Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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STRAIN=301 / Serotype 2a;
  NCBI_TaxID=623;
   Minor curlin subunit precursor, similar
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  Pseudomonadaceae; Pseudomonas.
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Last annotation updat
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   Score 104.5;
Pred. No. 0.0
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  analysis of the KT2440.";
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  update)
  57;
   16;
  Indels
  H., Qu D., Do
Ding K., Chen
Wen Y., Hou
  Length 160;
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∶
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  March 11, 2004, 18:33:51; Search time 171.3 Seconds (without alignments) 860.386 Million cell updates/sec
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779
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   10:
11:
12:
13:
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2: /cgn2_6/ptodata/2/paa/US06

3: /cgn2_6/ptodata/2/paa/US07
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Listing first 45 su
  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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   summaries
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  6019581
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|                | -                | _                |                   |                  | _              | _               | _                 | -            | ٠.           | •             | _              | _               |               | •               | Ť           | _                | _                | _                | ٠.               | •            | _       | _           |                 |                 | _               | •               | _          | •            | ٠.            | •              | -             | _             |             |               | _           | _               | _           | _             | ٠.          | •             | _             | _          |               | •                 |
|----------------|------------------|------------------|-------------------|------------------|----------------|-----------------|-------------------|--------------|--------------|---------------|----------------|-----------------|---------------|-----------------|-------------|------------------|------------------|------------------|------------------|--------------|---------|-------------|-----------------|-----------------|-----------------|-----------------|------------|--------------|---------------|----------------|---------------|---------------|-------------|---------------|-------------|-----------------|-------------|---------------|-------------|---------------|---------------|------------|---------------|-------------------|
| 98.5           | 8                |                  | 8                 | 8                | m              | 100             | 100               | 100          | 100          | 100           | 100            | 100.5           | •             | •               | 100.5       | 237              | •                | 335              | 347              | ω            | 439     | 7           | 481             | æ               | 481             | $\vdash$        | $\vdash$   | $\vdash$     | $\vdash$      | Ν              | o             | ω.            | 603         | 9             | 605         | 0               | $\vdash$    | $\vdash$      | $\vdash$    | v             | 9             | 695        | 696           | 779               |
| 12.6           | N                | N                |                   | 2                | 2              | ۲               | 2                 |              | 2            | 2             | 12.8           | •               | 12.9          | ۲               | 2           | 30.4             | ۳                | 43.0             | 44.5             | Ġ            | 56.4    | ننو         | μ               | μ               | ũ               |                 | ð          | 6            | ò             | 9              | Ľ             | 4.            | ٧.          | 7             | ١           | 80              | œ           | œ             | 8           | 4.            | œ             | 9          | 89            | 100.0             |
| 1028           | 2                | S                | 850               | ū                | œ              | 26              | 1249              | 1249         | 1249         | 4             | 445            | 186             | 186           |                 | 151         | 48               | 70               | 109              | 68               | 131          | 131     | 109         | s               | 158             | 5               | S.              | 151        | ū            | 151           | 151            | 120           | S             | 151         | лι            | S           | . س             | S           | S             | 151         | 151           |               | iσ         | 151           | iσ                |
| 20             |                  | w<br>W           |                   |                  |                |                 | ω<br>u            |              | 30           |               | 29             |                 | 16            |                 |             | 19               |                  | 19               | 19               | 21           |         | 19          |                 | 16              |                 | ω<br>w          | ယ          | 21           | 13            | 19             | σ             | 19            | 19          | 9             | 19          |                 |             |               | 19          | 19            | σ             |            | 19            |                   |
| -09-614-150A-1 | -09-614-150-1491 | -60-191-681-1901 | -60-191-637-24179 | -09-614-150A-240 | -09-614-150-24 | -10-179-131-931 | US-60-446-775-358 | v            | S            | 9-2063        | -10-369-493-20 | -10-417-886-583 | 09-252-6910-5 | -09-252-691-583 | 09-543-407- | US-09-543-407-39 | US-09-543-407-32 | US-09-543-407-35 | US-09-543-407-37 | 09-741-873B- | 78-878- | 9-543-407-3 | -10-417-886-583 | -09-252-691C-58 | -09-252-691-58  | -60-444-37      | 0-352-946- | -09-741-873B | S-08-978-878- | S-09-543-407-7 | 08-233-642A-5 | -09-543-407-1 | 09-543-407- | -09-543-407-2 | -09-543-407 | -09-543-407-3   | S-09-543-4  | -09-543-407-1 | -09-        | S-09-543-407- | -08-233-642A- | -09-543-4  | -09-543-407-1 | US-09-543-407-12  |
| quence 1       | equence 1491     | nce 1901         | equence 2417      | equence 24084,   | equence 24084, | e 9317,         | e 358             | equence 357, | equence 358, | equence 20638 | equence 20638, | equence 5833,   | e 5833,       | equence 583     | e<br>6,     | 39,              | e 32,            | equence 35,      | equence 37,      | equence 2, A | e 2,    | e 34, Ag    | e 5834,         | equence 5834,   | equence 5834, A | equence 2, Appl | equence 2, | equence 4,   | equence 4,    | Sequence 7,    | quence 55,    | Ø             | equence 30  | equence 22    | equence 28. | equence 31, App | equence 20, | equence 18,   | equence 26, | ce 24,        | 57,           | equence 5, | quence 14,    | Sequence 12, Appl |

# ALIGNMENTS

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RESULT 1

US-09-543-407-12

Sequence 12, Application US/09543407

Sequence 12, Application US/09543407

Sequence 12, Application US/09543407

Sequence 12, Application US/09543407

Sequence 12, Application P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406

CURRENT APPLICATION UNGER: US/09/543,407

CURRENT APPLICATION NOS: 59

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 151

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Result

Score

Query Match Length

DB ID

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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  RESULT 3
US-09-543-407-5
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  US-09-543-407-14
  RESULT 2
US-09-543-407-14
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   S
   밁
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   US-09-543-407-12
  Sequence 5, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
              APPLICANT: Collinson, S. Karen APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
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  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
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ORGANISM: Artificial Sequence
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  61
  61
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  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ--- 117
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Pred. No. 2e-65;
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   Length 151;
   Indels
  20;
   0
  Gaps
   60
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US-08-233-642A-57
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  RESULT 4
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   ; TYPE: PRT; ORGANISM: Salmonella US-09-543-407-5
  Sequence 57, Applicat
GENERAL INFORMATION
Query Match
Best Local Similarity
Matches 135; Conserv
   SOFTWARE: FastSEQ for SEQ ID NO 5
   Best Local Sin
Matches 136;
  TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEG ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
   Query Match
   NUMBER OF SEQ ID
   CURRENT FILING DATE:
   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
  TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
  APPLICATION NUMBER: US/0
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
   MOLECULE TYPE:
   LENGTH: 151
  CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
  APPLICANT:
  APPLICANT:
  TYPE: ami
TOPOLOGY:
   CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
  NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92
  STREET:
  ADDRESSEE:
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
   121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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  Application US/08233642A
  6300 Columbia
   Collinson, S. Karen
Clouthier, Sharon C.
Doran, James L.
   89.2%; ilarity 90.1%; Conservative
  Seed and Berry
   NOS:
  William W.
                88.6%;
   59
Windows Version 4.0
   enteritidis
   2000-04-05
  US/08/233,642A
  Center, 701 Fifth Avenue
  920043.403C3
                Score 690; DB 6; Length 151; Pred. No. 8.6e-65;
   Score 695; DB 19;
Pred. No. 2.5e-65;
4; Mismatches 11;
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   Length 151;
   Indels
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   Gaps
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Conservative

4;

Mismatches

0;

Gaps

0

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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
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  ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major: US-09-543-407-24
  ঠ
   US-09-543-407-26
   RESULT 5
US-09-543-407-24
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  Query Match
Best Local :
   NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24

LENGTH: 151
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   APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
   APPLICANT: White, Aaron P
APPLICANT: Doran, James 1
  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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  121 NNAALVNYDQLVTRVVTHEMAHA-------NNATANQY 151
  121
  121
  13
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   24, Application US/09543407
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  μ
  μ
  Similarity
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  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   Doran, James L.
Collinson, S. Karen
Kay, William W.
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RESULT 8 US-09-543-407-20

Sequence 20, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Asron P.
APPLICANT: Doran, James L.

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   US-09-543-407-18
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   US-09-543-407-18
  S
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Matches
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SEQ ID NO 18
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
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  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
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  Conservative
  Conservative
  Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
   78.7%;
80.8%;
   78.8%;
  6,
   Score 613; DB 19;
Pred. No. 1.4e-56;
7; Mismatches 22;
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Pred. No. 1
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  151
   DB 19;
   151
  PEPTIDE
   Length 151;
   Length 151;
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  0
  0
   Gaps
  Gaps
   120
   120
  60
  60
  120
   120
   60
  60
  0
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   ; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-31
  US-09-543-407-31
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   US-09-543-407-20
  Best Local Similarity Matches 116; Conserv
   Query Match
  SEQ ID NO 31
  Query Match
Best Local Similarity
Matches 122; Conserv
  FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
   APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  TYPE: PRT
ORGANISM: Artificial
   OTHER INFORMATION:
OTHER INFORMATION:
   LENGTH: 131
  FEATURE:
   OTHER INFORMATION:
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  121
   121
   61
   81
  21
   61
   61
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  GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                 AHANNATANOY 151
   VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEM 140
   VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV
  GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
  NNAALVNOTASDSSVMVROVGFGNNATANQY 151
   SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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  Application US/09543407
  Conservative
  Conservative
   Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment
   sequence containing the replacement fragmer encoding PT3 from GP63 of Leishmania major.
  78.4%;
80.8%;
  78.0%;
  4.
  7;
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Pred. No. 3.9e-56;
4; Mismatches 11
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Pred. No. 2.2e-56;
7; Mismatches 22;
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   PEPTIDE SEQUENCES
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   Length 151;
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  Indels
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  <u>.</u>
  Gaps
  Gaps
   120
  60
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; FEATURE:
; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragmen; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major US-09-543-407-22
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   US-09-543-407-22
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   ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragmen; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-28
  US-09-543-407-28
  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
  Sequence 22, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
        Matches 122;
                        Query Match
Best Local Similarity
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 151
TYPE: PRT
CURGANISM: Artificial Sequence
  GENERAL INFORMĀTION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENVATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
RUMBER OF SEO ID NOS: 59
   Matches 121;
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Best Local Similarity
  Sequence 28,
   TYPE: PRT
ORGANISM: Artificial Sequence
  FEATURE:
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  61
  61
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  SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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   PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
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   77.7%;
    Score 604; DB Pred. No. 1.2e 6; Mismatches
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   <u>ن</u>
   Score 605; DB 19;
Pred. No. 9.8e-56;
   Mismatches
    DB 19;
l.2e-55;
les 23;
  e replacement fragmer
of Leishmania major.
  PEPTIDE SEQUENCES
  Length 151;
  Length 151;
      Indels
   Indels
    0;
  0;
Gaps
  Gaps
    0;
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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  RESULT 13
US-09-543-407-16
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  밁
   US-09-543-407-30
   US-09-543-407-30
   APPLICANT: White, Aaron P.
APPLICANT: Colinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 30
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  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  TYPE: PRT ORGANISM: Artificial Sequence
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   FEATURE:
ORGANISM: Artificial Sequence
   LENGTH: 151
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   121
  121 NNAALVNYDQLVTRVVTHEMAHANNATANOY 151
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   61
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHNNGGGNSSGPDSTLSIYQYGSANAALALQ
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  Application US/09543407
  Conservative
   77.4%;
  6
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Pred. No. 1.6e-55;
6; Mismatches 23;
   151
  PEPTIDE SEQUENCES
   Length 151;
  Indels
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  Gaps
  120
   60
  60
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   US-08-233-642A-55
   US-09-543-407-16
  US-08-233-642A-55
Query Match 71.9%; Score 560; DB 6; Length 120. Best Local Similarity 100.0%; Pred. No. 4.5e-51; Matches 106; Conservative 0; Mismatches 0; Indels
   Sequence 55, Applicat GENERAL INFORMATION: APPLICANT: KAY, W
   Matches 121; Conservative
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Best Local Similarity
   TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 55:
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  APPLICANT:
APPLICANT:
  ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
   NUMBER OF SEQUENCES: 5
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS:
  SEQUENCE CHARACTERISTICS:
  REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  MOLECULE TYPE:
   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONBILLATITLE OF INVENTION: BASED VACCINES
   LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
   APPLICATION NUMBER: US/08/233,642A FILING DATE: 26-APR-1994 CLASSIFICATION: 424
   STREET: 6300 (
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
  STATE: Washington COUNTRY: U.S.A. ZIP: 98104-7092
   ADDRESSEE:
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
   61
  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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   1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
  Application US/08233642A
  6300 Columbia
  Kay, William W.
Collinson, S. Karen
Clouthier, Sharon C.
Doran, James L.
   Seed and Berry
  protein
   William W.
  74.5%;
80.1%;
  Center,
   920043.403C3
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Pred. No. 4.5e-53;
  701 Fifth Avenue
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  120
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S

22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV

81

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Sequence 7, Application US/09543407

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION UNMERSE: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRASESEQ for Windows Version 4.0
LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli
US-09-543-407-7
Search completed: March 11, 2004, 19:13:09 Job time: 172.3 secs
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   RESULT 15
US-09-543-407-7
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||||||| ||| |||||||||| 60
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  82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
  1 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
  GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
  GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
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  March 11, 2004, 18:35:05 ; Search time 5.3 Seconds (without alignments) 376.014 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| Regult<br>No. | Score | Query<br>Match | Length | BB  | ID                  | Description       |
|---------------|-------|----------------|--------|-----|---------------------|-------------------|
| 1             | 517   | 66.4           | 151    | 5 ! | US-09-741-873C-4    | Sequence 4, Appli |
| 2             | 439   | 56.4           | 131    | v   | -09-741-8           | Sequence 2, Appli |
| ω             | 92    |                | 1327   | ۲   | PCT-US04-02338-49   | e 49,             |
| 4             | 91.5  |                | 443    | 6   | 0-100-683-76        | e 760             |
| Ç)            |       | 11.6           | 234    | σ   | US-10-767-701-45603 | e 45603,          |
| 6             | 85    | 10.9           | 956    | o   | US-10-093-037A-63   | Sequence 63, Appl |
| 7             | 82    | 10.5           | 386    | σ   | US-10-100-683-10326 | e 1032            |
| 8             | 82    | 10.5           | 386    | თ   | US-10-100-683-10327 | e 103             |
| 9             | 81.5  | 10.5           | 1871   | _   | PCT-US03-02038-26   | e 26,             |
| 10            | 78.5  | 10.1           | 430    | ტ   | US-10-451-467A-314  | e 314             |
| 11            | 77    | 9.9            | 351    | ۲   | PCT-US04-05654-1755 | Sequence 1755, Ap |
| 12            | 76    | 9.8            | 250    | σ   | US-10-779-461-40    | e 40,             |
| 13            | 76    | •              | 321    | ۲   | PCT-US04-05654-590  | e 590,            |
| 14            | 76    | 9.8            | 382    | Q   | US-10-771-241-299   | e 299,            |
| 15            | 75    | 9.6            | 399    | _   | PCT-US04-05654-2748 | Sequence 2748, Ap |
| 16            | 75    | 9.6            | 424    | σ   | US-10-045-674A-591  |                   |
| 17            | 75    | 9.6            | 533    | 0   | US-10-045-674A-527  |                   |
| 18            | 74.5  |                | 1160   | σ   | US-10-603-150-2     | Sequence 2, Appli |
| 19            | 74    | 9.5            | 191    | σ   | US-10-767-701-47075 | e 47              |
| 20            | 74    |                | 250    | O   | US-10-779-461-6     | Sequence 6, Appli |
| 21            | 73    |                | 205    | σ   | US-10-767-701-40104 | Sequence 40104, A |
| 22            | 73    |                | 246    | δ   | US-10-779-461-41    | Sequence 41, Appl |
| 23            | 72.5  | 9.3            | 318    | σ   | US-10-417-884A-5818 | 581               |
| 24            | 72    | 9.2            | 434    | თ   |                     | 594, 1            |
| 25            | 71.5  | 9.2            | 179    | თ   | -10-767-701-42      | m.                |
| 26            | 71.5  | 9.2            | 251    | σ   | US-10-767-701-32417 | Sequence 32417, A |
|               |       |                |        |     |                     |                   |

|                    | 70 9             | 70 9                | 70 9                | 70 9                | -                   | -                 | -                 | -                 | 70.5 9              | -                 | -                 | 71 9             | 71 9                | 71 9             | 71 9              | 71 9            | 71 9                | 71.5 9            |
|--------------------|------------------|---------------------|---------------------|---------------------|---------------------|-------------------|-------------------|-------------------|---------------------|-------------------|-------------------|------------------|---------------------|------------------|-------------------|-----------------|---------------------|-------------------|
|                    | .0 245           |                     |                     |                     |                     |                   |                   |                   |                     |                   |                   | 9.1 619          |                     |                  |                   |                 | .1 125              | .2 471            |
| -                  | σ                | ტ                   | σ                   | 9                   | _                   | σ                 | σ                 | σ                 | σ                   | σ                 | σ                 | σ                | 1                   | σ                | σ                 | σ               | σ                   | σ                 |
| PCT-US04-05654-334 | US-10-779-461-59 | US-10-767-701-51583 | US-10-767-701-35342 | US-10-767-701-35046 | PCT-US04-05654-2086 | US-10-627-556-398 | US-10-627-556-402 | US-10-627-556-400 | US-10-767-701-45455 | US-10-627-556-396 | US-10-627-556-392 | US-10-695-499-70 | PCT-US04-05654-1756 | US-10-695-499-68 | US-10-695-499-192 | US-10-786-850-4 | US-10-767-701-58970 | US-10-746-795A-22 |
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| 334, App           | 59, Appl         | 51583, A            | 35342, A            | 35046, A            | 2086, Ap            | 398, App          | 402, App          | 400, App          | 45455, 1            | 396, App          | 392, App          | 70, Appl         | 1756, Ap            | 68, Appl         | 192, App          | 4, Appli        | 58970, 1            | 22, Appl          |

# ALIGNMENTS

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   CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1999-11-06
PRIOR PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR PRIOR DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1992-11-28
PRIOR FILING DATE: 1992-11-08
PRIOR FILING DATE: 1992-11-08
PRIOR FILING DATE: 1992-11-08
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  PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
  APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION. Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
  LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli
121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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   66.4%; Score 517; DB 5; Length 151; 66.2%; Pred. No. 1.2e-38; Length 151; 66.2%; Pred. No. 1.2e-38; Indels
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  PCT-US04-02338-49
  US-09-741-873C-2
   CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR TILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR PELICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
  US-09-741-873C-2
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Matches 82; Conserv
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  Sequence 49, Application PC/TUS0402338 GENERAL INFORMATION:
   SOFTWARE:
SEQ ID NO 2
  PRIOR APPLICATION NUMBER: US60/461,789
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US60/479,650
PRIOR FILING DATE: 2003-06-19
   Sequence 2, Application US/09741873C GENERAL INFORMATION:
  TITLE OF INVENTION: MARCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS TITLE OF INVENTION: USE FILE REFERENCE: EXO4-003C-PC CURRENT APPLICATION NUMBER: PCT/US04/02338 CURRENT FILING DATE: 2004-01-28 PRIOR APPLICATION NUMBER: US60/443,484 PRIOR APPLICATION NUMBER: US60/443,484 PRIOR FILING DATE: 2003-01-29
  PRIOR APPLICATION NUMBER: US60/447,358 PRIOR FILING DATE: 2003-02-11
  APPLICANT:
  NUMBER OF SEQ ID NOS:
  CURRENT APPLICATION NUMBER: US/09/741,873C
  TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation FILE REFERENCE: 012899-084
   APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
   TYPE: PRT
ORGANISM: Escherichia coli
   LENGTH: 131
NO 49
   APPLICATION NUMBER: US 07/970,846
FILING DATE: 1992-11-03
APPLICATION NUMBER: US 08/187,865
FILING DATE: 1994-01-28
APPLICATION NUMBER: US 08/318,519
  FILING DATE:
   141 AHANNATANOY 151
  121 GFGNNATAHOY 131
  61
  18
  21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                  PatentIn
  SEQ ID NOS:
   PatentIn version 3.0
   VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEM 140
  GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
   EXELIXIS, INC
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  2003-06-19
  1994-10-05
  56.4%;
  21;
  Score 439; DB 5;
Pred. No. 6.9e-32;
  Mismatches
  28;
  Length 131;
  Indels
  0,
  60
   80
   QF
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  ; ORGANISM: Homo sapiens US-10-100-683-7608
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US-10-100-683-7608
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  ; TYPE: PRT
; ORGANISM: Hom-
PCT-US04-02338-49
  Query Match
Best Local Similarity
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   Matches
  Sequence 7608, Appl. GENERAL INFORMATION
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SOFTWARE: PatentIn Ver. 2.0
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   CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
  TYPE: PRT
   PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
  TITLE OF INVENTION: Human Secreted Proteins
  FILE REFERENCE: PS900
   LENGTH: 443
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   APPLICATION NUMBER: US 60/043,576
FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,601
FILING DATE: 1997-05-23
  FILING DATE: 1997-05-23
   APPLICATION NUMBER: US 60/043,314 FILING DATE: 1997-04-11 APPLICATION NUMBER: US 60/047,632
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   FILING DATE: 1997-05-23
 298
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   99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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                                 VGQYGGN 121
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  Application US/10100683
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  11.7%;
26.0%;
  11.8%; Score 92; 1
30.4%; Pred. No. 2
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  Score 91.5; DB Pred. No. 0.72;
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   ore 92; DB 1; Length 1327 ed. No. 2.5; Mismatches 57; Indels
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   237
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RESULT

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  US-10-093-037A-63
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   ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82834_1.pep
US-10-767-701-45603
   US-10-093-037A-63
   US-10-767-701-45603
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   Sequence 63, Application US/10093037A GENERAL INFORMATION:
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   CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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   CURRENT APPLICATION NUMBER: US/10/093,037A CURRENT FILING DATE: 2002-03-06 PRIOR APPLICATION NUMBER: US 09/910,579 PRIOR FILING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: US 09/134,078 PRIOR APPLICATION NUMBER: US 09/134,078 PRIOR APPLICATION NUMBER: US 09/134,078 PRIOR APPLICATION NUMBER: US 08/949,026 PRIOR APPLICATION NUMBER: US 08/949,026 PRIOR FILING DATE: 1997-10-10
  APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
  APPLICANT: Kovalic, Dav
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwe
  NUMBER OF SEQ ID NOS:
  PRIOR FILING DATE: 1996-12-06
  TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF FILE REFERENCE: 564462001402
   APPLICANT:
   APPLICANT: Jay M. Short APPLICANT: Bylina, Edw
   TYPE: PRT
ORGANISM: Bankia
  TYPE: PRT
ORGANISM: Sorghum bicolor
  LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
  NAME/KEY: unsure LOCATION: (1)..(
  ENGTH:
  FEATURE:
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Local Similarity 21.5
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  103 QAGGSGS-----NGGAYAQGGAQGGGGGGGQYGGSGS 134
   83
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   61 GXYGEAGGSGXAYAQGGGQGGGGGGGGQYGGSG-----
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  1 MKLLKVAAFAAIVV--SGSALAGVVPQW---GGGGNHNGGGN------SSGPDSTL 45
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   QGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNA 123
   Swanson, Ronald V. Mathur, Eric J.
   Lam, David E.
   Bylina, Edward
   Application US/10767701
  for Windows Version 4.0
   David K.
   11.6%;
                 10.9%;
   19;
   12;
Score 85; DB
Pred. No. 6.8;
19; Mismatches
   Score 90.5; D
Pred. No. 0.4;
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  82
  60
   6
   9
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US-10-100-683-10327
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  US-10-100-683-10326
   US-10-100-683-10326
Sequence 10327, Application US/10100683
GENERAL INFORMATION:
APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS900
CURRENT APPLICATION NUMBER: US/10/100,683
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PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
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CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/40,162
PRIOR FILING DATE: 1997-03-07
PRIOR FILING DATE: 1997-03-07
   PRIOR FILING DATE: 1997-08-22
  PRIOR
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  ORGANISM: Homo sapiens
   TYPE: PRT
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  APPLICATION NUMBER: US 60/047,632 FILING DATE: 1997-05-23 APPLICATION NUMBER: US 60/056,892
   FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,845
  FILING DATE: 1997-08-22
APPLICATION NUMBER: US 60/043,314
   FILING DATE: 1997-04-11
   APPLICATION NUMBER: US 60/056,664
   FILING DATE: 1997-05-23
   APPLICATION NUMBER: US 60/047,599
  FILING DATE: 1997-04-11
  APPLICATION NUMBER: US 60/043,580
  FILING DATE: 1997-08-22
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   12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT
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   GDYWNIKDIEFKTGSKGIVLDNSNGSKLKN---LVVHDIGEEAIHLRDGSSN 475
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Pred. No.
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  B
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; ORGANISM: Mus musculus
PCT-US03-02038-26
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PCT-US03-02038-26
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   US-10-100-683-10327
  NUMBER OF SEQ ID NOS: 221
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 26
   Sequence 26, Application PC/TUS0302038
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
TITLE OF INVENTION: and Proteins
FILE REFERENCE: 07039/386W01
CURRENT APPLICATION NUMBER: PCT/US03/02038
CURRENT FILING DATE: 2003-01-23
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PRIOR PILING DATE: 2002-01-23
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SOFTWARE: PatentIn Ver. 2.0
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  LENGTH: 1871
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,845
FILING DATE: 1997-08-22
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  APPLICATION NUMBER: US 60/040,162 FILING DATE: 1997-03-07
  APPLICATION NUMBER: US 60/043,580 FILING DATE: 1997-04-11
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23.0%; Pred. No. 31;
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  Score 82;
Pred. No.
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  DB 1;
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  42;
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; Sequence 1755, Application PC/TUS0405654
; GENERAL INFORMATION:
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   US-10-451-467A-314
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US-10-451-467A-314
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  Ś
  멍
   SEQ ID NO 314
  Matches
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  APPLICANT: Sherman, Bradley K
APPLICANT: Sherman, Jose Luis
                  REPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYMOCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
   APPLICANT:
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   SOFTWARE:
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PRIOR FILING DATE: 2001-01-04
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CURRENT FILING DATE: 2003-06-19
  LENGTH: 43
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  NUMBER OF SEQ ID NOS: 732
  PRIOR APPLICATION NUMBER: EP 01870003.9 PRIOR FILING DATE: 2001-01-09
   PRIOR APPLICATION NUMBER: EP 00870318.3
   APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
   APPLICANT:
  APPLICANT: CONTRERAS, ROLAND HENRI
  ORGANISM: Saccharomyces cerevisiae
   APPLICANT:
  Local
  143 NN---DSYGSNNN---DSYGSNNND----SYGSNN 167
  INFORMAT
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  89 GSNNNDSYGSNNNDS---
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   314, Application US/10451467A
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1 Similarity 28.4%;
27; Conservative 1:
   98
   430
   PatentIn version 3.1
  Gutterson, Neal
Yu, Guo-Liang
Broun, Pierre E
   Repetti, Peter
Century, Karen
  DNTEL --
  Dubel
   Pineda, Omaira
  Haake, Volker
   Riechmann, Jose
Jiang, Cai-Zhong
  Keddie, James
   Heard, Jacqueline E
  LUYTEN, WALTER HERMAN MARIA LOUIS
  EBERHARDT,
  lman, Robert A
  l III, Arnold N
   Luc J
NUMBER: PCT/US04/05654
   Lynne
  INES
   Oliver
  12;
  Score 78.5; DB
Pred. No. 9.5;
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  Gaps
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PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2003-02 CURRENT FILING DATE:

2003-02-25

2004-03-03

10/374,780

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   PCT-US04-05654-590
  RESULT 13
   US-10-779-461-40
  ; OTHER INFORMATION: Orthologous to G1794 PCT-US04-05654-1755
  US-10-779-461-40
   Sequence 590, Application PC/TU
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
   Sequence 40, Applica GENERAL INFORMATION:
  PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1755
LENGTH: 351
  SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
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CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
   APPLICANT: MORTON, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR
FILE REFERENCE: 00980/1
  APPLICANT:
  APPLICANT:
                                  APPLICANT:
  TYPE: PRT ORGANISM: artificial FEATURE:
   TYPE: PRT
ORGANISM: Oryza saciva
  OTHER INFORMATION: phage display generated human antibody
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   9 FAAIVVSGSALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALAL 59
   YCAISPLRGLTADVFDVWGQGTLVTVSSGGGGGGGGGGGGGG
   AGYACGGAPSPEFAGSEQSSDTQSA--SAATMDEHHS----PVG--GGGNA 120
   SGYG-NGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNA 123
   SALARVVAGGGGGGGGDGDQWAWSSPSPSSS-----AAAAAARGVQERRREEQAMHEL
                          Heard, Jacqueline E
Haake, Volker
  Jiang, Cai-Zhong
   Application US/10779461
Creelman, Robert A
Ratcliffe, Oliver
  Riechmann,
  Application PC/TUS0405654
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  9.9%;
   30.6%;
  Jose Luis
  9.8%;
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Pred. No. 10;
  Score 76; I
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   20;
  Gaps
   Gaps
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   PCT-US04-05654-590
   SEQ ID NO 590
LENGTH: 321
TYPE: PRT
ORGANISM: Oryza sativa
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  TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN TITLE OF INVENTION: ESCHERICHIA COLI FILE REFERENCE: ELITRA, 001C1 CURRENT PALICATION NUMBER: US/10/771,241 CURRENT PILING DATE: 2004-02-03
  APPLICANT:
  NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
  PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
   CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR PPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
   APPLICANT:
  SOFTWARE: PatentIn version 3.2
   APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
   APPLICANT:
   APPLICANT:
  ORGANISM: E. Coli
  TYPE: PRT
  FEATURE: OTHER INFORMATION: G3384 Orthologous
   APPLICANT:
  APPLICANT:
   APPLICANT:
  Local Similarity
nes 38; Conserv
158 GNTHGGNTSSGTSGYSSLNYRGAYGNTNVGYSRSGDS--SQIYYGMSGGIIAHADGITFG
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  199 AAYASSADNIARLLQGWMRPGGG----GGGNGKGPEAS-----GSTSTTATTQQQPQCS 248
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  67 ETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATID--QWNAKNSDITVGQYGGNNA 123
   10 AAIVVSGSALAGVVPQW---GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKS 66
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  Pineda, Omaira
Repetti, Peter
Century, Karen
  Reuber, T. Ly
Keddie, James
  Yu, Guo-Liang
  Broun, Pierre E
   Dubell III, Arnold N
  Application US/10771241
  Conservative
  Conservative
   Luc J
  for Windows Version 3.0
   9.8%;
   9.8%;
   Lynne
   -GEGAASASASASQSGAAAAATAQTPECSTETSKMATGGGAGGPA 292
   13;
  18;
   Score 76; DB
Pred. No. 11;
   Score 76;
Pred. No.
  Mismatches
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  to G256
  DB 6; Length 382;
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  42;
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  Indels
  Indels
  36;
  30;
  Gaps
 215
```

```
APPLICANT: Century, Kareman APPLICANT: Gutterson, Neal APPLICANT: Gutterson, Neal APPLICANT: Yu, Guo-Liang APPLICANT: Broun, Pierre B APPLICANT: Broun, Pierre E APPLICANT: Broun, Pierre E APPLICANT: Pilgrim, Marsha L TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS FILE REFERENCE: MBI-0047 PCT CURRENT FILING DATE: 2004-03-03

PRIOR APPLICATION NUMBER: 10/374,780

PRIOR APPLICATION NUMBER: 10/374,780

PRIOR APPLICATION NUMBER: 10/675,852

PRIOR PILING DATE: 2003-09-30

NUMBER OF SEQ ID NOS: 2950

SOFTWARE: Patentin version 3.2

SEQ ID NO 2748

LENGTH: 399

TYPE: PRI
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G1882

PCT-US04-05654-2748

9.6%; Score 75; DB 1; Length 399;
Search completed: March 11, 2004, 19:14:15 Job time: 6.3 secs
   밁
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   В
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  밁
  RESULT 15
PCT-US04-05654-2748
  밁
  Ş
  GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
  APPLICANT:
APPLICANT:
APPLICANT:
   APPLICANT:
   PPLICANT:
   PPLICANT:
   PPLICANT:
  / Match 9.6%; Score 75; DB 1; Length 399;
Local Similarity 26.7%; Pred. No. 18;
les 32; Conservative 14; Mismatches 58; Indels
   215 NSNNNNILGLGSSLPPLKLMPPLDFTDNFTLQYGAVSAPSYHIGGGSSGGAAALLNGFDQ 274
  155 GGGGGSTSSGNSKSODSATSNDOYHHRAMANNOMGPPSSSSSLSSLLSSYNAGLIPGHDH 214
  77 --- NGADVGQGADNSTIBLTQN-GFRNNATIDQW--NAKNSDITVGQYGGNNAALVNYDQ 130
   270 ADNVELDETVVTVIPTH 286
   126 --- VNYDQLYTRVV-TH 138
   27 GGGGNHNGGGNSSGPDSTLSIYQY---GSANAALALQSDARKSETTITQSGYG----- 76
   83
  748, Application PC/TUS0405654
  QPLGDTMVLVKAPĠADNVKİĖ-NQTĞIHTD-----WRGYAILPFATEYRENRVALNANSL 269
   Riechmann, Jose Luis
Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
   Q------GADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAAL----- 125
  Reuber, T. Lynne
Keddie, James
Dubell III, Arnold N
   Repetti, Peter
Century, Karen
   Creelman, Robert A
   Ratcliffe, Oliver
  ineda, Omaira
   58; Indels 16; Gaps
```

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Fri Mar 1
```

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Database
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Perfect score:
  Maximum
  Minimum
  Scoring table:
   OM protein -
  Post-processing:
   Total number of hits satisfying chosen parameters:
   Searched:
   8
   DB seq length: 0
DB seq length: 2000000000
  Pending P
1: /cgn2
2: /cgn2
3: /cgn
4: /cgr
5: /cr
6: /c
7: /
8:
9:
  protein search, using sw model
               6019581 seqs, 976053577 residues
  Gapop 10.0 , Gapext 0.5
  BLOSUM62
  US-09-543-407-14
775
   March 11, 2004, 18:33:51 ; Search time 171.3 Seconds (without alignments) 860.386 Million cell updates/sec
  Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/2/paa/US085_COMB.pep:*
/cgn2_6/ptodata/2/paa/US095_COMB.pep:*
/cgn2_6/ptodata/2/paa/US090_COMB.pep:*
/cgn2_6/ptodata/2/paa/US100_COMB.pep:*
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  Copyright
   ding_Patents_AA_Main:*
/cgn2_6/ptodata/2/paa/PCTUS
/cgn2_6/ptodata/2/paa/US06_
/cgn2_6/ptodata/2/paa/US07_
  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
  COMB.pep:
  HASVMVRQVGFGNNATANQY 151
   6019581
```

# ALIGNMENTS

```
RESULT 1

US-09-543-407-14

Sequence 14, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Cay, William W.
ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 151

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
```

Regult No.

Score

Query Match Length DB

IJ

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

```
Sequence 24, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

APPLICANT: Kay, William W.

APPLICANT: Kay, William W.

ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER

CURRENT FAILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 151

TYPE: PRT
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   ₽
   S
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment oTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-24
  US-09-543-407-14
  S
   Ъ
   5
   밁
  5
   US-09-543-407-24
  B
   US-09-543-407-12
   Query Match
Best Local Similarity
Matches 151; Conserv
          Sequence 12, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Optan, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  Matches
  Query Match
Best Local Similarity
CURRENT APPLICATION NUMBER: US/09/543,407
   FEATURE:
  ORGANISM: Artificial Sequence
   121
   121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
  144;
  114
  121
  61
  61
   61
   19
   \vdash
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   _
  \vdash
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
  SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYDO 120
  SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDQWNAKNSDITVGQYDQ
  LVTRVVTHEMAHA-----SVMVRQVGFGNNATANQY 151
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNINGGGNSSGPDSTLSIYQYGSANAALALQ 60
  LVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
   SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKN---
   100.0%; Score 775; DB 19; illarity 100.0%; Pred. No. 6.1e-75; Conservative 0; Mismatches 0.
  Conservative
  92.1%;
  0;
  Score 714; DB 19;
Pred. No. 2.4e-68;
0; Mismatches 0
  0;
   PEPTIDE SEQUENCES
  PEPTIDE SEQUENCES
  Length 151;
   Indels
  Length
  Indels
  151;
  14;
   0,
  Gaps
   -YDQ
  120
   60
   60
   113
   60
   0
```

```
APPLICANT: White, Aaron P.
APPLICANT: Woran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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  밁
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  US-09-543-407-12
   US-09-543-407-5
   RESULT 4
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   , ORGANISM: Salmonella enteritidis US-09-543-407-5
                         Ş
  문
  뮍
   8
   CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12
LENGTH: 151
   SOFTWARE: FastSEQ for Windows Version SEQ ID NO 5
LENGTH: 151
  Query Match
Best Local (
   GENERAL INFORMATION:
   Matches 141;
  Matches
  Query Match
Best Local Similarity
   FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  ORGANISM: Artificial Sequence
  LENGTH: 1:
TYPE: PRT
  TYPE: PRT
   Local Similarity
   121
   118
                     121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
  137;
   61
  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ---
121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
   61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   NNAALVNYDOLVTRVVTHEMAHA------
   -----YDQLVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   Application US/09543407
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  Conservative
  Conservative
  89.8%;
  89.4%;
   0,
  ω
••
  Score 693; DB 19;
Pred. No. 4.4e-66;
3; Mismatches 11;
  Score 696; DB 19;
Pred. No. 2.1e-66;
   Mismatches
     151
  -NNATANQY
  PEPTIDE SEQUENCES
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  Length 151;
   Indels
  151
   20;
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   Gaps
  120
   117
   60
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RESULT 5
US-08-233-642A-57
; Sequence 57, Application US/08233642A
; GENERAL INFORMATION:
; APPLICANT: Kay, William W.

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collingon, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 151
  문
  В
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   US-09-543-407-30
  , MOLECULE TYPE: protein US-08-233-642A-57
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILLING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT
  Best Loc
Matches
   Sequence 30, Application US/09543407 GENERAL INFORMATION:
  Query Match
  ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Cen
   APPLICANT: Collinson, S. Karen APPLICANT: Clouthier, Sharon C. APPLICANT: Doran, James L. TITLE OF INVENTION: METHODS AND TITLE OF INVENTION: BASED VACCI
   NUMBER OF SEQUENCES:
   TOPOLOGY:
  TYPE: amino acids
  TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
  STATE: Washing
   Local
  ZIP: 98104-7092
   COUNTRY:
  121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
   121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
  tch 89.3%; al Similarity 90.7%; 137; Conservative
  61
  61
  ш
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   Washington
  BASED VACCINES
58
  METHODS AND COMPOSITIONS FOR SALMONELLA-
  Center,
  ω
••
  920043.403C3
  Score 692; DB 6; I
Pred. No. 5.6e-66;
3; Mismatches 11;
  701 Fifth
   AL SYSTEM FOR HETEROLOGOUS
  Version
  Avenue
  #
   Length 151;
   PEPTIDE
  Indels
   SEQUENCES
  <u>,</u>
  Gaps
  60
  60
  0
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RESULT 8 US-09-543-407-18

Sequence 18, Application US/09543407 GENERAL INFORMATION: APPLICANT: White, Aaron P. APPLICANT: Doran, James L.

```
; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-26
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                                 5
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  US-09-543-407-26
   밁
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  S
  US-09-543-407-30
   Query Match
Best Local S
Matches 123
   SEQ ID NO 26
LENGTH: 151
TYPE: PRT
  Sequence 26, Application US/09543407 GENERAL INFORMATION:
   Query Match
Best Local Similarity
Matches 136; Conserv
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
   FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
  NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
  ORGANISM: Artificial Sequence FEATURE:
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                        121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY
  121 LVTRVVTHEMAHA-------SVMVRQVGFGNNATANQY
   123;
   106 LVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
  61
   61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  ب
  1 MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSI YQYGSANAALALQ
  Similarity
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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   Conservative
  79.0%;
81.5%;
  85.0%;
   <u>ن</u>
   <u>,</u>
  Score 612; DB 19;
Pred. No. 2.5e-57;
  Score 659; DB 19;
Pred. No. 2.1e-62;
   Mismatches
   Mismatches
                                 151
 151
   23;
   0
  PEPTIDE SEQUENCES
   Length 151;
   Length 151;
   Indels
   Indels
   30;
   0,
   Gaps
   Gaps
  60
   60
  60
   60
   0
   N
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   US-09-543-407-20
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  US-09-543-407-20
   RESULT 9
   밁
   á
   US-09-543-407-18
  Matches
   Query Match
Best Local (
   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 20
  Sequence 20, Application US/09543407 GENERAL INFORMATION:
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
  Matches
   Query Match
Best Local :
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
   TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM TITLE OF INVENTION: PRESENTATION OF HETEROLOGISTIC REFERENCE: 920043.406
   APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial
  FEATURE:
  TYPE: PRT
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   LENGTH: 151
  TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
   Local Similarity
            61
   61
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   121
  123;
  61
   щ.
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   Similarity
  LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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  Conservative
  Conservative
   78.6%;
81.5%;
   Sequence
   78.8%;
81.5%;
  ი
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  Score 609; DB 19;
Pred. No. 5.2e-57;
6; Mismatches 22;
  Score 611; DB 19;
Pred. No. 3.2e-57;
6; Mismatches 22;
  HETEROLOGOUS PEPTIDE SEQUENCES
   FOR
   Length 151;
  Indels
   Length 151;
  Indels
  0,
  0;
  Gaps
  Gaps
   60
   60
  60
  0,
```

```
APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.

ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 131
TYPE: PRT
ORGANISM: Salmonella enteritidis
US-09-543-407-31
   APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI

FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 151
  US-09-543-407-28
  RESULT 11
US-09-543-407-28
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   문
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  Дb
  Ś
      Query Match
Best Local S
Matches 122
   US-09-543-407-31
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  Sequence 28, Application US/09543407 GENERAL INFORMATION:
   Query Match
Best Local Similarity
  Sequence 31, Applica GENERAL INFORMATION:
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  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
  APPLICANT: White, Aaron P.
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   121 GEGNNATANOY 131
   141 GFGNNATANOY
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Score 603; DB 19;
Pred. No. 2.3e-56;
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Pred. No. 9e-57;
   DB 19;
   11; Indels
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   PEPTIDE SEQUENCES
   Length 131;
    Indels
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   Gaps
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   0
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REFERENCE: 920043.406
CURRENT APPLICATION UNMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 16
LENGTH. . .
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   RESULT 13
US-09-543-407-16
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  US-09-543-407-22
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  US-09-543-407-22
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  FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
  Sequence 22, Applica GENERAL INFORMATION:
   Matches
  Query Match
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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81.5%;
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Pred. No. 3e-56;
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GENERAL INFORMATION:
APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
ITILE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 801723-1
EARLIER APPLICATION NUMBER: OB01723-1
   RESULT 15
US-08-978-878-4
  밁
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  ; TYPE: PRT
; ORGANISM: Escherichia
US-09-543-407-7
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   S
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US-09-543-407-7
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   NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
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Best Local Similarity
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  Query Match
Best Local Similarity
  GENERAL INFORMATION:
   APPLICANT: White, Aaron P.
APPLICANT: White, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM
TITLE OF INVENTION: PRESENTATION OF HETEROLOG
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
  FILE REFERENCE: 920043.406
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leighmania major.
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   Conservative
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   68.1%; Score 528; DB 19; 68.9%; Pred. No. 2.9e-48; tive 20; Mismatches 27;
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Pred. No. 1.2e-53;
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EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER FILING DATE: 1991-11-06
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1995-06-28
EARLIER APPLICATION NUMBER: US 08/318,519
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EARLIER FILING DATE: 1995-06-28
INUMBER OF SEQ ID NOS: 10
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SOSTWARE: PATENTIN Ver. 2.0
Search completed: March 11, 2004, 19:13:10 Job time: 172.3 secs
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   Query Match 67.7%; Score 525; DB 13; Length 151; Best Local Similarity 68.2%; Pred. No. 6.1e-48; Matches 103; Conservative 21; Mismatches 27; Indels 0;
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   121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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Maximum Match 100%
Listing first 45 summaries
   Minimum DB
Maximum DB
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  Title:
Perfect score:
  OM protein -
  Total number of hits satisfying chosen parameters:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  85.5
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| 8.8              | 8.8                 | 8.8                | 8.9             | 8.9             | 9.0                 | 9.0               | 9.0              | 9.0                 | 9.0                 | 9.1               | 9.1               | 9.1               | 9.1                 | 9.1               | 9.1               | 9.1                 | 9.1                 | 9.2                 |
| 251              | 175                 | 430                | 616             | 250             | 624                 | 348               | 245              | 199                 | 175                 | 521               | 505               | 505               | 351                 | 273               | 273               | 251                 | 226                 | 447                 |
| σ                | σ                   | σ                  | σ               | 9               | ۳                   | σ                 | σ                | σ                   | σ                   | σ                 | σ                 | 6                 | <b>ب</b>            | σ                 | σ                 | σ                   | 6                   | 9                   |
| US-10-779-461-30 | US-10-767-701-59665 | US-10-451-467A-314 | US-10-467-243-1 | US-10-779-461-6 | PCT-US04-05654-1466 | US-10-004-115B-34 | US-10-779-461-59 | US-10-767-701-51583 | US-10-767-701-35046 | US-10-627-556-398 | US-10-627-556-402 | US-10-627-556-400 | PCT-US04-05654-1755 | US-10-627-556-396 | US-10-627-556-392 | US-10-767-701-32417 | US-10-767-701-51685 | US-10-767-701-45219 |
| Sequence         | Sequence            | Sequence           | Sequence        | Sequence        | Sequence            | Sequence          | Sequence         | Sequence            | Sequence            | Sequence          | Sequence          | Sequence          | Sequence            | Sequence          | Sequence          | Sequence            | Sequence            | Sequence            |
| 30, Appl         | 59665, A            | 314, App           | 1, Appli        | 6, Appli        | 1466, Ap            | 34, Appl          | 59, Appl         | 51583, A            | 35046, A            | •                 | 402, App          | 400, App          | 1755, Ap            | 396, App          | 392, App          | 32417, A            | 51685, A            | 45219, A            |

# ALIGNMENTS

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FILE REFERENCE: 01289-084
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1990-05-04
PRIOR FILING DATE: 1990-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEO ID NOS: 11
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 4
LENGTH: 151
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  US-09-741-873C-4
  US-09-741-873C-4
   Query Match
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Matches 103;
   APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
  LENGTH: 151
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ORGANISM: Escherichia coli
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121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
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   67.7%; Score 525; DB 5
68.2%; Pred. No. 3e-40;
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   Its
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   60
   60
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CURRENT APPLICATION NUMBER: PCT/US04/0238
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US60/443,484
PRIOR FILING DATE: 2003-01-29
PRIOR PILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US60/447,358
PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US60/461,789
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
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  PCT-US04-02338-49
  ; TYPE: PRT ; ORGANISM: Escherichia coli US-09-741-873C-2
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SOFTWARE: PatentIn version 3.2 SEQ ID NO 49
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APPLICANT: EXELIXIS, INC.
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   PRIOR APPLICATION NUMBER: US60/479,650 PRIOR FILING DATE: 2003-06-19
  Sequence 2, Application US/09741873C GENERAL INFORMATION:
   PRIOR FILING DATE: 2003-05-14
   TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS TITLE OF INVENTION: USE
  FILE REFERENCE:
   SOFTWARE: PatentIn version 3.0
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  NUMBER OF SEQ ID NOS: 11
  PRIOR APPLICATION NUMBER: US 08/318,519 PRIOR FILING DATE: 1994-10-05
  APPLICANT: Olsen, Arne
TITLE OF INVENTION: Pibronectin Binding Protein
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
  PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
   APPLICATION NUMBER: US 08/978,878
FILING DATE: 1997-11-26
APPLICATION NUMBER: US 07/347,189
FILING DATE: 1989-05-04
APPLICATION NUMBER: US 07/789,437
FILING DATE: 1991-11-06
   APPLICATION NUMBER: US 07/970,846
FILING DATE: 1992-11-03
APPLICATION NUMBER: US 08/187,865
FILING DATE: 1994-01-28
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; OTHER INFORMATION: G1152 Paralogous to G1146
PCT-US04-05654-2086
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; ORGANISM: Homo sapiens
PCT-US04-02338-49
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PRIOR APPLICATION NUMBER: 10/374,780
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PRIOR APPLICATION NUMBER: 10/675,852
PRIOR TILING AND NUMBER: 10/675,852
  APPLICANT:
APPLICANT:
   APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
  TYPE: PRT
ORGANISM: Arabidopsis thaliana
  APPLICANT:
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   APPLICANT: Sherman, Bradley K
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   PPLICANT:
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  Gutterson, Neal
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   Broun, Pierre E
   Reuber, T. Lynne
   Creelman,
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  Jiang, Cai-Zhong
   entury, Karen
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   Application PC/TUS0405654
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  l III, Arnold
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  Jacqueline
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   James
   Robert A
  11.0%;
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  11.9%;
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GENERAL INFORMATION: NOUGETTE-Stamm
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   ঠ
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  ঠ
  ; ORGANISM: Homo sapiens
US-10-100-683-7608
  US-10-100-683-7608
   Sequence 7608, Appli
GENERAL INFORMATION:
APPLICANT: Rosen, 6
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Best Local Similarity
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   TITLE OF INVENTION: Human Secreted Proteins FILE REFERENCE: PS900 CURRENT APPLICATION NUMBER: US/10/100,683 CURRENT FILING DATE: 2002-03-19
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  PRIOR FILING DATE: 1997-03-07
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  PRIOR APPLICATION NUMBER: US 60/040,162
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FILING DATE: 1997-05-23
   APPLICATION NUMBER: US 60/056,845
  APPLICATION NUMBER: US 60/056,892
   APPLICATION NUMBER: US 60/043,314
   FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,664
  APPLICATION NUMBER: US 60/043,580 FILING DATE: 1997-04-11
  FILING DATE: 1997-08-22
   CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
   FILING DATE: 1997-05-23
   FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
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   CITY: Waltham
  Application US/10100683
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  1997-08-22
   100 Beaver Street
   1997-08-22
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NAME/KEY: misc feature
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; OTHER INFORMATION: Clone ID: 6858533.pep
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  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
  APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
  APPLICANT: Kovalic,
  NAME/KEY: unsure
LOCATION: (1)..(125)
OTHER INFORMATION: unsure at all Xaa locations
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nes 30; Conserv
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FILING DATE: 30-Jun-1998
APPLICATION UNMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
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  NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
  FILING DATE: 17-Apr-2003
  OPERATING SYSTEM: <Unknown>
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   TELEFAX:
   TELEPHONE: (781)893-5007
   Conservative
  David K.
   (781)893-8277
  10.0%; Score 77.5; D
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   APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
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NAME/KEY: unsure
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OTHER INFORMATION: unsure at all Xaa locations
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Cao, Yongwei
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TITLE OF INVENTION: Human Secreted Proteins
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APPLICANT: Morton, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR
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CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
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PRIOR FILING DATE: 2003-02-13
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CURRENT FILING DATE: 2002-03-06
   APPLICANT: Bylina, Edward
APPLICANT: Swanson, Ronald V.
APPLICANT: Mathur, Eric J.
APPLICANT: Lam, David E.
TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
   APPLICANT: Jay M. Short
APPLICANT: Byline, Edw
APPLICANT: Swanson, Ro
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  US-10-779-461-40
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
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TITLE OF INVENTION: ESCHERICHIA COLI
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CURRENT FILING DATE: 2004-02-03
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PRIOR APPLICATION NUMBER: 60/117,405
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   PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
  APPLICANT: Zyskind, Judith APPLICANT: Forsyth, R. Al
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ORGANISM: artificial
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(GENERAL INFORMATION:

APPLICANT: LADNER, ROBERT C.

APPLICANT: COHEN, EDWARD H.

APPLICANT: COHEN, EDWARD H.

APPLICANT: NASTRI, HORACIO G.

APPLICANT: NASTRI, HORACIO G.

APPLICANT: HOGI, RENE

APPLICANT: HOGINENCOM, HENDRICUS R. J. M.

TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY

TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY

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TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY

TITLE OF INVENTION: LIBRARIES

TITLE OF INVENTION: LIBRARIES

FILE REFERENCE: DYAX/002 CIP2

CURRENT FILING DATE: 2001-10-25

PRIOR APPLICATION NUMBER: 06/198,069

PRIOR APPLICATION NUMBER: 06/198,069

PRIOR APPLICATION NUMBER: 06/198,069

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  PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 424
TYPE: PRT
ORGANISM: Unknown Organism
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Search completed: March 11, 2004, 19:14:15 Job time : 5.3 secs
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; PEATURE:
; OTHER INFORMATION: Description of Unknown Organism: M13 protein; OTHER INFORMATION: sequence
US-10-045-674A-591
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C24509_1.pep
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   Score 75; DB 6; Length 424; Pred. No. 15; 8; Mismatches 35; Indels
  Score 75; DB 6; Length 191; Pred. No. 5.8; 9; Mismatches 46; Indels
   SGYGNG------ADVGQGADNSTIELTQNG 96
  46; Indels 28;
   35; Indels 42;
  Gaps
   Gaps
  FAMILY
```

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Database
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  Minimum DB seq length: 0
Maximum DB seq length: 200000000
  Sequence:
   Total number of hits satisfying chosen parameters:
  Scoring table:
   Title:
Perfect score:
  OM protein - protein search, using sw model
  BLOSUM62
Gapop 10.0 , Gapext 0.5
  US-09-543-407-16
757
   March 11, 2004, 18:33:51 ; Search time 171.3 Seconds (without alignments) 860.386 Million cell updates/sec
   6019581 seqs, 976053577 residues
   Pending_Patents_AA_Main:*
/cgn2_6/ptodata/2/paa/
/ Cgm2_6/ptodata/2/paa/VCTUS_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO7_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO7_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO8_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO82_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO82_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO83_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO83_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO83_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO83_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO86_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO86_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO89_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/VSO99_COMB.pep:*
/ Cgm2_6/ptodata/2/paa/USO99_COMB.pep:*
  MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
  GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
```

| 98<br>9.5<br>9.5<br>99.5<br>101                                                                                          | 757 658 658 668 668 679 579 579 577 577 577 578 578 578 578 578 578 578                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|--------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 13.3<br>13.1<br>13.1<br>13.1<br>12.9                                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 200444                                                                                                                   | 151<br>151<br>151<br>151<br>151<br>151<br>151<br>151<br>151<br>151                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 22222                                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 85<br>85<br>85<br>85<br>85<br>85<br>85<br>85                                                                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| Sequence 111371,<br>Sequence 111371,<br>Sequence 94843, A<br>Sequence 30765, A<br>Sequence 32862, A<br>Sequence 8854, Ap | equence 16, Applequence 57, Applequence 11, Applequence 11, Applequence 12, Applequence 26, Applequence 26, Applequence 27, Applequence 28, Applequence 27, Applequence 27, Applequence 27, Applequence 27, Applequence 27, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 37, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Applequence 28, Ap |

# ALIGNMENTS

```
US-09-543-407-16

Sequence 16, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Oran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
ITITE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043-406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
```

Result No.

Score

Query Match Length DB

ij

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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   ; ORGANISM: Salmonella enteritidis US-09-543-407-5
   US-09-5
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   US-09-543-407-16
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 5
  Matches 136;
   Query Match
  GENERAL INFORMATION:
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Key, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   Matches
   TYPE: PRT
  LENGTH: 151
STREET:
                          ADDRESSEE:
  Local Similarity
  Local
  121
  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   19
   61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120
   121
   151;
  121
  1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60
  61
   61
   1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60
   NNAALVNOTASDSSVMVROVGFGNNATANOV
  SDARKSETTÍTÓSGYGNGAÐVGÓGAÐNSTÍBLTONGFRNNATIDOMNAKNSDITVGÓYGG
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   Similarity
  Application US/09543407
   NNAALVNOTASDSSVMVROVGFGNNATANOY 151
  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
   MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60
    3: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
  Conservative
  Conservative
   86.9%;
90.1%;
   100.0%; Score 757; DB 19; 100.0%; Pred. No. 3.4e-76; tive 0; Mismatches 0;
   ω
••
  Score 658; DB 19;
Pred. No. 4.5e-65;
3; Mismatches 12;
   151
   PEPTIDE SEQUENCES
   Length 151;
  Indels
   Indels
  Length 151;
  0
   <u>,</u>
   Gaps
  Gaps
  120
   60
   120
  0
```

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
IAPPLICANT: Kay, William W.
ITITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITITLE OF INVENTION: BACTERIAL OF HETEROLOGOUS PEP
ITITLE REFERENCE: 92004.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: 2000-04-05
INUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
SEQ ID NO 18
LENGTH: 151
  ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-18
  RESULT 4
US-09-543-407-18
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  ; MOLECULE TYPE: protein US-08-233-642A-57
    Best Local Similarity 76. Matches 131; Conservative
  Sequence 18, Application US/09543407 GENERAL INFORMATION:
   Query Match 86.3%;
Best Local Similarity 89.4%;
Matches 135; Conservative 2
   NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
   TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS:
  ORGANISM: Artificial Sequence FEATURE:
   TYPE: amino acids
TOPOLOGY: line.
   ATTORNEY/AGENT INFORMATION: NAME: King, Joshua
   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   121
   61
   61 SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDQWNAKNSDITVGQYGG 120
  1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60
  3: Washington 
IRY: U.S.A. 
98104-7092
   MKLLKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSTYQYGSANAALALQ
  NNPALVNOTASDSSVMVROVGFGNNATANOY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                       81.6%;
Score 618; DB 19;
Pred. No. 1.4e-60;
0; Mismatches 0;
   Score 653; DB 6;
Pred. No. 1.6e-64;
3; Mismatches 13
   920043.403C3
   Length 151;
   PEPTIDE SEQUENCES
   Length 151;
   Indels
   0;
   Gaps
   120
   60
```

40;

Gaps

2

```
Sequence 31, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 131
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   RESULT 6
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   RESULT 5
US-09-543-407-12
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  밁
   US-09-543-407-31
  Query Match
Best Local S
Matches 121
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
  Sequence 12, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  09-543-407-12
   FEATURE: FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial Sequence
  TYPE: PRT
  121
  101 ATIDQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   121
   101
   61
   61
   41
  ... 76.6%;
Similarity 80.1%;
21; Conservative
   NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
  NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  PDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN 100
   SDARKSETTITQSGYGNGADVGQQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  MKLLKVAAFAAI VVSGSALAGV-----
  MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAH----
  --- ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN
  Score 580; DB 19;
Pred. No. 2.6e-56;
7; Mismatches 23;
  PEPTIDE SEQUENCES
  PEPTIDE SEQUENCES
   Length 151;
  Indels
  - YDQLVTRVVTHEMAHASG
|||||||||||||
  0
  Gaps
   120
  60
   60
   100
  57
```

```
Sequence 26, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PRESENTATION OF HETEROLOGOUS PRESENTATION APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION 1005: 59
NUMBER OF SEQ ID NOS: 59
   TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOI
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOU:
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
TYPE: PRT
  ; TYPE: PRT ; ORGANISM: Salmonella enteritidis US-09-543-407-31
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  US-09-543-407-14
  멍
  US-09-543-407-26
  US-09-543-407-14
  Query Match
Best Local Similarity
Matches 113; Conserv
   Sequence 14, Application US/09543407 GENERAL INFORMATION:
  Matches
   Query Match
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  ORGANISM: Artificial Sequence FEATURE:
   Local Similarity
  121
   121
  122;
  61
   61
  97
  17 NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
  77
   1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  LVTRVVTHEMAHASVMVROVGFGNNATANOV 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  FRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  FRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 131
  Conservative
  Conservative
   76.4%;
80.8%;
  76.5%;
98.3%;
  Score 578; DB 19;
Pred. No. 4.4e-56;
6; Mismatches 23;
  Score 579; DB 19;
Pred. No. 2.8e-56;
  Mismatches
  AL SYSTEM FOR HETEROLOGOUS
  PEPTIDE SEQUENCES
  PEPTIDE SEQUENCES
   Length 151;
   Length
  Indels
  Indels
  0
  ,
,
  Gaps
  Gaps
   60
  60
  76
   96
  0
```

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RESULT 10
US-09-543-407-20
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  В
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   US-09-543-407-24
  US-09-543-407-24
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   В
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   ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-26
  SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
TYPE: PRT
   Matches
  Query Match
Best Local Similarity
  Sequence
   SOFTWARE: rac
   GENERAL INFORMATION:
   Matches 122;
   Query Match
Best Local Similarity
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
  APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   APPLICANT: White, Aaron P. APPLICANT: Doran, James I
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial Sequence
   FEATURE:
   ORGANISM: Artificial Sequence
  FEATURE:
  121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   123;
  61
   61
  121
  121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
  24, Application US/09543407
  61
  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120
  MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
   LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  FastSEQ for Windows Version
  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
   Doran, James L.
   Conservative
   Conservative
   76.2%; Score 577; DB 19; Length 151; 80.8%; Pred. No. 5.7e-56; Vative 5; Mismatches 24; Indels
  76.0%;
81.5%;
   <u>ن</u>
   Score 575; DB 19;
Pred. No. 9.5e-56;
5; Mismatches 23;
   PEPTIDE SEQUENCES
  Length 151;
   Indels
   0,
   0,
   Gaps
   60
  60
  120
   60
  60
   0
```

Sequence 20,

Application US/09543407

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
CURRENT APPLICATION NUMBER: US/99/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARB: FastSEQ for Windows Version 4.0
SEQ ID NO 28
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   US-09-543-407-28
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  US-09-543-407-28
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   밁
   Ş
  US-09-543-407-20
   Matches 121;
  Query Match
  Sequence 28, Application US/09543407 GENERAL INFORMATION:
  Matches 122;
  Query Match
Best Local 9
  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 20
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   GENERAL INFORMATION:
   APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  ORGANISM: Artificial Sequence
  TYPE: PRT
  APPLICANT: White, Aaron
APPLICANT: Doran, James
APPLICANT: Collinson, &
  FEATURE:
  NUMBER OF SEQ ID NOS:
   CURRENT APPLICATION NUMBER: US/09/543,407 CURRENT FILING DATE: 2000-04-05
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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ORGANISM: Artificial Sequence
FEATURE:
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  Similarity
                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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80.1%;
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   2000-04-05
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Pred. No. 5.8e-55;
4; Mismatches 26;
   DB 19;
.2e-55;
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US-09-543-407-30

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APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 151
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  US-09-543-407-30
   US-09-543-407-22
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   US-09-543-407-22
  몽
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 22
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   Sequence 22,
  Matches 122; Conservative
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Best Local Similarity
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  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
  APPLICANT: White, Aaron P
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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  Application US/09543407
   Application US/09543407
  74.9%;
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7.5e-55;
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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SEQ ID NO 34
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; Sequence 55, Application US/08233642A
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; TYPE: PRT
; ORGANIEM: Salmonella enteritidis
US-09-543-407-34
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   RESULT 14
US-09-543-407-34
   RESULT 15
  Matches 109;
   GENERAL INFORMATION:
   Query Match
Best Local :
   Query Match
Best Local Similarity
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   APPLICANT: White, Aaron P. APPLICANT: Doran, James L.
  APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
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STATE: Washing
  STREET:
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  73.2%; Score 554; DB 19; 100.0%; Pred. No. 1.4e-53; tive 0; Mismatches 0;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
LURENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 920043.403C3
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
US-08-233-642A-55
Search completed: March 11, 2004, 19:13:10 Job time : 171.3 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd

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Result
No.
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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  Total number of hits satisfying chosen parameters:
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Perfect score:
   OM protein -
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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73.5
73.5
73.7
73.5
71.5
71.5
71.5
71.5
71.5
69.5
68.5
68.5
68.5
68.5
68.5
68.5
  69.
   93
78.5
75.5
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seq length: 2000000000
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   Match
  BLOSUM62
Gapop 10.0 , Gapext 0.5
  March 11, 2004, 18:35:05; Search time 5.3 Security (without alignments 376.014 Million cel
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US-10-667-701-42417
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US-10-661-678-38
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US-10-781-477-830
US-10-781-978-314
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47075, A
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34, Appl
34, Appl
40444, A
44, Appl
42417, A
      44208, A
6, Appli
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| 45                  | 44                                            | <b>4</b> ω        | 42                 | 41                  | 40                  | 39                 | 38                  | 37                  | 36                  | 35<br>5           | 34                | မ                   | 32               | 31                  | 30                  | .29                 | 28                  | 27                |
|---------------------|-----------------------------------------------|-------------------|--------------------|---------------------|---------------------|--------------------|---------------------|---------------------|---------------------|-------------------|-------------------|---------------------|------------------|---------------------|---------------------|---------------------|---------------------|-------------------|
| 63                  | 63.5                                          | 63.5              | 63.5               | 63.5                | 63.5                | 64                 | 64                  | 64.5                | 64.5                | 64.5              | 65                | 65 .                | 65.5             | 65.5                | 65.5                | 66                  | 66.5                | 67                |
| 8.3                 | 8.4                                           | 8.4               | 8.4                | 8.4                 | 8.4                 | 8.5                | æ<br>.5             | 8.5                 | 8<br>5              | 8.5               | 8.6               | 8.6                 | 8.7              | 8.7                 | 8.7                 | 8.7                 | 8.8                 | 8.9               |
| 179                 | 526                                           | 467               | 263                | 175                 | 154                 | 1645               | 198                 | 1221                | 795                 | 135               | 1230              | 620                 | 3668             | 772                 | 178                 | 708                 | 172                 | 595               |
| 6                   | <u>, , , , , , , , , , , , , , , , , , , </u> | 0                 | Ļ                  | σ                   | 6                   | თ                  | σ                   | σ                   | 0                   | თ                 | თ                 | σ                   | σ                | σ                   | σ                   | σ                   | σ                   | σ                 |
| US-10-767-701-35342 | PCT-US04-04280-9                              | US-10-771-241-381 | PCT-US04-05654-126 | US-10-767-701-59665 | US-10-767-701-39935 | US-10-451-467A-452 | US-10-767-701-59434 | US-10-417-884A-3959 | US-10-417-884A-5429 | US-10-091-007A-38 | US-10-786-892-150 | US-10-767-701-46258 | US-10-746-795A-4 | US-10-417-884A-5724 | US-10-767-701-32700 | US-10-417-884A-6047 | US-10-767-701-49464 | US-10-786-892-166 |
|                     | Sequence 9                                    | Sequence 31       | Sequence 1:        | Sequence 59         | Sequence 39         | Seguence 4!        | Sequence 51         | Sequence 3:         | Sequence 5          | Sequence 31       | Sequence 1:       | Sequence 40         | Sequence 4       | Sequence 5'         | Sequence 3:         | Sequence 60         | Sequence 4:         | Sequence 1        |
| 35342, A            | Appli                                         | 81, App           | 126, App           | 59665, A            | 39935, A            | 452, App           | 59434, A            | 3959, Ap            | 5429, Ap            | 38, Appl          | 150, App          | 46258, A            | 4, Appli         | 5724, Ap            | 32700, A            | 6047, Ap            | 4                   | 166, App          |

#### ALIGNMENTS

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APPLICANT: NOTMARK, Staffan
APPLICANT: Olsen, Arne
FITTLE OF INVENTION: Fibronectin Binding Protein As
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 8001723-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1994-01-28
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   US-09-741-873C-4
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Best Local Similarity
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   Application US/09741873C
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  63.5%; Score 481; DB 5; 66.2%; Pred. No. 2.6e-41; cive 19; Mismatches 32
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  0;
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  120
  120
  60
  60
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US-10-004-115B-34

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PRIOR FILING DATE: 2000-12-07
  APPLICANT: ITO, NOBUYA
APPLICANT: WAKITA, RYUHEI
TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE
TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE
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   APPLICANT: ASAKO, APPLICANT: MATSU
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ORGANISM: Corynebacterium sp
   CURRENT APPLICATION NUMBER: US/09/741,873C CURRENT FILING DATE: 2000-12-2 PRIOR APPLICATION NUMBER: SE 8801723-1 PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: US 08/978,878 PRIOR FILING DATE: 1997-11-26 PRIOR APPLICATION NUMBER: US 07/347,189
  SOFTWARE:
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   09-741-873C-2
  APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
   ORGANISM: Escherichia coli
  NITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
  ENGTH: 131
  Local Similarity
  APPLICATION NUMBER: US 07/970,846
FILING DATE: 1992-11-03
APPLICATION NUMBER: US 08/187,865
FILING DATE: 1994-01-28
  APPLICATION NUMBER: US 08/318,519
   FILING DATE: 1989-05-04
APPLICATION NUMBER: US 07/789,437
FILING DATE: 1991-11-06
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  99 NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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US-10-767-701-40444
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  NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 40444
LENGTH: 358
CURRENT APPLICATION NUMBER: PCT/US03/32645
CURRENT FILING DATE: 2003-10-15
NUMBER OF SEQ ID NOS: 234
SOFTWARE: PatentIn version 3.0
SEQ ID NO 44
LENGTH: 1531
  APPLICANT: Progulske-Fox, Ann
TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans Antigens
TITLE OF INVENTION: in the Diagnosis, Treatment, and Monitoring of Periodontal Dise
FILE REFERENCE: MBHB01-662B
  Matches
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  Sequence 40444, Application US/10767701
  APPLICANT: Handfield, Martin
APPLICANT: Hillman, Jeffrey
APPLICANT: Progulske-Fox, Ar
  Matches
   Query Match
Best Local :
  APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
  APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
  CURRENT FILING DATE:
   TYPE: PRT
   FEATURE:
  ORGANISM: Sorghum bicolor
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US-10-093-037A-63

Sequence 63, Application US/10093037A

GENERAL INFORMATION:

APPLICANT: Jay M. Short

APPLICANT: Bylina, Edward

APPLICANT: Swanson, Ronald V.

APPLICANT: Swanson, Ronald V.

APPLICANT: Mathur, Eric J.

APPLICANT: Mathur, Eric J.

APPLICANT: Lam, David E.

FILE REFERENCE: 564462001402

FILE REFERENCE: 564462001402
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  Ś
  NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 42417
LENGTH: 386
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE: OTHER INFORMATION: Clone ID: SORBI-28MAY03-C47268_1.pep
US-10-767-701-42417
   RESULT 7
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  밁
   US-10-767-701-42417
   RESULT 6
  ঠ
   ; TYPE: PRT ; ORGANISM: Actinobacillus actinomycetemcomitans PCT-US03-32645-44
   Query Match
Best Local S
Matches 28
  Sequence 42417, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
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   336 KASQDNVVAIGKYATATESG---SMAIGQGAKSTFKNSLALGTGTIVNSVDGGQSKFTAQ 392
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  393 NYDANNGVVAVAN-AGKERRIINVAGGRNDTDAVNIAQLKEVNDNLA 438
  293 LSKKADKAIAVGTSALA----QKESAIAFGYQANASGIN----
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PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/134,078
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PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/056,916
PRIOR FILING DATE: 1996-12-06
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 63
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   밁
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  문
   ; ORGANISM: Mus musculus US-10-603-150-2
   S
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   밁
  US-10-603-150-2
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CURRENT FILING DATE: 2003-06-24
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   146 A 146
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   11 AIVVSGSALAGVYD-----QLYTRVVTH-EMAHASGPDSTLSIYQYGSANAALALQSD
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  8 AFAAIVVSGSALAGVYDOLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSE 67
   VLNGRAGFGGALNT----NATFGGVLNGSAGFGGAMNTNATFG--GALNSNAGFGGAIS
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TSTNFGGALNNSAGFGGAMNTSASFGGVLNNSAGFGGAINTSAN
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  ARKSETTITOSGYGNGADVGQGADNSTIEL--TQNGFRNNATI------ 103
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Pred. No. 27;
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   615
   476
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; ORGANISM: Phanerochaete chrysosporium US-10-641-678-38
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  В
  RESULT 10
US-10-641-678-38
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   ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C24509_1.pep
US-10-767-701-47075
  RESULT 9
US-10-767-701-47075
Query Match
Best Local Similarity
  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 38 LENGTH: 449
   APPLICANT: Day,
APPLICANT: Goed
APPLICANT: Gual
  Sequence 38, Application US/10641678 GENERAL INFORMATION:
  Matches
   NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 47075
  Sequence 47075, Application US/10767701 GENERAL INFORMATION:
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   PRIOR APPLICATION NUMBER: US 60/458,696
PRIOR FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/456,368
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2003-03-21
   PRIOR APPLICATION NUMBER: US 60/404,063 PRIOR FILING DATE: 2002-08-16
   PRIOR APPLICATION NUMBER: US 60/458,853 PRIOR FILING DATE: 2003-03-27
  CURRENT APPLICATION NUMBER: US/10/641,678
CURRENT FILING DATE: 2003-08-15
  APPLICANT: Stahlberg, Jerry
TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
TITLE OF INVENTION: Cellulases
FILE REFERENCE: GC772-3
  APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
CURRENT FILING DATE: 2004-01-29
  NUMBER OF SEQ ID NOS:
   APPLICANT:
   APPLICANT:
   APPLICANT: Kovalic, David K.
   TYPE: PRT ORGANISM: Sorghum bicolor FEATURE:
  ENGTH: 191
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   127 NQTASD 132
   124 SAGAASSGTAGSÁSAGAGAASS----
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   AAAAAGAASGSAAAG------SASGSAAT-----GSGSAGAAGSSTTLAS 123
  Gualfetti, Peter
Mitchinson, Colin
Neefe, Paulien
  Shaw, Andrew
   Sandgren, Mats
  Jay, Anthony, G. Goedegebuur, Fr
  Conservative
   2002-08-16
  9.5%;
26.1%;
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Pred. No.
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CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: 60/442,582
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 191
SOPTWARE: Patentin version 3.2
SEQ ID NO 185
LENGTH: 583
    Ş
   ; TYPE: PRT; ORGANISM: Homo sapiens US-10-764-425-185
   RESULT 12
US-10-764-425-185
   밁
   밁
  ; ORGANISM: Homo sapiens PCT-US04-02188-185
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   g
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  SOFTWARE: PatentIn version 3.2 SEQ ID NO 185
  Query Match
Best Local Similarity
   Matches
  GENERAL INFORMATION:
   Query Match
Best Local
   APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Eveleigh, Deepa
APPLICANT: Bigwood, Douglas
APPLICANT: Bigwood, Douglas
APPLICANT: Taylor, Ian
TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
FILE REFERENCE: 5151
CURRENT APPLICATION NUMBER: US/10/764,425
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: 60/442,582
PRIOR APPLICATION NUMBER: 60/142,582
PRIOR FILING DATE: 2003-01-24
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  NUMBER OF SEQ ID NOS: 191
   APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Eveleigh, Deepa
APPLICANT: Bigwood, Douglas
APPLICANT: Taylor, Ian
   FILE REFERENCE: 5151
   PPLICANT: Taylor, Ian
  ENGTH: 583
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   182 NSKLSLTPNCSSTLNITQSQIHFLSPDSFVNNSHGANNELELVTCLSSD 230
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  213 ATTGTGSYGSCCTELDIWEANSNAAALTPHTCTNNA----QTRCSGSNCTSN 260
27 VTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD
   111 SDITVGQYG------GNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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   Application US/10764425
   Application PC/TUS0402186
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29.4%; Pred. No. 17;
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  S
  RESULT 13
US-10-771-241-364
  RESULT 14
US-10-767-701-44555
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  밁
   ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C21806_1.pep
US-10-767-701-44555
   US-10-771-241-364
   밁
  Sequence 4455, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21 (53535) B
CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128
Query Match
Best Local Similarity 28.0
Matches 23; Conservative
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 364
   Sequence 364, Application US/10771241 GENERAL INFORMATION:
   SEQ ID NO 44555
LENGTH: 281
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Best Local Similarity 22.7%; Pred. No. 29;
Matches 34; Conservative 19; Mismatches
   APPLICANT: Zyekind, Judith
APPLICANT: Forsyth, R. Allyn
APPLICANT: Forsyth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA, 001C1
CURRENT APPLICATION NUMBER: 105/10/771,241
CURRENT APPLICATION NUMBER: 09/492,709
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
   PRIOR FILING DATE: 1999-01-27
   PRIOR APPLICATION NUMBER: 60/117,405
   TYPE: PRT
ORGANISM: Sorghum bicolor
   ORGANISM: E. Coli
   FEATURE:
   LENGTH: 878
  705
   591 DQMLALNVNIPFSHWLRSDSK---SQWRHASASYSMSHDLNGRMTNLAGVYGTLLEDNNL
  122 -NAALVNOTASDSSVMVROVGFGNNATANO 150
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  71 ---TQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN-----
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Search completed: March 11, Job time: 6.3 secs
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   ; ORGANISM: Candida albicans US-10-451-467A-462
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LENGTH: 829
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
   APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKWANS, RIEKA JOSEPHIM.
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
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  GFPIPGSPDETTRPNS----IFGGHTRGLFSSRLSESQSVLYQQYAIADD-TVGDY 731
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Listing first 45 summaries
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cgn2_6/ptodata/2/paa/US07_
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|---|----------------|--------------|----------------|-----------------|--------------|------------------|-------------------|----------|----------------|-----------|----------------|------------------|--------------|----------------|-----------------|------------------|----------------|----------------|---------|---------------|-----------------|------------|--------------|---------------|-----------------|----------------|---------------|-------------|---------------|---------------|--------------|---------------|-------------|---------------|-------------|----------------|-----------------|----------------|--------------|----------------|-----------------|----------------|----------------|----------------|-------------------|
|   | œ.             | 9.           | 99.5           | 100             | 101          | 101              | 101               | 101      | 101            | ٥.        | 107.5          | 8                | 8            | 116            | 116             | 116              | 175            | 250.5          | 276     | 359.5         | 444             | 444        | 457          | S             | ū               | 8              | 506           | -           | $\vdash$      | N             | 520          | N             | 599         | 20            | ٥ د         | 000            | ) F             | 611            | 613          |                | N               | 675            | œ              | 9              | œ                 |
| ; | 12.8           | 12.8         |                | •               | 12.9         | •                | 12.9              | 'n       | 12.9           | 13.7      |                | ω.               | ω.           | 14.9           | 14.9            | 14.9             | 22.4           | 32.1           | 5       | 46.1          | 6               | 56.9       | 58.6         | 8             | ω.              |                | ٠.            | σ           | 66.4          | σ             | 66.7         | 7 :           | <u>ه</u> :  | , ת           | ٦:          | <br>           | , 0             | 70.0           | ٠:           | ٠.             | ۰               | ٥,             | 7.             | 88             |                   |
|   | 24             | N            | 4              | 30              | σ            | σ                |                   | σ        | ທ              | G         | 151            | 4                | 4            |                | œ               | æ                | 48             |                | 89      |               | 131             | 131        | 5            | ū             | 5               | 0              | 120           | ū           | 151           | S             | 151          | σ,            | 151         | лί            |             |                | ٦ (             | лυ             |              |                | л               |                | ū              | 151            |                   |
|   | W              | ü            | 30             |                 | 33           | 33               | 20                | 20       | ω<br>ω         | 19        | 19             | ü                |              | 30             | 16              |                  | 19             | 19             | 19      | 19            | 21              | 13         | 30           | 16            | 16              | 19             | σ             | w<br>W      | w<br>W        | 21            | 3            | 19            |             | ָ<br>מ        | 2 5         | י ב            | ,               | ,              |              |                | 19              | 19             |                | 19             |                   |
|   | -60-446-775-35 | 60-385-568-3 | -10-455-719-35 | -10-179-131-514 | -681-2056    | -60-191-637-2595 | -09-614-150A      | 50-2581  | 73-464-2155    | 7-6       | -09-543-40     | -60-360-039-2063 | -10-369-493- | 0-417-886-5833 | -09-252-691C-58 | -09-252-691-5833 | -09-543-407-39 | -09-543-407-3  | 3-407-3 | -09-543-407-3 | -741-873B-      | 78-878-2   | -417-886-583 | -09-252-691C- | -09-252-691-583 | S-09-543-407-3 | 08-233-642A-5 | 60-444-371- | -60-352-946-2 | S-09-741-873E | -08-978-878- | -09-543-407-7 | 09-543-407- | -09-543-407-2 | 3-407-3     | 5-09-543-407-2 | 7-101-101-10-1  | 407-1          | -00-5/3-407- | -09-543-407-1  | -09-543-407-2   | S-09-543-407-  | -08-233-642A-5 | -09-543-407-5  | US-09-543-407-18  |
|   | equence 358,   | equence 357, | 58,            | equence 5148,   | equence 2056 | equence 25957,   | Sequence 25818, A | e 25818, | equence 21553, | e 6, Appl | equence 8, App | equence 20638,   | equence      | e 5833,        | equence 5833,   | equence 5833,    | equence 39, Ap | equence 32, Ap | 37,     | equence 35,   | equence 2, Appl | equence 2, | 583          | equence 583   | equence 58      | ce 34          | quence        | equence 2,  | e<br>2,       | equence 4,    | equence 4    | equence 7.    | <u>س</u>    | equence 22.   | מינות מני ש | equence 24, Ap | equence 11, App | equence 14 App | מקיני מינים  | equence 16. Ap | equence 20, App | equence 26, Ap | quence 57, A   | quence 5, Appl | Sequence 18, Appl |

## ALIGNMENTS

```
RESULT 1

US-09-543-407-18

(Sequence 18, Application US/09543407)

(SEMERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043,406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEO ID NO 18

SEO ID NO 18

SEO ID NO 18

LENGTH: 151

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
```

Result No.

Score

Query Match Length DB

Ħ

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

```
US-08-233-642A-57
; Sequence 57, Application US/08233642A
; GENERAL INFORMATION:
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.406
FILE REFERENCE: 920043.406
CURRENT APPLICATION UMBER: US/09/543,407
CURRENT APPLICATION UMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
   В
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  밁
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   ; SEQ ID NO 5
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-5
  US-09-543-407-5
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   S
   US-09-543-407-18
  Matches
  Query Match
  GENERAL INFORMATION:
   Matches
  Query Match
Best Local
                                       NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
   APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
       ADDRESSEE:
STREET: 6
   Local
  Local
   121
   121
  137;
   61
  121
  61
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   151;
  61
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGUNHNGGGNGSGPDYDQLVTRVVTHEMAHALQ
  61
   Similarity
  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  Similarity
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60
   Application US/09543407
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
   MKLLKVAAFAAIVVSGSALAGVVFQWGGGGNHNGGGNSSGFDYDQLVTRVVTHEMAHALQ 60
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  NNAAL VNQTASDSSVMVRQVGFGNNATANQY 151
E: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
  Conservative
   Conservative
   88.6%;
   58
   100.0%; Score 780; DB 19; 100.0%; Pred. No. 3.7e-75; tive 0; Mismatches 0;
  Score 691; DB 19;
Pred. No. 1.4e-65;
3; Mismatches 11
   DB 19;
  11;
   PEPTIDE SEQUENCES
   Length 151;
  Indels
   Indels
   Length 151;
  0
   0
   Gaps
  60
  60
  120
  120
   120
  0;
```

```
FILE REPERENCE: 920043.406

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 151

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella entertidies 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   S
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   US-09-543-407-26
  RESULT
  ; MOLECULE TYPE: protein
US-08-233-642A-57
  Sequence 26, Application:
  Query Match
   Query Match 87.9%;
Best Local Similarity 90.1%;
Matches 136; Conservative
  APPLICANT: White, Aaron P. APPLICANT: Doran, James L. APPLICANT: Collinson, S. ... APPLICANT: Kay, William W
  APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
   TELEFAX: (206) 682-6031
TELEX: 372336 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
  REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHAX: (206) 682-6031
  ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  LENGTH: 151 amino acids TYPE: amino acid TOPOLOGY: linear
  STATE: W
   APPLICATION NUMBER: US/08/233,642A FILING DATE: 26-APR-1994 CLASSIFICATION: 424
  COMPUTER: IBM PC
OPERATING SYSTEM:
   121
   121
  26, Application US/09543407
   61
   61
   1 MKLIKVAAFAAIVVSGSAIAGVVPQWGGGGHHNGGGNSSGPDYDQLVTRVVTHEMAHAIQ 60
   RY: U.S.A.
98104-7092
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   Doran, James L.
  3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                     86.5%;
   ω
••
Score 675; DB 19;
Pred. No. 7.3e-64;
0; Mismatches 0;
   920043.403C3
   Score 686; DB 6;
Pred. No. 4.8e-65;
3; Mismatches 12;
  PEPTIDE SEQUENCES
   Length 151;
                                      Length 151;
   Indels
   0
   Gaps
```

0

Best Local Similarity 81. Matches 136; Conservative

0

30;

Gaps

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTE
TITLE OF INVENTION: PRESENTATION OF HETEROL
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
   밁
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  밁
   8
  RESULT 5
US-09-543-407-20
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  RESULT
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   US-09-543-407-16
  US-09-543-407-20
   밁
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 151
   Sequence 16, Application US/09543407 GENERAL INFORMATION:
   Sequence 20, Application GENERAL INFORMATION
  Query Match
Best Local Similarity
  Sequence
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collingon, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial Sequence FEATURE:
  TYPE: PRT
   106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   106
  98
   98
  3
  _
   128;
  61
  46 LVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ
   61 SDARKYDQLVTRVVTHEMAHA-----
   RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  -----YDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
  MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  RNNATIDQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPD----
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
  Application US/09543407
   Conservative
  79.7%;
73.6%;
   0;
   Score 622; DB 19,
Pred. No. 3.6e-58,
0; Mismatches (
  -----GYGNGADVGQGADNSTIELTQNGFRNNATIDQ
   OF HETEROLOGOUS
  DB 19;
   0
   PEPTIDE
  PEPTIDE
  Length 151;
   Indels
   -GQGADNSTIELTQNGF
  SEQUENCES
   46;
  105
   60
  97
  60
   105
   97
   42
```

US-09-543-407-14

Sequence 14, Application US/09543407 GENERAL INFORMATION:

APPLICANT: White, Aaron APPLICANT: Doran, James

RESULT 8

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   ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-12
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   8
   US-09-543-407-12
  US-09-543-407-16
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
TYPE: PRT
  Best Loc
Matches
  Sequence 12, Application US/09543407 GENERAL INFORMATION:
   Query Match
Best Local Similarity
   Query Match
  Matches 131;
  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
   FILE REFERENCE: 920043.406
   APPLICANT: White, Aaron P. APPLICANT: Doran, James I
  FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial FEATURE:
  TYPE: PRT ORGANISM: Artificial Sequence
  Local Similarity 80.8
les 122; Conservative
                                   121
   101
121
  101 ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  61
   61
  58
   41 PDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAH----
                                   NNAALVNOTASDSSVMVROVGFGNNATANOY 151
   SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGG
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
NNAALVNYDQLVTRVVTHEMAHANNATANQY
   ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
   MKLLKVAAFAAI VVSGSALAGV----
  Conservative
  Sequence
  78.6%;
80.8%;
   79.2%;
   ALQSDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNN
  0;
  Score 613; DB 19;
Pred. No. 3.4e-57;
   Score 618; DB 19;
Pred. No. 9.8e-58;
  Mismatches
  Mismatches
   ----YDQLVTRVVTHEMAHASG
  0
  PEPTIDE SEQUENCES
   Length 151;
   Length 151;
  Indels
  Indels
  40;
  0
  Gaps
  Gaps
   120
  60
   60
  100
   40
  57
  120
   100
  0
  2
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В
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  US-09-543-407-24
  RESULT 9
US-09-543-407-24
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   В
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   US-09-543-407-14
  Query Match
Best Local
   SEQ ID NO 24
LENGTH: 151
  Sequence 24, Application US/09543407 GENERAL INFORMATION:
   Query Match
Best Local
  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14
  FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
  APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L
APPLICANT: Collinson, S.
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
   APPLICANT: KAY, WILLIAM W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major
   FILE REFERENCE: 920043.406
  APPLICANT: Collinson, S. Karen
  ORGANISM: Artificial Sequence FEATURE:
   ORGANISM: Artificial Sequence FEATURE:
   OTHER INFORMATION:
   TYPE: PRT
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
   ENGTH: 151
  Local Similarity
   Local Similarity
   124;
  123;
  INFORMATION: sequence containing the replacement fragmen INFORMATION: encoding PT3 from GP63 of Leishmania major.
      61
   61
   121 LVTRVVTHEMAHASVMVROVGFGNNATANOY 151
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
   61
  61
   ۳
  _
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNNNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60
                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDOWNAKNYDQLVTRVVT 120
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
  Doran, James L
   Conservative
  Conservative
   77.9%;
82.1%;
   78.3%;
   Karen
   υ
••
  6
   Score 608; DB 19;
Pred. No. 1.2e-56;
5; Mismatches 22;
   Score 611; DB
Pred. No. 5.5e
6; Mismatches
  DB 19;
.5e-57;
  Length 151;
   Length 151;
   Indels
  Indels
   0
   0
   Gaps
   60
   60
  60
   0
```

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   US-09-543-407-28
  US-09-543-407-31
   US-09-543-407-31
  밁
   Ş
Query Match
Best Local Similarity
Matches 122; Conserv
  CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 151
   Sequence 28, Applica GENERAL INFORMATION:
  SEQ ID NO 31
LENGTH: 131
  APPLICANT: Doran, James L. APPLICANT: Collinson, S. K APPLICANT: Kay, William W.
   Matches 117;
   Query Match
Best Local Similarity
  Sequence 31,
   TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
   TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

NUMBER OF SEQ ID NOS: 59

NUMBER OF RESISE FASTSEQ for Windows Version 4.0
   FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   APPLICANT: White, Aaron P.
  APPLICANT: White, Aaron P. APPLICANT: Doran, James L APPLICANT: Collinson, S. APPLICANT: Kay, William W
  ORGANISM: Artificial Sequence
   TYPE: PRT
  ORGANISM: Salmonella enteritidis
   141
  121 GEGNNATANOY 131
   INFORMATION:
  121
   121 NNAALVNOTASDSSVMVROVGFGNNATANOY 151
  81 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
   21 GVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGAD 80
   GFGNNATANOY 151
   VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV
  GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
  HEMAHANQTASDSSVMVRQVGFGNNATANQY
  Application US/09543407
  Collinson, S. K. Kay, William W.
  Doran, James L.
  Application US/09543407
        Conservative
   Conservative
   77.4%;
89.3%;
                        77.1%;
   Karen
   Karen
   3;
      Score 601; DB 19;
Pred. No. 6.6e-56;
4; Mismatches 25;
   Score 604; DB 19;
Pred. No. 2.6e-56;
   Mismatches
  151
   PEPTIDE SEQUENCES
   Length 151;
  Length 131;
        Indels
   Indels
      ٥,
  <u>,,</u>
      Gaps
  Gaps
  60
      0
```

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 22
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PE:
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 30
   RESULT 13
US-09-543-407-30
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   US-09-543-407-22
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  US-09-543-407-22
   Sequence 22, Applica
GENERAL INFORMATION:
   Sequence 30, Applica GENERAL INFORMATION:
  Best Local Sim
Matches 123;
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  FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
TYPE: PRT
ORGANISM: Artificial
   LENGTH: 151
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   Application US/09543407
   Application US/09543407
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  76.9%;
81.5%;
Sequence
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  Score 600; DB 17;
Pred. No. 8.4e-56;
   PEPTIDE SEQUENCES
  PEPTIDE SEQUENCES
  Length 151;
  Indels
  ٥,
  Gaps
   120
   120
  60
   120
  60
   60
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US-08-978-878-4
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   ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-543-407-7
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  8
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   밁
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  US-09-543-407-30
   US-09-543-407-7
  Sequence 4, Application US/08978878 GENERAL INFORMATION:
  SOFTWARE: FastSEQ
SEQ ID NO 7
   GENERAL INFORMATION:
APPLICANT: White, Aaron P.
   Matches
   Best Local Similarity Matches 123; Conserv
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Best Local Similarity
  Sequence
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APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
   APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
   FEATURE:
OTHER INFORMATION: R
OTHER INFORMATION: G
OTHER INFORMATION: G
   NUMBER OF SEQ ID NOS:
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  NNAALVNOTASDSSVMVROVGFGNNATANOY 151
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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  Application US/09543407
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81.5%;
  Score 599; DB 19;
Pred. No. 1.1e-55;
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   27;
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EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1991-11-06
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER APPLICATION NUMBER: US 08/318,519
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Datentin Ver. 2.0
SEQ ID NO 4
LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli
Search completed: March 11, 2004, 19:13:11 Job time: 172.3 secs
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   Query Match 66.7%; Score 520; DB 13; Length 151; Best Local Similarity 68.2%; Pred. No. 3.4e-47; Matches 103; Conservative 21; Mismatches 27; Indels 0;
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Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 0.5
  125546 seqs, 13197846 residues
Pending_Patente_AA, New:*

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  GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result<br>No. | Score | Query<br>Match | Length | B        | ID                  | Description       |
|---------------|-------|----------------|--------|----------|---------------------|-------------------|
| 1             | 520   | 66.7           | 151    | σį       | US-09-741-873C-4    | Sequence 4, Appli |
| N             | 444   | 56.9           | 131    | ហ        | -09-741-873C-       | æ                 |
| ω             | 82.5  | 10.6           | 434    | ტ        | -10-045-674A-       | 59                |
| 4             | 81.5  | •              | 424    | σ        | -10-045-674A-       | e 59              |
| IJ            | 81.5  | •              | 533    | σ        | US-10-045-674A-527  | e 52              |
| o,            | 79.5  |                | 956    | σ        |                     | e 63              |
| 7             | 78.5  |                | 480    | -        | PCT-US04-05654-1498 | e 14              |
| 8             | 77.5  |                | 234    | σ        | US-10-767-701-45603 | 456               |
| 9             | 77.5  |                | 443    | 6        | US-10-100-683-7608  | 7608              |
| 10            | 76.5  |                | 179    | 6        | °                   | 3534              |
| 11            | 76.5  |                | 348    | σ        | US-10-004-115B-34   | e 34,             |
| 12            | 74.5  |                | 430    | σ        | US-10-451-467A-314  |                   |
| 13            | 74    |                | 305    | بر       | PCT-US04-05654-1406 | e 1406            |
| 14            | 73    |                | 310    | <u>ب</u> | PCT-US04-05654-1412 | 1412,             |
| 15            | 73    | 9.4            | 386    | σ        | US-10-767-701-42417 | e 424             |
| 16            | 73    |                | 1327   | _        | PCT-US04-02338-49   |                   |
| 17            | 72    |                | 654    | _        |                     | 156               |
| 18            | 72    |                | 654    | 6        | US-10-764-425-156   | 156,              |
| 19            | 71.5  |                | 386    | σ        | 1032                | 10326             |
| 20            | 71.5  |                | 386    | σ        | US-10-100-683-10327 | æ                 |
| 21            | 71.5  |                | 772    | σ        |                     | Ç                 |
| 22            | 71    |                | 391    | -        | PCT-US04-05654-336  | е 336, А          |
| 23            | 70.5  |                | 173    | თ        | US-10-767-701-39649 | 39649             |
| 24            | 70    |                | 1160   | σ        | US-10-603-150-2     | 2                 |
| 25            | 69.5  |                | 449    | Φ        | -10-641-678         |                   |
| 26            | 69    | 20             | 245    | Þ        | US-10-779-461-19    | 19                |

| US-10-767-701-41435 |
|---------------------|
| US-10-767-701-46086 |
| Ö                   |
| PCT-US04-05654-2038 |
| US-10-767-701-58351 |
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|                     |
| PCT-US04-05654-2586 |
| US-10-767-701-40444 |
| CT-US04-05654-2080  |
| PCT-US04-05654-1756 |
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|                     |
|                     |
|                     |

## ALIGNMENTS

RESULT 1

```
APPLICANT: Normark, Staffan

APPLICANT: Olsen, Arne

FITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873C

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: SE 8801723-1

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/789,437

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PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/318,519

PRIOR APPLICATION NUMBER: US 08/318,519

PRIOR PILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 11
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   US-09-741-873C-4
   US-09-741-873C-4
  SEQ ID NO 4
LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli
  Sequence 4, Application US/09741873C GENERAL INFORMATION:
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   Query Match
  SOFTWARE: PatentIn version 3.0
  Local Similarity
121 GNGAAVDOTASNSSVNVTOVGFGNNATAHOY 151
                          121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 594
  RESULT 3
US-10-045-674A-594
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  US-09-741-873C-2
   CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR REPLICATION NUMBER: US 07/347,189
PRIOR RILING DATE: 1989-05-04
PRIOR RILING DATE: 1989-05-04
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 07/970,846
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PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 07/970,846
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  Query Match
  SOFTWARE: PatentIn version 3.0 SEQ ID NO 2
  Sequence 2, Application US/09741873C GENERAL INFORMATION:
   APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM
TITLE OF INVENTION: OF PROTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
   APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: WASTRI, HORACIO G.
APPLICANT: WASTRI, HORACIO G.
  TITLE OF INVENTION: LIBRARIES FILE REFERENCE: DYAX/002 CIP2
  PRIOR FILING DATE: 1994-
NUMBER OF SEQ ID NOS: 11
   APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne
   ·09-741-873C-2
   TYPE: PRT
ORGANISM: Escherichia coli
   FILE REFERENCE: 012889-084
  TITLE OF INVENTION: Fibronectin Binding Protein As Well
   LENGTH: 131
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FILING DATE: 1994-01-28
APPLICATION NUMBER: US 08/318,519
   INFORMATION:
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  141 GFGNNATANOY 151
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   Application US/10045674A
   1994-10-05
  56.9%; Score 444; 65.6%; Pred. No. 2.
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APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOGE, RENE
APPLICANT: HOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR PILING DATE: 2001-04-17
PRIOR PILING DATE: 2001-04-17
PRIOR PILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
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   US-10-045-674A-591
   US-10-045-674A-591
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  ; OTHER INFORMATION: Description of Artificial Sequence: M13-III; OTHER INFORMATION: protein sequence US-10-045-674A-594
   SOFTWARE: Pa
   Matches
  Query Match
Best Local Similarity
  GENERAL INFORMATION:
   Sequence 591,
  Query Match
Best Local Similarity
  Matches
  APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACTO G.
APPLICANT: ROOKEY, KRISTIN L.
  OTHER INFORMATION: OTHER INFORMATION:
   TYPE: PRT
ORGANISM: Unknown Organism
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25.2%; Pred. No. 3.8;
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  US-10-045-674A-527
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  -10-093-037A-63
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  GENERAL INFORMATION:
   PILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION.
  PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/134,078
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 08/949,026
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/056,916
   CURRENT APPLICATION NUMBER: US/10/093,037A CURRENT FILING DATE: 2002-03-06
   APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OP INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM:
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
  APPLICANT: LAM, DAVÍD E.
TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: 564462001402
  APPLICANT: Jay M. Short
  PRIOR APPLICATION NUMBER: US 09/910,579
   APPLICANT:
   NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2
  CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
  PRIOR FILING DATE: 2001-04-17
   OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS OTHER INFORMATION: protein sequence
   ORGANISM: Artificial Sequence FEATURE:
  TYPE: PRT
   ENGTH: 533
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   FILING DATE:
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  COHEN, EDWARD H.
  VGFGNNA 146
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   VGDGDNS 462
   Bylina, Edward
Swanson, Ronald V.
Mathur, Eric J.
   Application US/10093037A
  NASTRI, HORACIO G. ROOKEY, KRISTIN L.
  Application US/10045674A
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   RENE
   1996-12-06
   2000-04-17
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  US-10-093-037A-63
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  RESULT 7
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LENGTH: 956
  SOFTWARE: Patentin
SEQ ID NO 1498
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Best Local Similarity
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   Matches
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  PRIOR FILING DATE:
   PRIOR APPLICATION NUMBER: 10/374,780 PRIOR FILING DATE: 2003-02-25 PRIOR APPLICATION NUMBER: 10/675,852
   APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
   APPLICANT:
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   Riechmann, Jose Luis
Jiang, Cai-Zhong
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  Dubell III, Arnold
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  PRIOR APPLICATION NUMBER: US 60/040,162
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PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
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  APPLICANT: Rosen, et al.
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NAME/KEY: unsure
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  APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
  APPLICANT: Kovalic, APPLICANT: Zhou, Y
  TYPE: PRT
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US-10-767-701-35342
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   APPLICANT: Kovalic,
APPLICANT: Zhou, Y
APPLICANT: Cao, Yo
  Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 13468
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Sequence 34, Application US/10004115B GENERAL INFORMATION:

APPLICANT: ASAKO, HIROYUKI APPLICANT: MATSUMURA, KEN APPLICANT: SHIMIZU, MASAT

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US-10-451-467A-314
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  APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION
TITLE OF INVENTION: YEAST AND FUNGI
   PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: JP 2001-026594
PRIOR FILING DATE: 2001-02-02
   APPLICANT: WAKITA, RYUHEI
TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE
TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE
FILE REFERENCE: 7372-72249
CURRENT APPLICATION NUMBER: US/10/004,115B
CURRENT FILING DATE: 2001-12-06
  PRIOR APPLICATION NUMBER: EP 00870318.3 PRIOR FILING DATE: 2000-12-22
   APPLICANT: CONTRERAS, ROLAND HENRI APPLICANT: EBERHARDT, INES
  PRIOR APPLICATION NUMBER: JP 2000-372704 PRIOR FILING DATE: 2000-12-07 PRIOR APPLICATION NUMBER: JP 2001-006144
   APPLICANT:
  PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
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  PRIOR FILING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 37
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TYPE: PRT
  ORGANISM: Saccharomyces cerevisiae
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82 ---GOGADNSTIELTONGFRNNATIDOWNAKNS-----DITVGOYGGNNAA- 124
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SEQ ID NO 1406
LENGTH: 305
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   APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780.
PRIOR PPLICATION NUMBER: 10/675,852
PRIOR PILING DATE: 2003-02-25
PRIOR PILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR PILING DATE: 2003-09-30
   APPLICANT: Sherman,
  NUMBER OF SEQ ID NOS: 2950
   OTHER INFORMATION: Orthologous to G1073
  ORGANISM: Oryza sativa FEATURE:
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  Pineda, Omaira
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   Haake, Volker
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Sherman, Bradley K Riechmann, Jose Luis Jiang, Cai-Zhong

Creelman, Robert A

łaake, Volker

Jacqueline E

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RESULT 15
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Sequence 42417, Application US/10767701
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
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   PPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
ITTLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
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ORGANISM: Glycine max
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   Query Match
Best Local Similarity
Matches 27; Conserv
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|-------------|-----------------|----------------|-----------------|-----------------|----------------|------------------|-----------------|------------------|-----------------|---------------|-----------------|----------------|-----------------|------------------|--------------|-----------------|----------------|---------------|---------------|---------------|---------------|--------------|-----------------|-----------------|--------------|---------------|----------------|--------------|-------------------|--------------|--------------|---------------|-------------|---------------|---------------|-----------------|-----------------|-----------------|-----------------|----------------|---------------|-------------------|--------------|---------------|------------------|--|
| 3           | 0 '             | 99             | 99              | 99              | 99             | 99               | 99              | 99               | 99              | 99            | 99              | 99             | 101.5           | 01.              |              | 05.             | ū              |               | σ             | 4             | 447           | 4            | 466             | 466             | 466          | 470           | 504            | 523          | 523               | 525          | 525          | 528           | 574         | 597           | 500           | 606             | 609             | 611             | 619             | 622            | 662           | æ                 | 689          |               | 774              |  |
|             | ١               |                | .~              | ۶               | .2             | 2                | N               |                  |                 |               |                 |                |                 | ω.               | w            | ω.              | 9              |               |               | 44.3          | 7.            | 7.           |                 |                 |              | 0             |                | 7.           |                   | 7.           | 7.           | œ             | φ.          | 7:            | 7 :           | 200             | 200             | œ               | 0               | .0             | 85.5          | 8                 | 9            |               | 0                |  |
| 6           | 2               | S              | 20              | 65              | ū              | 23               | င္မ             | ū                | ū               | J             | 4               | 9              | 445             | 4                | 145          | 145             | 48             | 70            |               | 0             | 131           | w            | ū               | S               | ū            |               | N              | S            | 151               | v            | S            | 151           | s           | 151           | ., (          | 151             | J I             | ū               | 151             | ū              | ū             |                   | 151          | 151           |                  |  |
| ţ           |                 | 19             | 19              | 19              | 19             | 24               | 24              | 24               | 24              | 21            | 21              | 21             | ω<br>ω          | 29               | 23           | 21              | 19             | 19            | 19            | 19            | 21            | 13           | 30              | 16              | 16           | 9             |                | ယ            | ω<br>W            | 21           | 13           | 19            | 19          |               |               |                 |                 |                 |                 |                | 19            | თ                 |              | 19            |                  |  |
|             | -09-573-6558-66 | -09-573-655B-3 | -09-573-655A-66 | -09-573-655A-34 | 09-570-581A-18 | -09-935-625-2515 | -09-935-625-794 | 8-09-935-625-251 | -09-935-625-794 | 9-708-427-765 | -09-708-427-765 | 09-708-427-765 | -60-360-039-206 | -10-369-493-2063 | -09-803-110- | -09-739-449-885 | -09-543-407-39 | -09-543-407-3 | -09-543-407-3 | -09-543-407-3 | -09-741-873B- | -08-978-878- | -10-417-886-583 | -09-252-691C-58 | 9-252-691-58 | S-09-543-407- | -08-233-642A-5 | -60-444-371- | S-60-352-946-2    | -09-741-873B | -08-978-878- | -09-543-407-7 | 09-543-407- | -09-543-407-3 | -09-543-407-3 | S-09-543-407-2  | -09-543-407-    | -09-543-407-1   | -09-543-407-    | S-09-543-407-1 | -09-543-407-2 | US-08-233-642A-57 | -09-543-407- | S-09-543-407- | US-09-543-407-20 |  |
| cancina oc. | emience 667     | equence 349,   | equence 667,    | equence 349, A  | nce 1851,      | equence 25157,   | equence 7945,   | e 25158,         | equence 7946,   | equence 7655, | equence 7656,   | equence 765    | equence 206     | equence 206      | 885          | equence 885     | equence 39,    | equence 32,   | equence 37    | equence 35    | nce           | equence 2,   | equence 58:     | equence 58:     | e 58         | Sequence 34   | quence 55,     | equence 2,   | Sequence 2, Appli | equence 4,   | equence 4,   | equence 7,    | e 16        | eguence 30    | ednesde 11    | equence 24. App | equence 14. App | equence 12, App | equence 22, App | e 18, App      | equence 28,   | 57, Appl          | e 5, Appl    | e 26,         | equence 20, App  |  |

#### ALIGNMENTS

```
RESULT 1

US-09-543-407-20

Sequence 20, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: LOran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: WINDER: US/09/543,407

CURRENT APPLICATION UNUMBER: US/9/543,407

CURRENT FILING DATE: 2000-04-05

INUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 20

LENGTH: 151

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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RESULT 3
US-09-543-407-5
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   US-09-543-407-26
   US-09-543-407-26
  US-09-543-407-20
  Sequence 5, Application US/09543407 GENERAL INFORMATION:
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
   Matches
  Query Match
Best Local Similarity
   Sequence 26, Application US/09543407 GENERAL INFORMATION:
              APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   Matches
   Query Match
CURRENT APPLICATION NUMBER: US/09/543,407
  APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  FILE REFERENCE: 920043.406
  APPLICANT: White, Aaron P.
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial Sequence FEATURE:
  TYPE: PRT
   Local Similarity
   113
   143;
  121
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  58
  61
   151;
  61
   61
   1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  ----YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
   SDARKYDQLVTRVVTHEMAHA-------GQGADNSTIELTQNGFRNNATIDQWNAKNSD
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
  SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  SDARKYDQI/TTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  NNAALVNOTASDSSVMVROVGFGNNATANOY 151
   Doran, James
   Conservative
   100.0%; Score 774; DB 19; llarity 100.0%; Pred. No. 3.3e-75; Conservative 0; Mismatches 0;
   91.6%;
  Score 709; DB 19;
Pred. No. 3.8e-68;
0; Mismatches 0
  0;
  PEPTIDE SEQUENCES
  PEPTIDE SEQUENCES
   Length 151;
  Indels
   Length
   Indels
   151;
  16;
   0;
  Gaps
  112
  57
  N
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  RESULT 4
US-08-233-642A-57
   В
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   US-08-233-642A-57
  밁
  S
   S
  US-09-543-407-5
   Best Loc
Matches
Query Match
Best Local Similarity 90:
Matches 136; Conservative
   CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 5
   GENERAL INFORMATION:
  Query Match
  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
   LENGTH: 151
TYPE: PRT
  ORGANISM: Salmonella enteritidis
   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  TOPOLOGY: li
   TELEPHONE: (206) 622-4900
  ATTORNEY/AGENT INFORMATION:
   APPLICANT:
  NUMBER OF SEQUENCES:
   CORRESPONDENCE ADDRESS:
   TITLE OF INVENTION:
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
  TELEPHONE: (200) 682-6031
  NAME: King, Joshua REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
   APPLICATION NUMBER: FILING DATE: 26-APPLICATION: 424
   Local Similarity hes 137; Conserv
  STREET:
  LENGTH:
  COUNTRY:
   ADDRESSEE:
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   ب
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   amino acid
  3723836 SEEDANBERRY
  Seattle
   Washington
  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   Application US/08233642A
  151 amino acids
  6300 Columbia Center, 701 Fifth Avenue
  U.S.A.
   Collinson, S. Karen
Clouthier, Sharon C.
  Doran, James L.
   Conservative
   Seed and Berry
  protein
  26-APR-1994
  William W.
  2000-04-05
   Windows Version
  89.0%;
88.4%; Score 684; DB 6; Length 151; 90.1%; Pred. No. 1.9e-65; tive 3; Mismatches 12; Indels
   BASED VACCINES
  METHODS AND COMPOSITIONS FOR SALMONELLA-
   US/08/233,642A
   35,570
   ω
••
  920043.403C3
   Score 689; DB 19;
Pred. No. 5.6e-66;
  Mismatches
   Version
   Length 151;
   Indels
  Gaps
   120
  120
   60
  0
```

0,

Gaps

```
Sequence 18, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI

FILE REFERENCE: 920043.406

CURRENT APPLICATION UNMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 151
  APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S.
APPLICANT: Collinson, S.
APPLICANT: Collinson, S.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 151
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   ঠ
   RESULT 5
US-09-543-407-28
   ঠ
   US-09-543-407-18
   밁
   용
  Query Match
Best Local S
Matches 136
   Sequence 28, Applica GENERAL INFORMATION
   -09-543-407-28
  FEATURE: FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  TYPE: PRT ORGANISM: Artificial Sequence
   106
   106
   121
   121
  2
  61
  62
   61
   _
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  -
  Similarity 81.9
36; Conservative
  WNAKONSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  NNPALVNOTASDSSVMVRQVGFGNNATANQY 151
  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA------
   MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  SDARK-----YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQ
  Application US/09543407
   85.5%;
81.9%;
  <u>,</u>
  Score 662; DB 19;
Pred. No. 4.7e-63;
0; Mismatches 0
   DB 19;
  0
   PEPTIDE SEQUENCES
   PEPTIDE
  Length 151;
  Indels
   SEQUENCES
  30;
  FRNNATIDO
  Gaps
  105
  105
   60
   60
  120
   120
   60
```

```
RESULT 8
US-09-543-407-12
; Sequence 12, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.
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  US-09-543-407-22
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   US-09-543-407-18
   US-09-543-407-22
  Query Match
Best Local S
Matches 129
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
  GENERAL INFORMATION:
   Sequence
   Matches
  Query Match
Best Local Similarity
  TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
   APPLICANT: White, Aaron P. APPLICANT: Doran, James L.
  APPLICANT: Collinson, S. Karen APPLICANT: Kay, William W.
  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
  FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial Sequence
   TYPE: PRT
  Local Similarity
   128;
  104
  129;
  99
   61
  61
   22, Application
  86
   98
  43
   61
   Н
  RNNATIDOWNAKNSDITYGOYGGNNAALVNOTASDSSVMVRQVGFGNNATANQY 151
  SDARKYDQLVTRVVTHEMAHA------
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  ----YDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
  ----DQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPD-----
  Conservative
   Conservative
  80.0%;
  80.4%;
   US/09543407
  ------YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFR
   0;
  <u>,</u>
  Score 619; DB 19;
Pred. No. 2.2e-58;
0; Mismatches 0;
  Score 622; DB 19;
Pred. No. 1e-58;
   Mismatches
  0
   0
  PEPTIDE SEQUENCES
   Length 151;
  Length
  Indels
   -GOGADNSTIELTONGF
  44;
   46;
  Gaps
   Gaps
  98
   60
   97
  42
  60
  103
  97
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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   US-09-543-407-14
  US-09-543-407-12
   Matches
   Query Match
  Sequence 14, Application US/09543407 GENERAL INFORMATION:
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   Matches 122;
   Query Match
Best Local
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragmen OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  TYPE: PRT
ORGANISM: Artificial Sequence
   Local Similarity
             61
  61
   123;
  121
   121
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNNNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  61
   5
   Similarity
  1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
                            SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   Conservative
   Conservative
  PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
  78.7%;
81.5%;
   78.9%; Score 611; DB 19;
80.8%; Pred. No. 1.6e-57;
tive 7; Mismatches 22;
   6;
   Score 609; DB 19;
Pred. No. 2.7e-57;
6; Mismatches 22;
  PEPTIDE SEQUENCES
  Length 151;
   Indels
  Length 151;
   Indels
   <u>,,</u>
   o
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  120
   120
  60
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   US-09-543-407-31
   RESULT 11
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   US-09-543-407-24
  RESULT 10
US-09-543-407-24
   Ş
   Sequence 31, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  밁
   FILE REPERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 131
   Query Match
   Query Match
Best Local S
Matches 124
  Matches
  Sequence 24, Application US/09543407 GENERAL INFORMATION:
   SEQ ID NO 24
LENGTH: 151
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collingon, S. Karen
APPLICANT: Collingon, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT FULUENTION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FRESEQ for Windows Version 4.0
  TYPE: PRT ORGANISM: Salmonella enteritidis
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragme: OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major
  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
  Local
   Local Similarity
nes 124; Conserv
   121
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAH
  61
  61
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
   121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
  Similarity
  SDARKSETTITOSGYGNGADVGOGADNSTIBLTONGFRNNATIDOWNAKNYDOLVTRVVT 120
   SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
   Conservative
   Conservative
  77.8%;
89.3%;
  78.3%;
82.1%;
   ω
-.
                                     Score 602; DB 19;
Pred. No. 1.3e-56;
3; Mismatches 11;
  Score 606;
Pred. No. 5.
   Mismatches
  DB 19;
5.7e-57;
   151
  PEPTIDE SEQUENCES
   Length 131;
                                       Indels
   Indels
   fragment a major.
                                     0
   0;
                                   Gaps
   Gaps
   60
```

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILLE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT TILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
   RESULT 13
US-09-543-407-16
  र्
  В
   ঠ
   밁
  ફ
   RESULT 12
US-09-543-407-30
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CURRENT FILING DATE: 2000-04-05
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   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
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   120
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APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
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PREPARATION

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EARLIER FILING DATE: 1994-10-05
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| Sequence 59520, A   | Sequence 1838, Ap   | Sequence 170, App | Sequence 169, App | Sequence 5134, Ap   | Sequence 70, Appl | Sequence 119, App | Sequence 120, App  | Sequence 5818, Ap   | Sequence 43, Appl | Sequence 48913, A   | Sequence 2, Appli | Sequence 2, Appli | Sequence 43919, A   | Sequence 42650, A   | Sequence 138, App | Sequence 1466, Ap   | Sequence 37331, A   | Sequence 34, Appl |

#### ALIGNMENTS

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PRIOR FILING DATE: 1998-05-06
PRIOR PELICATION NUMBER: US 08/978,878
PRIOR PELICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1999-05-04
PRIOR PELING DATE: 1999-11-06
PRIOR PELING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR PILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PILING DATE: 1994-10-05
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GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
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GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its
   APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
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   APPLICANT: LADNER, ROBERT C. APPLICANT: COHEN, EDWARD H.
  CURRENT APPLICATION NUMBER: US/10/779,461
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PRIOR APPLICATION NUMBER: 60/447,073
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PCT-US04-05654-590

Sequence 590, Application PC/TUS0405654
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis

APPLICANT: APPLICANT: APPLICANT:

Riechmann, Jose Luis Jiang, Cai-Zhong Heard, Jacqueline I Haake, Volker

Creelman, I Ratcliffe,

Robert A

RESULT 8

```
FILE REFERENCE: DYAX/OO2 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PALENTIN Ver. 2.1
SOFTWARE: PALENTIN Ver. 2.1
TYPE: DDT.
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  RESULT 7
US-10-045-674A-527
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   8
  US-10-045-674A-527
  Sequence 527, Application:
  Query Match
Best Local 9
   APPLICANT: HOOGENBOON
TITLE OF INVENTION: NO
TITLE OF INVENTION: OF
TITLE OF INVENTION: OF
TITLE OF INVENTION: OF
  Matches
   APPLICANT: LADNER, ROBERT APPLICANT: COHEN, EDWARD
   APPLICANT:
   APPLICANT:
  OTHER INFORMATION: Description of Artificial Sequence: Vector pCES5 OTHER INFORMATION: protein sequence
   FEATURE:
   ORGANISM: Artificial Sequence
  Local Similarity les 37; Conserv
451 SQMA---
  352
   123 AALVNQTASDSSVMVRQVGFGNNA 146
  319 DDYKRSTSGQVQPTKSESN--NRPITFGSEKGSN 350
  236 INGGGGGGVNQQWNATTTNPSGGQSSQIWDFNLGQSRGPEDT
   I: HOET, RENE

T: HOSTENBOOM, HENDRICUS R. J. M.

T: HOSGENBOOM, HENDRICUS R. J. M.

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TI HOSGENBOOM, HENDRICUS R. J. M.

TI HOSGENBOOM, HENDRICUS R. J. M.

T
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   15 SGSALAGVVPQWGG--GGNHNGGGNSSGPDSTLSIYQ-YGSANAAL-----ALQSDA 63
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   14 VSGSALAGVVPOWGGGGNHNGGGNSS-----
  KGKLDSVAT-----DYGAAID-----
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  ROOKEY,
  Application US/10045674A
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  ROBERT C.
EDWARD H.
HORACIO G.
KRISTIN L.
  9.5%; Score 73.5;
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  Gaps
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  FAMILY
  411
   122
  277
   62
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PPLICANT:

Keddie, James Dubell III, Arnold N

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   US-10-045-674A-594
  PCT-US04-05654-590
   SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 594
  SOFTWARE: Pat
SEQ ID NO 590
LENGTH: 321
  Sequence 594, Application US/10045674A
  APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM.
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR APPLICATION NUMBER: 03/837,306
PRIOR ENTING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 03/837,306
  GENERAL INFORMAT:
  Matches
  Query Match
  PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
OTHER INFORMATION: Description of Artificial Sequence: M13-III OTHER INFORMATION: protein sequence
   TYPE: PRT
ORGANISM: Artificial Sequence
  APPLICANT:
   CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR PILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
   APPLICANT:
  APPLICANT: LADNER,
  PPLICANT:
  APPLICANT:
  ENGTH:
   OTHER INFORMATION: G3384 Orthologous to G256
  TYPE: PRT
ORGANISM: Oryza sativa
  APPLICANT:
  FEATURE:
  PPLICANT: Kumimoto, Roderick W

APPLICANT: Pilgrim, Marsha L

TITLE OF INVENTION: POLYMOCLEOTIDES AND POLYPEPTIDES IN PLANTS

TILE REFERENCE: MBI-0047 PCT
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  PPLICANT:
   PPLICANT:
   Local
  199
  67 DQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATID--QMNAKNSDITVGQYGGNNA 123
  10 AAIVVSGSALAGVVPQW----GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKY 66
  434
  28;
   Similarity
   PatentIn version 3.2
  AAYASSADNIARLLQGWMRPGGG----GGGNGKGPEAS-----GSTSTTATTQQQPQ-- 246
   Pineda, Omaira
Repetti, Peter
Century, Karen
   Broun, Pierre E
  Yu, Guo-Liang
   Conservative
  ION:
   RENE
   ROBERT C.
EDWARD H.
   HORACIO G.
KRISTIN L.
  9.4%; Score 73; DB 1; Length 321; 23.5%; Pred. No. 14;
   -CSGEGAASASASASQSGAAAAATAQTPECSTETSKMATGGGAGGPA 292
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NAME/KEY: misc_feature;
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LOCATION: (B) LOCATION 1...708;
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SEQUENCE DESCRIPTION: SEQ ID NO: 60.
US-10-417-884A-6047
  RESULT 10
US-10-417-884A-6047
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  밁
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  US-10-045-674A-594
      Query Match
Best Local Similarity
  Sequence 6047,
  Matches
   Query Match
Best Local
   TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6047:
   SQUENCE 6047, Application US/10417884A
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532

FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
   FEATURE:
  MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
   SEQUENCE CHARACTERISTICS:
   CURRENT APPLICATION DATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
   NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
  351 NSOMAQVGDGDNS 363
   134 SVMVRQVGFGNNA 146
  257 GGSGGGSGGSEGG--
   87 NSTIELTONGFRNNATIDOWNAKNS-DITVGOYG-----GNNAALVNOTA-----SDS 133
   27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGAD 86
  l Similarity 25.6
34; Conservative
   ORGANISM: Enterococcus faecium
  LENGTH: 708 amino acids
TYPE: amino acid
  APPLICATION NUMBER: US/10/417,884A
FILING DATE: 17-Apr-2003
   TOPOLOGY: linear
  NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
  TELEPHONE: (781)893-5007
  SOFTWARE: ASCI
  OPERATING SYSTEM: <Unknown>
   STATE: Massachusetts
  STREET: 100 Beaver Street
  -----MTENADENAL---OSDAKGKLDSVATDYGAAIDGFIGDVSGLANGNGATGDFAGS 350
   COUNTRY: USA
   ADDRESSEE: GENOME THERAPEUTICS CORPORATION
   25.6%;
      9.3%;
24.9%;
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  17; Mismatches
      Score 72;
Pred. No.
   Score 72.5;
Pred. No. 2
   GTC-012
  GSEGGGSGGGGGGDFDY----EKMANANKGA- 298
  6047:
  and David Bush
AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAI
DB
48;
                        6
   DB 6;
  43; Indels
   Length 434;
  39;
  Gaps
  THERAPEUTICS
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Length 708;

RESULT 11 PCT-US04-0

-US04-03808-14

APPLICANT:

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430

Matches

43,

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ORGANISM: Gallus gallus PCT-US04-03808-14
  Sequence 63, Application US/10093037A
GENERAL INFORMATION:
APPLICANT: Jay M. Short
APPLICANT: Bylina, Edward
APPLICANT: Swanson, Ronald V.
  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14
   Sequence 14, Application PC/TUS0403808 GENERAL INFORMATION:
   FILE REFERENCE: 38586-332
CURRENT APPLICATION NUMBER: PCT/US04/03808
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: US 60/445,672
PRIOR FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 14
  FILE REFERENCE: 564462001402
CURRENT APPLICATION NUMBER: US/10/093,037A
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US 09/910,579
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/134,078
PRIOR FILING DATE: 1998-08-13
   PRIOR APPLICATION NUMBER: US 08/949,026 PRIOR FILING DATE: 1997-10-10
   TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS
  APPLICANT: The Regents of the University of California
   ITLE OF INVENTION: Nell Peptide Expression Systems and ITLE OF INVENTION: Formation Activity of Nell Peptide
                     APPLICATION NUMBER: US 60/056,916
FILING DATE: 1996-12-06
  545 KISEITGKANNYTDGKVSEINSQLTASINEVDTTAKDA----
  102 TIDOWNAKNSDITVGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNNATA 148
  486 ATKG-AVQIEWLKLEKGNTRTPNISEYKYRGTGMRDSNNPKDYVWDLAPEYVEDNLATDI
  81 LRNKYE--FTILVTLKQAHLNSGVIFSIHHLDHRYLELESSGHRN 123
   62 DARKYDQLVTRVVTHEMAHAGQGA-----DNSTJELTQNGFRN 99
   53 ANAALALQSDARKYDQLVTRVVT-HEMAHAGQGADNS-----TIELTQNGFRNNA 101
  4 LKVAAFAAIVVSGSALAGV--VPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQS 61
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   LTVQSFAVYIAAGRVKVGDMKPTEGLANTWELTFTVTKQH----IDSGVTNYLEIYQYPS
   Swanson, Ronald V.
Mathur, Eric J.
Lam, David E.
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   Kuroda, Shunichi
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   Indels
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  38;
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   52
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US-10-767-701-37968
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  RESULT 13
US-09-126-816C-6
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   ; ORGANISM: Bankia
US-10-093-037A-63
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Matches
   Sequence 37968, Application US/10767701 GENERAL INFORMATION:
  SEQ ID NO 6
  Sequence 6, Applicat GENERAL INFORMATION:
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SEQ ID NO 63
LENGTH: 956
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
   APPLICANT: VON EICHEL-STREIBER, CHRISTOPH
APPLICANT: BOQUET, PATRICE
APPLICANT: THELESTAM, MONICA
  APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
   NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
  PRIOR APPLICATION NUMBER: PCT/EP97/00426
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: 96 101 469.3
PRIOR FILING DATE: 1996-02-02
   FILE REFERENCE: 98501/254992/bet
CURRENT APPLICATION NUMBER: US/09/126,816C
CURRENT FILING DATE: 1998-07-31
  TITLE OF INVENTION: METHOD OF INACTIVATION OF RAS SUBFAMILY PROTEINS AND TITLE OF INVENTION: AGENTS THEREFOR
  TYPE: PRT ORGANISM: Clostridium sordellii
   TYPE: PRT
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  Similarity
  Application US/09126816C
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   Conservative
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  9.2%; Score 71.5; I
19.8%; Pred. No. 79;
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   9.2%; Score 71.5; DB 5;
28.1%; Pred. No. 2.5e+02;
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  Length 956;
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   49;
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28

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Query Match Best Local :

916

Matches

RESULT 12

US-10-093-037A-63

SEQ

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CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: Patentin version 3.2
SEQ ID NO 2748
LENGTH: 399
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SEQ ID NO 37968
LENGTH: 363
  APPLICANT: Gutterson, Neal
APPLICANT: Yu, Guo-Liang
APPLICANT: Broun, Pierre
APPLICANT: Kumimoto, Roderick W
APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REPERENCE: MBI-0047 PCT
  APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
   APPLICANT:
  APPLICANT:
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   APPLICANT:
  FEATURE:
OTHER INFORMATION: G1882
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  PPLICANT
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Ratcliffe, Oliver
   Repetti, Peter
Century, Karen
   Pineda, Omaira
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Reuber, T. Lynne
  Dubell III, Arnold N
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   273
  215 NSNNNNILGLGSSLPPLKLMPPLDFTDNFTLQYGAVSAPSYHIGGGSSGGAAALL-NGF-
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Search completed: March 11, Job time : 5.3 secs 2004, 19:14:17

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
  Total number of hits satisfying chosen parameters:
   Searched:
   Scoring table:
   Sequence:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
   March 11, 2004, 18:33:51; Search time 171.3 Seconds (without alignments) 860.386 Million cell updates/sec
Match Length DB
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  US-09-543-407-22
776
  6019581 seqs, 976053577 residues
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   1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
  Pending_Patents_AA_
: /cgn2_6/ptodata/
  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
   / Cgn2_6/ptodata/2/paa/US082_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US082_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US082_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US085_COMB.pep: *
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/ Cgn2_6/ptodata/2/paa/US100_COMB.pep: *
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/ Cgn2_6/ptodata/2/paa/US105_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US105_COMB.pep: *
/ Cgn2_6/ptodata/2/paa/US105_COMB.pep: *
  2 6/ptcdata/2/paa//PCTUS_COMB.pep:*
2 6/ptcdata/2/paa/US06_COMB.pep:*
2 6/ptcdata/2/paa/US07_COMB.pep:*
2 6/ptcdata/2/paa/US080_COMB.pep:*
2 6/ptcdata/2/paa/US080_COMB.pep:*
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  SUMMARIES
  2/paa/PCTUS_COMB.pep:*
  6019581
Description
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| •                  |                      | -              |                    |                | _                | _             |               | _                |                | -             |                   |                |                  |                 | _              | _             | _          | -             |             |               |               |                |                  |                 | _              | _            | _            | -         |              |              |              |              | •             | _             | _            | _             | _             | •             | -             | -               |                |              |                   |
|--------------------|----------------------|----------------|--------------------|----------------|------------------|---------------|---------------|------------------|----------------|---------------|-------------------|----------------|------------------|-----------------|----------------|---------------|------------|---------------|-------------|---------------|---------------|----------------|------------------|-----------------|----------------|--------------|--------------|-----------|--------------|--------------|--------------|--------------|---------------|---------------|--------------|---------------|---------------|---------------|---------------|-----------------|----------------|--------------|-------------------|
| 93.5               | 94                   | 95             | 95                 | 95             | 95               | 95.5          | 96            | 96               | 96             | 96            | 96                | 97.5           | 104.5            | 104.5           |                | 159.5         | 215        | 256           | 30.         | 440           | 4             | 6              | σ,               | 465             | o v            | 497          |              | 516       | л U          | 521          | 567          | 595          | 600           | 0             | 602          | 0             | 609           | r             | u             | 7               | 682            |              | 776               |
| 12.0               | 12.1                 | 'n             | 12.2               | 9              | ۲                | 12.3          | ٠             | •                | •              | •             | •                 | •              | •                | 13.5            |                |               |            | 33.0          | 4.          |               |               |                |                  |                 |                |              |              | , o       |              | 67.1         | •            | ٠            | 7             | 7             |              | •             | 8             | 9             | 4             | 7               | 7              |              | 100.0             |
| 145                | 271                  | 597            | 597                | 445            | 445              | 252           | 30            | 30               | 2309           | 30            | 30                | 520            | 186              | 186             | 186            | 70            | 48         | 68            | 109         | ا سا          | w             | 0              | <b>5</b> 1       | S               | 158            | N) I         | 151          | 15.       | 101          | 151          | 151          | 131          | 151           | 151           | 151          | 151           | 151           | 151           | 151           | 151             | 151            | 151          | 151               |
| 21                 | 30                   | 22             | ۲                  | ü              | 29               | ш             | ü             | ü                | 20             | 20            | ω<br><del>u</del> | μ              | 30               | 6               | 16             | 9             | 19         | 19            | 19          | 21            | <u>ا</u> ۵    | 19             | ω<br>0           | 16              | 16             | מי           | w t          | ۰<br>۲    | ا د          | 19           | 19           | 19           | 19            |               |              |               | 19            | 19            | 19            | o į             |                | 19           | 9                 |
| US-09-739-449-8854 | US-10-437-963-147343 | 09-793-306-146 | PCT-US01-05992-146 | -60-360-039-20 | -10-369-493-2063 | -US03-13414-2 | -60-191-681-2 | -60-191-637-2560 | 9-614-150A-254 | -09-614-150-2 | -60-161-932-68    | -US02-18256-21 | -10-417-886-5833 | -09-252-691C-58 | -09-252-691-58 | -09-543-407-3 | -09-543    | -09-543-407-3 | -09-5       | -09-741-873B- | -08-978-878-2 | -09-543-407-34 | -10-417-886-5834 | -09-252-691C-58 | S-09-252-691-5 | 08-233-642A- | -60-444-371- | 352-945-2 | -08-9/8-8/8- | -09-543-407- | -09-543-407- | -09-543-407- | -09-543-407-1 | -09-543-407-2 | -09-543-407- | -09-543-407-1 | -09-543-407-2 | -09-543-407-2 | S-09-543-407- | -08-233-642A-   | S-09-543-407-5 | -09-543-407- | IIS-09-543-407-22 |
| 8854,              | Sequence 147343,     | e 146,         | 146,               | æ              | e 206            | N             | equence 202   | Ø                | equence 25488, | equence 2548  | equence 688,      | quence 21,     | equence 5833     | e 5833          | equence 5833   | equence 32    | equence 39 | equence 3     | equence 35. | equence 2     | equence 2     | equence 34.    | equence 5834,    | equence 5834.   | Sequence 583   | quence 55.   | equence      | •         | equence 4,   | equence 7,   | equence 16,  | equence 31,  | equenc        | equence 26,   | equence 14,  | equence       | equence 24,   | equence 20,   | equence 30,   | quence 57, Appl | equence 5      | e 28         | Seguence 22. Appl |

# ALIGNMENTS

```
US-09-543-407-22

US-09-543-407-22

Sequence 22, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22

LENGTH: 151

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
```

```
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543.407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
  US-09-543-407-5
  RESULT 3
  В
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   밁
  Ś
  8
            Sequence 5, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043,406
   US-09-543-407-28
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   US-09-543-407-28
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  S
  US-09-543-407-22
  Query Match 91.8%; Score 712; DB 19; Best Local Similarity 91.1%; Pred. No. 9.1e-68; Matches 144; Conservative 0; Mismatches C
  Sequence 28, Application US/
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
CURRENT APPLICATION NUMBER: US/09/543,407
   Matches
   Query Match
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  ORGANISM: Artificial Sequence
  FEATURE:
   Local
   114
   114 TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   PRT
  61
  61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA------DQNNAKNSDI 113
  121
  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   _
   1 MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   19
   61
   151,
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  SDARKSETTITQSGYGNGAD-----YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDI
   Similarity
  MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
   SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
  Application US/09543407
   Conservative
   100.0%; Score 776; DB 19; 100.0%; Pred. No. 1.2e-74; Mismatches 0;
   DB 19;
  0
                                    PEPTIDE
   PEPTIDE SEQUENCES
   Length 151;
  Indels 14;
   Indels
   Length
                                    SEQUENCES
   <u>,</u>
   Gaps
   60
  60
   120
   0
```

```
; MOLECULE TYPE: protein US-08-233-642A-57
  Ş
   ; CURRENT FILING DATE: 2000-04-05; NUMBER OF SEQ ID NOS: 59; SOFTWARE: FastSEQ for Windows Version SEQ ID NO 5; SEQ ID NO 5; LENGTH: 151
; TYPE: PRT
; ORGANISM: Salmonella enteritidis US-09-543-407-5
  US-08-233-642A-57
   RESULT 4
  밁
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  Ś
    Query Match
Best Local Similarity
Matches 136; Conserv
   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 950043.403
TELEPHONE: (206) 682-4900
TELEPHONE: (206) 682-4900
TELEPHONE: (206) 682-491
  Sequence 57, Applicat GENERAL INFORMATION:
  TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
  Query Match
Best Local Similarity
  Matches
   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
   TOPOLOGY:
   STREET: 6300 Colum
CITY: Seattle
STATE: Washington
   LENGTH:
  COUNTRY: U.S.A. ZIP: 98104-7092
   121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  137;
   61 SDARKSETTITQSGYGNGADVGQQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
   1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   amino acids
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  Application US/08233642A
   Kay, William ...
Collinson, S. Karen
Clouthier, Sharon C.
  87.9%; Score 682; DB 19; milarity 90.7%; Pred. No. 1.5e-64; Conservative 2; Mismatches 12.
   Doran, James L.
                    87.2%;
90.1%;
   US/08/233,642A
   920043.403C3
Score 677; DB 6; Length 151;
Pred. No. 5.2e-64;
2; Mismatches 13; Indels
   Version
  4.0
   Length 151;
  Indels
  0;
  Gaps
   120
  0
```

Conservative

2

0;

Gaps

```
Sequence 20, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEE

FILE REFERENCE: 920043,406

CURRENT APPLICATION UNMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 20

LENGTH: 151
   RESULT 6
US-09-543-407-20
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   RESULT 5
US-09-543-407-30
  S
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   Query Match
Best Local S
Matches 136
   NUMBER OF SEQ ID NOS: 59
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 151
  Sequence 30, Applica GENERAL INFORMATION:
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  .09-543-407-30
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
   FEATURE: FRATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial Sequence
  TYPE; PRT
   106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  121
   tch 84.7%; al Similarity 81.9%; 136; Conservative
   13
  61
   61
   61
  ۳
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  Н
  SDARKSETTITQSGYGNGADVGQQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA--
  SDARKSETTITOSGYGNGADVGQGADN---------YDQLVTRVVTHEMAHADQ 105
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  NNPALVNOTASDSSVMVRQVGFGNNATANQY
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   Application US/09543407
  GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   <u>,</u>
   Score 657; DB 19;
Pred. No. 7.4e-62;
0; Mismatches 0;
  PEPTIDE
   PEPTIDE
   Length 151;
   Indels
  SEQUENCES
   SEQUENCES
   30;
   Gaps
  60
   60
   120
   120
  60
```

RESULT 8 US-09-543-407-12

Sequence 12, Application US/09543407 GENERAL INFORMATION: APPLICANT: White, Aaron P. APPLICANT: Doran, James L.

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  ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-24
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   US-09-543-407-24
  US-09-543-407-20
  CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
TYPE: PRT
  Sequence 24, Application US/09543407 GENERAL INFORMATION:
   Best Local Similarity Matches 128; Conserv
  Query Match
   Matches 129;
   Query Match
Best Local Similarity
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  CURRENT APPLICATION NUMBER: US/09/543,407
   ORGANISM: Artificial Sequence FEATURE:
  OTHER INFORMATION:
OTHER INFORMATION:
  FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
   TYPE: PRT ORGANISM: Artificial Sequence
  104 -----DOWNAKUSDITYGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
121
                                  86
   61
   61
  61 SDARK-----
  μ.
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                            HEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  SDARKSETTITQSGYGNGADVGQGAD------
 HEMAHA----
   Conservative
   Conservative
  sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
   79.8%;
   78.5%; Score 609; DB 19;
73.6%; Pred. No. 1.1e-56;
tive 0; Mismatches 0;
   -----YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFR
   0
   Score 619; DB 19;
Pred. No. 8.9e-58;
0; Mismatches 0;
 -NQTASDSSVMVRQVGFGNNATANQY
   ,
,
  PEPTIDE SEQUENCES
  Length 151;
  Length 151;
   Indels
   Indels
  -NYDQLVTRVVT
   44;
   46;
 151
                                    151
   Gaps
   Gaps
   97
  60
  103
   120
   N
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   B
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   US-09-543-407-14
   RESULT 9
US-09-543-407-14
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  В
   S
  US-09-543-407-12
  Matches
   Query Match
Best Local S
Matches 122
  Query Match
   Sequence 14, Application US/09543407 GENERAL INFORMATION:
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRStSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM
TITLE OF INVENTION: PRESENTATION OF HETEROLOG
FILE REFERENCE: 920043.406
  SOFTWARE: FastSEQ for Windows Version SEQ ID NO 12
   ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  APPLICANT: KAY, William W.
TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CIPRENT REFERENCE: 920043.406
CURRENT FAPILICATION NUMBER: US/09/543,407
CURRENT FILLING DATE: 2000-04-05
CURRENT FILLING DATE: 2000-04-05
CURRENT FILLING DATE: 2000-04-05
CURRENT FILLING DATE: 2000-04-05
  TYPE: PRT
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmes
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major
  TYPE: PRT
ORGANISM: Artificial
   FEATURE:
   LENGTH: 151
   Local Similarity
  Local Similarity
  123;
          61
   121
   121
  61
   122;
   5
  61
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                    SDARKSETTITQSGYGNGADVGQGGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
  MKILKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  MKLLKVAAFAAIVVSGSALAGVVFQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
  NNAALVNYDOLVTRVVTHEMAHANNATANOY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   SDARKSETTITQSGYGNGADVGQGADVYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
  MKLLKVAAFAAIVVSGSALAGVVÞQWGGGGNHNGGGNSSGÞDSTLSIYQYGSANAALALQ 60
   NNAAL VNOTASDSSVMVRQVGFGNNATANOY 151
   Collinson,
  Conservative
   Conservative
   77.6%;
81.5%;
  Sequence
  80.8%;
   S. Karen
   Score 602; DB 15,
Pred. No. 6e-56;
""amatches 23;
  Score 604; DB 19;
Pred. No. 3.6e-56;
   Mismatches
  AL SYSTEM FOR HETEROLOGOUS
   Leishmania major.
   23;
   PEPTIDE SEQUENCES
  Length 151;
   Indels
   Length 151;
   Indels
   0
   0;
   Gaps
  60
   60
   120
   120
```

```
; Sequence 18, Application US/09543407
; GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043,406
; CURRENT APPLICATION UNMBER: US/99/543,407
; CURRENT PILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FRASTSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 151
  CURRENT APPLICATION NUMBER: US/09/543,407; CURRENT FILING DATE: 2000-04-05; NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0; SEQ ID NO 26; LENGTH: 151
TYPE: PRT
TYPE: Artificial Sequence; FERATURE:
  RESULT 11
US-09-543-407-18
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   밁
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   В
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   US-09-543-407-26
   US-09-543-407-26
   밁
  Ş
  GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William v
   Matches
  Query Match
Best Local :
  OTHER INFORMATION: Recombina OTHER INFORMATION: sequence OTHER INFORMATION: encoding
   TYPE: PRT
ORGANISM: Artificial Sequence
  TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
  FEATURE:
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  FEATURE:
  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   123;
   61 LYTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  61
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   Conservative
Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragmen encoding PT3 from GP63 of Leishmania major
   77.4%;
81.5%;
   Score 601; DB 19;
Pred. No. 7.7e-56;
   Mismatches
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   Length 151;
  Indels
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  Gaps
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Query Match

77.3%;

Score 600;

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19;

Length 151

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Sequence 31, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER

FILE REFERENCE: 920043.406

CURRENT APPLICATION MUMBER: US/09/543,407

CURRENT APPLICATION MUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 31

LENGTH: 131
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  RESULT 12
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  US-09-543-407-31
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PastSEQ for Windows Version 4.0
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LENGTH: 151
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Best Local Similarity
   APPLICANT: White, Aaron P. APPLICANT: Doran, James L. APPLICANT: Collinson, S. K APPLICANT: Kay, William W.
   TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
   FILE REFERENCE: 920043.406
TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Salmonella
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  141 GEGNNATANOY 151
  121
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   19
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  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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89.3%;
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Pred. No. 2.8e-55;
2; Mismatches 12;
  Pred. No. 9.8e-56;
5; Mismatches 23;
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   Indels
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  Gaps
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  120
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   120
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  60
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US-08-978-878-4
  US-09-543-407-7
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  US-09-543-407-16
  Sequence 4, Application US/08978878 GENERAL INFORMATION:
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SEQ ID NO 7
  Sequence 7, Application US/09543407 GENERAL INFORMATION:
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Best Local Similarity
Matches 122; Conser
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  Query Match
Best Local Similarity
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS FILE REFERENCE: 012889-081 CURRENT EPPLICATION NUMBER: US/08/978,878 CURRENT FILING DATE: 1997-11-26 EARLIER APPLICATION NUMBER: SE 8801723-1 EARLIER FILING DATE: 1988-05-06
   APPLICANT: NORMARK, Staffan APPLICANT: OLSEN, Arne
   FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  NUMBER OF SEQ ID NOS:
  APPLICANT: White, Aaron P.
   LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  FEATURE:
  121
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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  121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  61
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  61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
  1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ
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EEARLIER FILLING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER FILLING DATE: 1991-11-06
EEARLIER FILLING DATE: 1992-11-03
EEARLIER FILLING DATE: 1992-11-03
EEARLIER APPLICATION NUMBER: US 08/187,865
EEARLIER FILLING DATE: 1994-01-28
EEARLIER FILLING DATE: 1994-01-28
EEARLIER APPLICATION NUMBER: US 08/318,519
EEARLIER APPLICATION NUMBER: US 08/318,519
EEARLIER APPLICATION NUMBER: US 08/495,959
EMALIER FILLING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
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SEQ ID NO 4
LENGTH: 151
TYPE: PAT
ORGANISM: Escherichia coli
US-08-978-878-4
Search completed: March 11; 2004, 19:13:12 Job time : 171.3 secs
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  Ś
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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
   OM protein -
  Total number of hits satisfying chosen parameters:
  and is derived by analysis of the total score distribution.
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
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    80
79.5
79
   80.5
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110.4
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US-09-741-873C-2
US-10-767-701-45603
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### ALIGNMENTS

Application US/09741873C

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CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1999-11-26
PRIOR FILING DATE: 1999-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-03
PRIOR PPLICATION NUMBER: US 08/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-01-28
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR PRIOR PRIOR DATE: 1994-10-05
UNMBER OF SEQ ID NOS: 11
SOFTWARE: PACENTIN VETSION 3.0
SEQ ID NO 4
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  US-09-741-873C-4; Sequence 4, Applicat; GENERAL INFORMATION:
   US-09-741-873C-4
  Query Match
Best Local S
Matches 104
   APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
FILE REFERENCE: 012889-084
   LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli
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121
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   Conservative
  66.8%; Score 518; DB 5; 68.9%; Pred. No. 8.6e-39; cive 18; Mismatches 29
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03+C82834_1.pep US-10-767-701-45603
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  В
   US-10-767-701-45603
  ; TYPE: PRT; ORGANISM: Escherichia coli US-09-741-873C-2
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LENGTH: 234
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  GENERAL INFORMATION:
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Best Local Similarity
  SOFTWARE: PatentIn version 3.0 SEQ ID NO 2
  Sequence 2, Applicat: GENERAL INFORMATION:
   APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 388-21(5355)B
FILE REFERENCE: 388-21(5355)B
  CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
   PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 08/187,865
  PRIOR APPLICATION NUMBER: US 08/318,519 PRIOR FILING DATE: 1994-10-05
   APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
   NAME/KEY: unsure
LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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PRIOR FILING DATE: 1991-11-06
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PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
  CURRENT APPLICATION NUMBER: US/09/741,873C CURRENT FILING DATE: 2000-12-22
  ORGANISM: Sorghum bicolor
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   FILING DATE: 1998-05-06
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  56.7%; Score 440; DB 5; 65.6%; Pred. No. 4.9e-32; ative 17; Mismatches 28
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   US-10-779-461-19
   US-10-451-467A-314
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  Sequence 19, Application US/10779461 GENERAL INFORMATION:
   SOFTWARE: Pa
APPLICANT: MORTON, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR
FILE REFERENCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
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Best Local Similarity 24.8:
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  NUMBER OF SEQ ID NOS: 732
  PRIOR APPLICATION NUMBER: EP 01870002.1 PRIOR FILING DATE: 2001-01-04 PRIOR APPLICATION NUMBER: EP 01870003.9 PRIOR FILING DATE: 2001-01-09
  PRIOR APPLICATION NUMBER: EP 00870318.3 PRIOR FILING DATE: 2000-12-22
  CURRENT APPLICATION NUMBER: US/10/451,467A CURRENT FILING DATE: 2003-06-19
   APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
   FILE REFERENCE: JAB-1667
  ORGANISM: Saccharomyces cerevisiae
   APPLICANT: CONTRERAS, ROLAND HENRI
  LENGTH: 430
TYPE: PRT
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  139
  142 FGNN 145
  193 NDDSYGSSNKKKSSYGSSNNDSYGSNNDD----SYGSNNNDSYGSNNDDSYGSSNKKKSS 248
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   28 GGGNHNGGGNSSGPDSTLSIYQYGS-ANAALALQSDARKSETTITQSGYGNGADVGQGA-
  61
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  1 MKLLKVAAFAAIVV--SGSALAGVVPQW---GGGGNHNGGGN------SGGPDSTL 45
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   YGSN 252
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   QGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNA 123
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  QAGGS-----GSNGGAYA-QGGAQGGGGGGGQYGGSGS 134
   EBERHARDT, INES
LUYTEN, WALTER HERMAN MARIA LOUIS
  Application US/10451467A
  Conservative
  10.3%; Score 80; DB 24.2%; Pred. No. 6.8;
   10.4%; Score 80.5; D
24.8%; Pred. No. 2.9;
tive 14; Mismatches
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  THE TREATMENT OF
  DB 6;
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  SGYGSGSGYG
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   Gaps
   82
   60
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```
Sequence 6, Application US/10779461
GENERAL INFORMATION:
APPLICANT: MOTION: Philip A
FITLE OF INVENTION: ANTIBODIES TO C-MET FOR THI
FILE REFERENCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION UMMEER: 60/447,073
PRIOR FILING DATE: 2003-02-13
PRIOR FILING DATE: 2003-02-13
PRIOR FILING DATE: 2003-02-13
PRIOR FILING DATE: 2003-02-13
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   RESULT 7
  US-10-779-461-6
   RESULT 6
  ; NUMBER OF SEQ ID NOS: 161
; SOPTWARE: PatentIn version
; SEQ ID NO 19
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; TYPE: PRT
; ORGANISM: artificial
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US-10-779-461-6
   US-10-779-461-19
   SOFIWALL 250
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (5.5358)
CURRENT APPLICATION INVESER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 35342
LENGTH: 179
   Sequence 35342, Application US/10767701 GENERAL INFORMATION:
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   APPLICANT: Kovalic,
   SOFTWARE: PatentIn version 3.2
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ORGANISM: artificial
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   163 GSSSDIGDYNHVSWYQQHPGKAPKLMIYDVNKWPSGVPDRFSGSKSGNTASL 214
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Pred. No. 3
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TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR TITLE OF INVENTION: ESCHERICHIA COLI FILE REFERENCE: ELITRA.001C1
CURRENT APPLICATION UNMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR PILING DATE: 1909-01-27
NUMBER: 05/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER: 05/10 NOS: 485
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  ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C129260_1.pep US-10-767-701-32417
   S
  ; OTHER INFORMATION: Clone ID: US-10-767-701-35342
  RESULT 8
US-10-767-701-32417
   US-10-771-241-299
  RESULT 9
  Sequence 299, Application US/10771241
GENERAL INFORMATION:
APPLICANT: Syskind, Judith
APPLICANT: Forsyth, R. Allyn
  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(5355)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 32417
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   Sequence
   APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
  SOFTWARE:
   TYPE: PRT ORGANISM: Sorghum bicolor
   FEATURE:
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   FEATURE:
  LENGTH: 251
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  140 VGFGNNA 146
  16 GSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQY-GSANAALALQSDARKSETTITQSG
   32417, Application US/10767701
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FastSEQ for Windows Version
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   David
   10.1%;
25.2%;
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29.4%; Pred. No. 4.8;
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RESULT 11
US-10-779-461-40
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; ORGANISM: E. Coli
US-10-771-241-299
   PCT-US04-02338-49
  PCT-US04-02338-49
  Sequence 40, Application US/10779461 GENERAL INFORMATION:
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Matches
   Sequence 49, Application PC/TUS0402338 GENERAL INFORMATION: APPLICANT: EXELIXIS, INC.
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  SEQ ID NO 49
                                   APPLICANT: MORTON, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
FILE REFERENCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
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PRIOR FILING DATE: 2003-02-13
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                    NUMBER OF SEQ ID NOS: 161
   PRIOR APPLICATION NUMBER: US60/447,358
PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US60/461,789
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR FILING DATE: 2003-05-14
   PRIOR APPLICATION NUMBER: US60/479,650
PRIOR FILING DATE: 2003-06-19
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CURRENT APPLICATION NUMBER: PCT/US04/02338
CURRENT FILING DATE: 2004-01-28
  TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS TITLE OF INVENTION: USE
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26.1%; Pred. No. 9.
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   Gaps
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  RESULT 12
US-10-767-701-61422
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   ; FEATURE: , OTHER INFORMATION: phage display generated human antibody US-10-779-461-40
   Sequence 591, Application US/10045674A
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
   CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 61422
LENGTH: 134
TYPE: PRT
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LENGTH: 250
  APPLICANT:
  APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
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T: HOOGENBOOM, HENDRICUS R. J. M.
INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
INVENTION: LIBRARIES
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PRIOR FILING DATE: 2000-04-17
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
NUMBER: OF SEQ ID NOS: 635
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 527
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   ; OTHER INFORMATION: Description of Unknown Organism: M13 protein
; OTHER INFORMATION: sequence
US-10-045-674A-591
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US-10-045-674A-527
  Sequence 527, Application US/10045674A GENERAL INFORMATION:
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SOFTWARE: PATENTIN VEY: 2.1
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   APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OP INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
   APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO
APPLICANT: ROOKEY, KRISTIN
APPLICANT: HOET, RENE
   PILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
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PRIOR PILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
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US-10-767-701-56903
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  В
   US-10-767-701-56903
   Sequence 56903 Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated ITITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(5535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NO 56903
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#### SUMMARIES

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No. Score Match Length DB ID

Description

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|-------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------|
| 92.5<br>92.5<br>5                                                                         |                                                                                            | 248.5<br>237<br>111<br>111<br>107<br>107<br>107<br>107<br>98.5                                                      |                                                                                                        | 600<br>600<br>600<br>600<br>600<br>600<br>500<br>500<br>500<br>500                                                                                                                                                                                                      | @ W O H J                                                                                            |
| 11.9<br>11.9<br>11.9                                                                      | 111122                                                                                     | 32.1<br>30.6<br>14.3<br>13.8<br>13.8<br>13.8                                                                        | 1108844                                                                                                | 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                 |                                                                                                      |
| 1028<br>1028<br>1028<br>1028                                                              | 85585                                                                                      |                                                                                                                     | 0000000                                                                                                | វសេហហហហហហហហហហហហហ                                                                                                                                                                                                                                                        | 151<br>151<br>151                                                                                    |
| 33<br>33                                                                                  |                                                                                            | 19<br>29<br>16<br>16<br>19                                                                                          | 16<br>30<br>19<br>19<br>19                                                                             |                                                                                                                                                                                                                                                                         | 19<br>19<br>19                                                                                       |
| US-09-614-150-14916<br>US-09-614-150A-14916<br>US-60-167-217-14978<br>US-60-173-464-12194 | -09-914-543<br>-09-543-407<br>-09-614-150<br>-09-614-150A<br>-60-191-637<br>-60-191-681-   | -09-543-407-3<br>-09-543-407-3<br>-10-369-493-2<br>-60-360-039-2<br>-09-252-691-5<br>-09-252-691C-<br>-10-417-886-5 | -09-252-691C-<br>-10-417-886-5<br>-09-543-407-3<br>-08-978-878-2<br>-09-741-873B-<br>-09-543-407-3     | US-09-543-407-12 US-09-543-407-22 US-09-543-407-26 US-09-543-407-20 US-09-543-407-20 US-09-543-407-20 US-09-543-407-16 US-09-543-407-17 US-09-543-407-17 US-09-543-407-17 US-08-978-878-4 US-09-543-407-17 US-08-978-878-4 US-08-978-878-878-878-878-878-878-878-878-87 | US-09-543-407-24<br>US-09-543-407-14<br>US-09-543-407-30<br>US-09-543-407-5<br>US-08-233-642A-57     |
| Sequence 14916, A<br>Sequence 14916, A<br>Sequence 14978, A<br>Sequence 12194, A          | equence 44 equence 8, equence 24 equence 24 equence 24 equence 24                          | 58333<br>68333<br>7                                                                                                 | equence 5834, equence 5834, equence 2, Apr equence 2, Apr equence 2, Apr equence 35, Ar equence 37, Ar | equence 12,<br>equence 22,<br>equence 26,<br>equence 18,<br>equence 20,<br>equence 21,<br>equence 16,<br>equence 4,<br>equence 4,<br>equence 4,<br>equence 2,<br>equence 55,<br>equence 55,                                                                             | Sequence 24, Appl<br>Sequence 14, Appl<br>Sequence 30, Appl<br>Sequence 5, Appl<br>Sequence 57, Appl |

## ALIGNMENTS

US-09-543-407-24

Sequence 24, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

INMBER OF SEQ ID NOS: 59

SOFTWARE: FastSQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 151

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.

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RESULT 3
US-09-543-407-30
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   RESULT 2
US-09-543-407-14
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   밁
   US-09-543-407-14
   S
  US-09-543-407-24
  Sequence 30, Application US/09543407 GENERAL INFORMATION:
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FAST-SEQ for Windows Version 4.0
SEQ ID NO 14
   Matches
   Query Match
  GENERAL INFORMATION:
  Sequence 14, Application US/09543407
   Matches
   Query Match
Best Local
                  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
   APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  APPLICANT: White, Aaron P.
  OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
   LENGTH: 151
  Local Similarity
   Local Similarity
  121
   114 LYTRYVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
   144;
   121
   121
  61
   61
  151,
   61
   61
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN----
  LVTRVVTHEMAHA-----
  HEMAHANQTASDSSVMVRQVGFGNNATANQY
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
   HEMAHANOTASDSSVMVRQVGFGNNATANOY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   Conservative
   Conservative
   Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
  92.1%;
91.1%;
   100.0%; Score 775; DB 19; 100.0%; Pred. No. 2.7e-74;
   0
  0,
  Score 714; DB 19;
Pred. No. 9.2e-68;
   Mismatches .
  Mismatches
   151
   DB 19;
   0
  0
  151
                                    PEPTIDE SEQUENCES
  PEPTIDE SEQUENCES
   Length 151;
   Indels 14;
  Length
  Indels
  151;
  0
   ---YDQ 113
   Gaps
  Gaps
   120
   60
   60
  60
   2
```

```
RESULT 5
US-08-233-642A-57
i Sequence 57, Application US/08233642A
; GENERAL INFORMATION:
; APPLICANT: Kay, William W.
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  밁
  Š
   ; TYPE: PRT ; ORGANISM: Salmonella US-09-543-407-5
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  US-09-543-407-5
  밁
  8
   밁
   밁
  S
   US-09-543-407-30
  ; CUMRENT FILING DATE: 2
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for W
; SEQ ID NO 30
; LENGTH: 151
  Best Loc
Matches
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
   Query Match
Best Local Similarity
   GENERAL INFORMATION:
   Sequence
   Matches
   Query Match
Best Local (
  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
   APPLICANT: White, Aaron P. APPLICANT: Doran, James I
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial Sequence FEATURE:
  TYPE: PRT
  121
   121
  138;
  113
  121 HEMAHA-----NOTASDSSVMVRQVGFGNNATANQY
  61
   61
   13
  61
   143;
   Н
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  Similarity
   HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHNNGGGNSSGPDSTLSIYQYGSANAALALQ
  SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYGG
   Application US/09543407
   HEMAHAGGNNAALVNOTASDSSVMVROVGFGNNATANOY
   SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNAT----
  SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  Conservative
   Conservative
  enteritidis
   2000-04-05
59
Windows Version
  89.0%;
   90.3%;
   2
   .
.
   Score 690; DB 19;
Pred. No. 3.4e-65;
2; Mismatches 11.
   Score 700; DB 19;
Pred. No. 2.9e-66;
   Mismatches
  DB 19;
   0
  PEPTIDE
   151
  151
   Length 151;
  Length 151;
   Indels
   Indels
  SEQUENCES
   16;
   ,
,
   Gaps
   Gaps
  120
  120
  60
   112
   60
  60
   0
```

APPLICANT: APPLICANT: APPLICANT:

Collinson, S. Karen Clouthier, Sharon C. Doran, James L.

```
APPLICANT: COLLINGON, S. KAYEN
APPLICANT: KAY, WILLIAM W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
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  밁
  S
   밁
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  US-09-543-407-12
   Query Match
Best Local S
Matches 138
  Sequence 12, Application US/09543407 GENERAL INFORMATION:
  MOLECULE TYPE: protein -08-233-642A-57
   APPLICANT: White, Aaron P. APPLICANT: Doran, James L.
  TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
CLASSIFICATION: 424
  REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
  NUMBER OF SEQUENCES:
   ATTORNEY/AGENT INFORMATION: NAME: King, Joshua
  CORRESPONDENCE ADDRESS:
   TITLE OF INVENTION:
   TYPE: amino acid
   Local Similarity 91.
   TOPOLOGY:
  COUNTRY: U.S.A. ZIP: 98104-7092
   CITY: Seattle
  LENGTH:
  ADDRESSEE:
  121
   121
  19
  61
  1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNINGGGNSSGPDSTLSIYQYGSANAALALQ
   HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
  NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
  SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNYDOLVTRVVT
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  Washington
  151 amino acids
   E: Seed and Be
   linear
   88.9%;
   BASED VACCINES
58
  METHODS AND COMPOSITIONS FOR SALMONELLA-
   l Berry
Dia Center,
   2
   Score 689; DB 6;
Pred. No. 4.4e-65;
   Mismatches
   701
   Fifth Avenue
   Length 151;
   PEPTIDE SEQUENCES
   Indels
   0
   Gaps
  120
   60
  60
```

```
RESULT 8
US-09-543-407-26
; Sequence 26, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
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  S
   US-09-543-407-22
  US-09-543-407-22
  US-09-543-407-12
   RESULT 7
   Query Match
Best Local S
Matches 128
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
  Sequence 22, Application US/09543407 GENERAL INFORMATION:
  Matches 134;
  Query Match
Best Local Similarity
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
   TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmen OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  Local Similarity
   121
  121
  110
   86
   61
   61
  13
  13
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   -----NYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAK------
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   HEMAHADOWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
   HEMAHA-----
   SDARKSETTITQSGYGNGADVGQGAD
  NNAALVNYDQLVTRVVTHEMAHA-----NNATANQY 151
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   Conservative
  Conservative.
  78.6%;
73.6%;
   84.5%;
79.8%;
  0,
   0;
  Score 609; DB 19;
Pred. No. 1.6e-56;
   Score 655; DB 19;
Pred. No. 1.9e-61;
   Mismatches
  Mismatches
   NQTASDSSVMVRQVGFGNNATANQV
  0;
  PEPTIDE SEQUENCES
   Length 151;
   Length 151;
   Indels
  Indels
   NYDQLVTRVVT
   46;
  34;
  151
   Gaps
  Gaps
   60
  109
   97
   120
   60
  60
```

APPLICANT: Collinson, S. Karen

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  US-09-543-407-18
  US-09-543-407-18
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   US-09-543-407-26
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 151
   Query Match
Best Local
  Sequence 18, Application US/09543407 GENERAL INFORMATION:
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
   Matches 124; Conservative
  Query Match
  APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  APPLICANT: White, Aaron P. APPLICANT: Doran, James L
  FILE REFERENCE: 920043.406
  FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major
   TYPE: PRT
ORGANISM: Artificial Sequence
  APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  ORGANISM: Artificial Sequence FEATURE:
  TYPE: PRT
   Match 78.6%;
Local Similarity 82.1%;
      61
  121
  121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
   61
   61
   61
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   Similarity
SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
   NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
   Doran, James L
  LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  Conservative
  78.5%;
82.1%;
   Score 608; DB 15,
Pred. No. 2.1e-56;
"" ematches 22;
   4
   Score 609; DB 19;
Pred. No. 1.6e-56;
  Mismatches
   PEPTIDE SEQUENCES
   Length 151;
  Indels
   Indels
   fragment
a major.
  0;
   60
   60
```

```
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-31
   RESULT 11
US-09-543-407-31
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   5
  US-09-543-407-20
   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 31
                 Query Match
Best Local Similarity
   Sequence 31, Application US/09543407 GENERAL INFORMATION:
  Best Loc
Matches
  GENERAL INFORMÁTION:
APPLICANT: White, ABRON P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043,406
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  Query Match
  SEQ ID NO 20
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
   ENGTH: 131
  Local Sin
   121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
  121 NNAALVNOTASDSSVMVROVGFGNNATANOY
   121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
  61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIBLTQNGFRNNATIDQWNAKNSDITVGQYGG 120
   61
   1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  Similarity
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  NNAALVNOTASDSSVMVROVGFGNNATANOY
   Application US/09543407
  Conservative
                      77.8%;
   78.2%;
82.1%;
  ت
--
Score 603; DB 19;
Pred. No. 5.9e-56;
2; Mismatches 11.
   Score 606; DB 19;
Pred. No. 3.4e-56;
5; Mismatches 22;
  PEPTIDE SEQUENCES
  Length 131;
  Length 151;
   0,
   Gaps
   60
```

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21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD 80

Matches 118;

Conservative

2

Indels

0;

Gaps

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF
FILE REFERENCE: 92004.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
TYPE: DET
  RESULT 13
US-09-543-407-16
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  밁
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  밁
   US-09-543-407-28
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   밁
  밁
   US-09-543-407-28
  FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 28
   Sequence 16, Application:
  Sequence 28, Applica GENERAL INFORMATION:
   Matches 123;
   Query Match
Best Local Similarity
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. K.
APPLICANT: Collinson, K.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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US-08-978-878-4
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  밁
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   US-09-543-407-7
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APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, ATHE
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
   Query Match
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
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  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER FILING DATE: 1992-11-03
EARLIER APPLICATION NUMBER: US 08/187,865
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EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1995-06-28
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ORGANISM: Escherichia coli
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Job time : 172.3 secs
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Maximum Match 100%
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Maximum DB
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|---------------------|-------------------|---------------------|-------------------|-------------------|---------------------|---------------------|---------------------|---------------------|-------------------|---------------------|---------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
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| 8.8                 | 8.8               | 8.8                 | 8.9               | 8.9               | 9.0                 | 9.0                 | 9.0                 | 9.0                 | 9.0               | 9.0                 | 9.0                 | 9.1                 | 9.1               | 9.1               | 9.1               | 9.1               | 9.1               | 9.1               |
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| US-10-767-701-59665 | US-10-779-461-30  | US-10-767-701-47075 | PCT-US03-02038-26 | US-10-779-461-6   | PCT-US04-05654-1755 | PCT-US04-05654-1466 | US-10-767-701-45219 | PCT-US04-05654-2748 | US-10-779-461-59  | US-10-767-701-51583 | US-10-767-701-35046 | PCT-US04-05654-2086 | US-10-093-037A-63 | US-10-627-556-398 | US-10-627-556-402 | US-10-627-556-400 | US-10-627-556-396 | US-10-627-556-392 |
| Sequence 59665, A   | Sequence 30, Appl | Sequence 47075, A   | Sequence 26, Appl | Sequence 6, Appli | Sequence 1755, Ap   | Sequence 1466, Ap   | Sequence 45219, A   | Sequence 2748, Ap   | Sequence 59, Appl | Sequence 51583, A   | Sequence 35046, A   | Sequence 2086, Ap   | Sequence 63, Appl | Sequence 398, App | Sequence 402, App | Sequence 400, App | •                 | Sequence 392, App |

### ALIGNMENTS

US-09-741-873C-4

Sequence 4, Application US/09741873C GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1999-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR RPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1994-01-28
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
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Best Local Similarity
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   APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
FILE REFERENCE: 012889-084
   LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia
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CURRENT APPLICATION NUMBER: PCT/US04/02338
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US60/443,484
PRIOR FILING DATE: 2003-01-29
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PRIOR APPLICATION NUMBER: US60/461,789
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PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-04-10
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PRIOR PILING DATE: 2003-05-14
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US-09-741-873C-2
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APPLICANT: EXELIXIS, INC.
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  TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF TITLE OF INVENTION: USE
   Sequence 2, Applicat GENERAL INFORMATION:
   -09-741-873C-2
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CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
   APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
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PCT-US04-02338-49
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APPLICANT: Porsyth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION
TITLE OF INVENTION: ESCHERICHIA COLI
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CURRENT FILING DATE: 2004-02-03
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PRIOR FILING DATE: 2000-01-27
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PRIOR FILING DATE: 1999-01-27
  APPLICANT: POTSYTH, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
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   APPLICANT: Zyskind, Judith APPLICANT: Forsyth, R. Al
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SOFTWARE: PastSEQ for Windows Version 3.0 SEQ ID NO 364

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PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485

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US-10-771-241-364
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TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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CT-US04-05654-590
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Best Local Similarity
Matches 32; Conserv
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  PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: PatentIn version 3.
   APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
  PRIOR APPLICATION NUMBER: 10/374,780 PRIOR FILING DATE: 2003-02-25
   CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
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  Adam, Luc J
Reuber, T. Lynne
  Riechmann, Jose 1
Jiang, Cai-Zhong
  Yu, Guo-Liang
Broun, Pierre E
  Heard, Jacqueline
Haake, Volker
  Gutterson, Neal
   Century, Karen
   Pineda, Omaira
  Keddie, James
Dubell III, Arnold N
   Ratcliffe, Oliver
   Creelman, Robert A
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   version 3.2
   Peter
9.9%; Score 76.5; Di
22.5%; Pred. No. 8.2;
tive 19; Mismatches
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   DB 6; Length 878
                                  DB
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; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS900
; CURRENT APPLICATION NUMBER: US/10/100,683
; CURRENT FILING DATE: 2002-03-19
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   US-10-100-683-10326
   밁
   S
   US-10-100-683-10326
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   SOFTWARE: PatentIn Ver. SEQ ID NO 10326
   Sequence 10326, App
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   FILE REFERENCE: PS900
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
  PRIOR APPLICATION NUMBER: US 60/056,892 PRIOR FILING DATE: 1997-08-22
  PRIOR FILING DATE: 1997-05-23
   PRIOR FILING DATE: 1997-04-11 PRIOR APPLICATION NUMBER: US
  PRIOR APPLICATION NUMBER: US 60/047,599
   PRIOR APPLICATION NUMBER: US 60/043,580 PRIOR FILING DATE: 1997-04-11
  PRIOR APPLICATION NUMBER: US 60/047,601 PRIOR FILING DATE: 1997-05-23
  PRIOR FILING DATE: 1997-04-11
   PRIOR APPLICATION NUMBER: US 60/040,162 PRIOR FILING DATE: 1997-03-07
  TITLE OF INVENTION: Human Secreted Proteins
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  PRIOR FILING DATE: 1997-08-22
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US-10-100-683-10327
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LENGTH: 386
  Query Match
Best Local
   Sequence 7608, Appli
GENERAL INFORMATION:
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   CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
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PRIOR FILING DATE: 1007-03-07
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PRIOR APPLICATION NUMBER: US 60/047,601
   APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
  SOFTWARE: PatentIn Ver.
  Remaining Prior Application data NUMBER OF SEQ ID NOS: 13468
   PRIOR FILING DATE:
  FILE REFERENCE: PS900
  PRIOR APPLICATION NUMBER: US 60/056,892 PRIOR FILING DATE: 1997-08-22
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                                       FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,892
   FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,599
FILING DATE: 1997-05-23
   APPLICATION NUMBER: US 60/047,632
  FILING DATE: 1997-04-11
   APPLICATION NUMBER:
   APPLICATION NUMBER: US 60/056,664
  APPLICATION NUMBER: US 60/056,845
  FILING DATE:
   FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
  FILING DATE: 1997-05-23
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   APPLICATION NUMBER: US 60/040,162
  FILING DATE:
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  238 GGGSSNSGGGSGSGSGSGSNGDNNNGS 267
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CATION NUMBER: US 60/043,580
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NUMBER: US 60/043,314
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US-10-767-701-40104
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  ; OTHER INFORMATION: phage display generated human antibody
US-10-779-461-40
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US-10-779-461-40
   밁
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   밁
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; ORGANISM: Homo sapiens
US-10-100-683-7608
   SEQ ID NO 40104
LENGTH: 205
TYPE: PRT
  CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin version 3.2
SEQ ID NO 40
SEQ ID NO 40
   Sequence 40104, Application US/10767701 GENERAL INFORMATION:
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   Sequence 40, Application US/10779461 GENERAL INFORMATION:
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   TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29
   APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
   APPLICANT: MORTON, Philip A TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS FILE REFERENCE: 00980/1
   NUMBER OF SEQ ID NOS: 63128
  LENGTH: 250
TYPE: PRT
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  ORGANISM: artificial
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                    FEATURE:
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   185
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  26;
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   443
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   GNGAD---VGQGADNSTIELTQNGFRNNAT 102
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RESULT 13
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   Sequence 527, Application US/10045674A
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                  APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROCKEY, KRISTIN L.
  FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION TIME CONTROL OF THE PRIOR APPLICATION TO THE PRI
  APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM.
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
   PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: Patentin Ver. 2.1
  CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
  PRIOR APPLICATION NUMBER: 09/837,306
   APPLICANT:
  APPLICANT:
  APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
  OTHER INFORMATION: Descript
OTHER INFORMATION: sequence
   ORGANISM: Unknown Organism FEATURE:
  TYPE: PRT
  LENGTH: 424
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   similarity 22.2%;
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RENE
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8; Mismatches
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```

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PCT-US04-02188-187
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  ; OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS; OTHER INFORMATION: protein sequence US-10-045-674A-527
  ; ORGANISM: Homo sapiens
PCT-US04-02188-187
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SEQ ID NO 187
LENGTH: 588
   SOFTWARE: PatentIn Ver.
SEQ ID NO 527
LENGTH: 533
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Best Local Similarity
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   PRIOR APPLICATION NUMBER: 60/442,582
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: PAFARE:
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   Matches
   FILE REFERENCE: 5151
CURRENT APPLICATION NUMBER: PCT/US04/02188
CURRENT FILING DATE: 2004-01-23
   PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
  APPLICANT: Taylor, Ian
TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND
  APPLICANT:
  APPLICANT: Bayer Pharmaceuticals Corporation APPLICANT: Eveleigh, Deepa
   CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
  TITLE OF INVENTION: NOVEL MET TITLE OF INVENTION: DISPLAYE TITLE OF INVENTION: OF PEPTI TITLE OF INVENTION: LIBRARIE. FILE REFERENCE: DYAX/002 CIP2
  CURRENT APPLICATION NUMBER: US/10/045,674A
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  FEATURE:
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  412 KGKLDSVATDYGAAIDGFIGDVSGLANGNGATGDFAGSNSQMAQVGDG-DNSPL---MNN 467
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   23 VPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVG 82
   97 FR 98
  64 R-KSETTITQ-----SGYGNG------ADVGQGADNSTIELTQNG
   37;
   15 SGSALAGVVPQWGG--GGNHNGGGNSSGPDSTLSIYQ-YGSANAAL-----ALQSDA
  I: HOOGENBOOM, HENDRICUS R. J. M.
INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
INVENTION: OF PEFTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
  QGADNSTIEL-TQNGFRNNATIDQWNA-KNYDQLVTRVVTHEMAHANQTASDSSVMVRQ 139
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  Eveleigh, Deepa
Bigwood, Douglas
   9.5%; Score 74; DB ilarity 26.1%; Pred. No. 29; Conservative 17; Mismatches
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   9.7%;
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;-
   Score 75;
Pred. No.
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   Mismatches
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   DB 6;
   37;
   35;
   Length 588
   Length 533
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US-10-764-425-187

US-10-764-425-187

US-10-764-425-187

US-10-764-425-187

US-10-764-425-187

US-10-764-425-187

Sequence 187, Application US/10764425

GENERAL IMPORNATION:

APPLICANT: Bayer pharmaceuticals Corporation

APPLICANT: Eveleigh, Despa

APPLICANT: Eveleigh, Despa

APPLICANT: Eveleigh, Despa

APPLICANT: Everence 1515

INTILE OF INVENTION: EXCRESSION PROFILES FOR COLON CANCER AND METHODS OF USE

INTILE OF INVENTION: EXCRESSION PROFILES FOR COLON CANCER AND METHODS OF USE

CURRENT PILING DATE: 2004-01-24

UNMBER: COPICATION NUMBER: US/10/764,425

CURRENT PILING DATE: 2003-01-24

UNMBER OF EGO ID NOS: 191

SEQ ID NO 187

PRIOR APPLICATION NUMBER: 60/442,582

PRIOR APPLICATION NUMBER: 60/442,582

PRIOR APPLICATION NUMBER: 60/442,582

PRIOR APPLICATION NUMBER: 60/442,582

PRIOR APPLICATION NUMBER: 60/442,582

PRIOR PILING DATE: 2003-01-24

UNMBER OF EGO ID NOS: 191

SEQ ID NO 187

SEQ ID NO 187

CURRENT SERVE PROFILES FOR COLON CANCER AND METHODS OF USE

PRIOR FILING DATE: 2003-01-24

UNMBER OF EGO ID NOS: 191

SEQ ID NO 187

CURRENT SERVE PROFILES FOR COLON CANCER AND METHODS OF USE

PRIOR FILING DATE: 2003-01-24

UNMBER: 60/442,582

PRIOR APPLICATION UNMBER: US/10/764,425

CURRENT SEQ ID NO 187

SEQ ID NO 187

ORGANISM: Homo sapiens

US-10-764-425-187

Query Match

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ORGANISM: Homo sapiens

US-10-764-425-187

Query Match

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Matches 31; Conservative 17; Mismatches 37; Indels 34; Gaps 6;

ORGANISM: Homo sapiens

US-10-764-425-187

Query Match

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Matches 31; Conservative 17; Mismatches 37; Indels 34; Gaps 6;

ORGANISM: Homo sapiens

US-10-764-425-187

Query Match

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Matches 31; Conservative 17; Mismatches 37; Indels 34; Gaps 6;

ORGANISM: Homo sapiens

US-10-764-425-187

Query Matches 187

ORGANISM: Homo sapiens

ORGANISM
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Pending_Patents_AA_Main:*

1: <a href="mailto:cgm2">cgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <a href="mailto:cgm2">cfgm2</a> <
   March 11, 2004, 18:33:51 ; Search time 171.3 Seconds (without alignments) 860.386 Million cell updates/sec
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   1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
  US-09-543-407-26
782
   6019581 seqs, 976053577 residues
   GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
  6019581
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Result No.

Score

Query Match Length DB

ä

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| RESULT 1  US-99-543-407-26  Sequence 26, Application US/0  GENERAL INFORMATION:  APPLICANT: White, Aaron P. APPLICANT: Doran, James L. APPLICANT: Collinson, S. Ka APPLICANT: Kay, William W. TITLE OF INVENTION: BACTERIA TITLE OF INVENTION: BACTERIA TITLE OF INVENTION: PRESENT FILE REFERENCE: 920043.406  CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2000-0  NUMBER OF SEQ ID NOS: 59 SOFTWARE: FastSEQ for Window SEQ ID NO 26 LENGTH: 151 TYPE: PRT ORGANISM: Artificial Sequen FEATURE: INFORMATION: Recombin OTHER INFORMATION: encoding                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |            | 44444433333333333333333333333333333333                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
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| -407-26 I 26, Appl: I NORMATIO INFORMATIO INFORMATIO INFORMATIO INFORMATIO INFORMATIO INFORMATIO INFORMATIO INFORMATIO INFORMATIO INFORMATIO INFORMATIO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |            | 782 792 692 693 687 6114 6114 601 600 600 600 600 600 600 600 600 600                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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| tion US/0954340 aron P. James L. James L. James L. BACTERIAL FIME PRESENVATION 043.406 NUMBER: US/09/ 2000-04-05 S: 59 or Windows Vers al Sequence Recombinant Sa sequence conta                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |            | 155<br>155<br>155<br>155<br>155<br>155<br>155<br>155<br>155<br>155                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| Kare<br>MITAL<br>NITAT<br>USA<br>1-04-<br>lence<br>lence<br>lence<br>cence<br>ong py                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |            | $\begin{array}{cccccccccccccccccccccccccccccccccccc$                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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APPLICANT: White, Maron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF
ILE REFERENCE: 920043, 406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: 05/09/543,407
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 151
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  Вb
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   RESULT 3
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  US-09-543-407-20
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   US-09-543-407-26
  Sequence 5, Application US/09543407 GENERAL INFORMATION:
  Query Match
Best Local Sim
Matches 151;
                    APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
IITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
  Matches
   Query Match
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  Sequence 20, Application US/09543407
CURRENT APPLICATION NUMBER: US/09/543,407
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  ORGANISM: Artificial Sequence
  FEATURE:
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  121
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  61 SDARKYDQLVTRVVTHEMAHA------GQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
   58
   61
  61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQNNAKNSDITVGQYGG 120
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
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  Conservative
  90.7%;
   100.0%; Score 782; DB 19;
100.0%; Pred. No. 1.8e-75;
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,
  Score 709; DB 19;
Pred. No. 1.3e-67;
   Mismatches
   DB 19;
  PEPTIDE SEQUENCES
  Length 151;
  Indels 16;
  Length 151;
  0;
  57
   60
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RESULT 4
US-08-233-642A-57
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; GENERAL INFORMATION:
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  US-09-543-407-5
Query Match
Best Local Similarity
Matches 136; Conserv
  CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 5
  Query Match
Best Local
   Matches
  TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 57:
  ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION UNMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
  LENGTH: 151
TYPE: PRT
ORGANISM: Salmonella
   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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  ZIP: 98104-7092
COMPUTER READABLE FORM:
   TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: BASED VACCINES NUMBER OF SEQUENCES: 58
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  APPLICATION NUMBER: FILING DATE: 26-APF CLASSIFICATION: 424
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STATE: Washington
   MEDIUM TYPE:
   LENGTH:
   COUNTRY:
  STREET:
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  137;
  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
  amino
   Similarity
   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  Application US/08233642A
   151 amino acids
  6300 Columbia Center, 701 Fifth Avenue
   U.S.A.
   Collinson, S. Karen
Clouthier, Sharon C.
Doran, James L.
  linear
   Conservative
  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
   Seed and Berry
  acid
   Floppy disk
   26-APR-1994
   William W.
               87.9%;
90.1%;
   enteritidis
  Windows Version
   2000-04-05
  88.5%;
   US/08/233,642A
  920043.403C3
Score 687; DB 6
Pred. No. 3e-65;
2; Mismatches
  2
  Score 692; DB 19;
Pred. No. 8.7e-66;
  Mismatches
  Version
                               DB 6; Length 151;
   FOR SALMONELLA-
   Length 151;
  Indels
  <u>.</u>
  120
   120
  6
   60
  0
```

2;

0

Gaps

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043, 406
FULL REFERENCE: 920043, 407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 151
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 151
  RESULT 6
US-09-543-407-28
  밁
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   RESULT 5
US-09-543-407-18
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   Sequence 28, Application US/09543407 GENERAL INFORMATION:
  Sequence 18, Applica GENERAL INFORMATION:
   Query Match
Best Local
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   TYPE: PRT ORGANISM: Artificial Sequence
  FEATURE:
  106 WNAKNSDITYGQYGGNNAALVNQTASDSSVMYRQVGFGNNATANQY 151
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   121
   46
  13
   61
  61 LVTRVVTHEMAHA-------GYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
   _
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
  -
   h 86.3%;
Similarity 81.9%;
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   LVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ
   NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
   MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPD------YDQ
   Application US/09543407
   Conservative
  0,
   Score 675; DB 19;
Pred. No. 5.9e-64;
   Mismatches
   PEPTIDE
  PEPTIDE
   Length 151;
   Indels
  30;
  Gaps
   105
   45
   60
   120
  60
   120
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  ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-28
                                  S
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  S
   US-09-543-407-12
   US-09-543-407-12
   Sequence 12, Application US/09543407 GENERAL INFORMATION:
  SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12
LENGTH: 151
TYPE: PRT
   Query Match
Best Local Similarity
Matches 122; Conserv
  Query Match
Best Local Similarity
Matches 128; Conserv
  TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
   APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
  APPLICANT: White, Aaron P.
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  ORGANISM: Artificial Sequence FEATURE:
   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
121
                              121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
   61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   86
   98 RNNATIDOWNAKNSDITYGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
  61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA----
   58
  _
   μ
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHNGGGNSSGPDSTLSIYQYGSANAALYDQ
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
   LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
NNAALVNYDQLVTRVVTHEMAHANNATANQY
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
  ------| YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGF
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   Conservative
  Conservative
   78.9%;
73.6%;
   78.5%; Score 614; DB 19;
80.8%; Pred. No. 2.2e-57;
tive 6; Mismatches 23;
  0;
  Score 617; DB 19;
Pred. No. 1e-57;
0; Mismatches 0;
  151
                                      151
  0,
   PEPTIDE SEQUENCES
  Length 151;
   Length 151;
  Indels
   Indels
  46;
   0,
   Gaps
   151
  Gaps
   120
  60
   97
   120
  97
   0
  N
```

US-09-543-407-14
; Sequence 14, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.

```
APPLICANT: COLLINSON, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PE
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
TYPE: PRT
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  US-09-543-407-24
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   US-09-543-407-24
   US-09-543-407-14
  Query Match
Best Local Similarity
   Sequence 24, Application US/09543407 GENERAL INFORMATION:
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
  Matches
   Matches 123;
  Query Match
Best Local
   APPLICANT: White, Aaron P. APPLICANT: Doran, James L.
   APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
  OTHER INFORMATION:
OTHER INFORMATION:
  FEATURE:
   ORGANISM: Artificial Sequence
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmer
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial Sequence FEATURE:
   TYPE: PRT
   Local Similarity
   121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
  61
  61
   61
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
   ۲
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
                                 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
  Conservative
   Conservative
   Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
   PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
  77.9%;
82.1%;
   78.3%;
81.5%;
   ა
--
  4; Mismatches
   Score 612; DB 19;
Pred. No. 3.6e-57;
5; Mismatches 23;
   Score 609; DB 19; Pred. No. 7.5e-57;
   23;
  Indels
   Length 151;
   Indels
   0;
   0;
   Gaps
   Gaps
   60
   120
   60
   0
```

```
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
  RESULT 11
US-09-543-407-22
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  뮍
  APPLICANT: White, Aaron P.

APPLICANT: Collingon, S. Karen
APPLICANT: Collingon, S. Karen
APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
  US-09-543-407-22
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   ; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-31
  RESULT 10
US-09-543-407-31
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  Query Match
Best Local S
Matches 123
  Sequence 22, Applica GENERAL INFORMATION:
   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 131
  Query Match 77.4%;
Best Local Similarity 89.3%;
Matches 117; Conservative
   Sequence 31, Application GENERAL INFORMATION:
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
    123;
  141 GFGNNATANOY 151
  121 GFGNNATANOY 131
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
  13
  81 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV
  21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGAD
  1 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                       Similarity
  VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 120
   HEMAHANQTASDSSVMVRQVGFGNNATANQY
  Application US/09543407
    Conservative
                 76.9%;
81.5%;
   US/09543407
  4;
   2
  Score 601; DB 19;
Pred. No. 5.5e-56;
4; Mismatches 24
  Score 605; DB 19;
Pred. No. 1.7e-56;
2; Mismatches 12;
  151
   PEPTIDE SEQUENCES
  PEPTIDE SEQUENCES
  Length 131;
                                      Length 151;
   Indels
    Indels
  0,
   <u>,,</u>
Gaps
   Gaps
   140
  60
   80
  0
   0
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60

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  US-09-543-407-16
   RESULT 13
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  US-09-543-407-30
  US-09-543-407-30
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FABUSEQ for Windows Version 4.0
SEQ ID NO 30
                                   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILLMG DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
  Sequence 16, Application US/09543407 GENERAL INFORMATION:
  Query Match
Best Local (
   Matches
  Sequence 30, Applica GENERAL INFORMATION:
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
   APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  APPLICANT: White, Aaron P.
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   TYPE: PRT
ORGANISM: Artificial Sequence
  TYPE: PRT
ORGANISM: Artificial
   FEATURE:
   LENGTH: 151
   121
   121
  121
  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  61
   61
  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNINGGGGNSSGPDSTLSIYQYGSANAALYDQ
  Similarity
   NNAALVNQTASDSSVMVRQVGFGNNATANQY
   NNAALVNOTASDSSVMVROVGFGNNATANOY 151
  NNAALVNQTASDSSVMVRQVGFGNNATANQY
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
   LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   Application US/09543407
   Doran, James L.
   Conservative
  76.7%;
81.5%;
Sequence
   Score 600; DB 12,
Pred. No. 7e-56;
"" amatches 24;
   151
  151
  PEPTIDE SEQUENCES
  PEPTIDE SEQUENCES
  Length 151;
   Indels
   ٥,
   120
  60
  60
  60
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RESULT 15
US-08-978-878-4
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  US-09-543-407-7
  US-09-543-407-7
   뭐
  US-09-543-407-16
   NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 7
   Sequence 4, Application US/08978878 GENERAL INFORMATION:
   Sequence 7, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
  Query Match
Best Local Similarity
   Matches 104;
  APPLICANT:
APPLICANT:
APPLICANT:
   Matches 122;
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
  Best Local Similarity
   Query Match
  APPLICANT: NORMARK, Staffan APPLICANT: OLSEN, Arne
   TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN
  TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
   CURRENT FILING DATE:
  CURRENT APPLICATION NUMBER: US/09/543,407
   TYPE: PRT
ORGANISM: Escherichia
   OTHER INFORMATION:
OTHER INFORMATION:
  LENGTH: 151
   121
   121 NNAALVNOTASDSSVMVROVGEGNNATANOV 151
   121
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  61 TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG
  61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  61
   61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
  MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
   NNAALVNOTASDSSVMVROVGFGNNATANOY 151
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
  Collinson, S. K
Kay, William W.
  Doran, James L.
   Conservative
   Conservative
   Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
  66.98;
   PRESENTATION OF HETEROLOGOUS
   Windows Version
  73.8%;
   coli
   2000-04-05
   Karen
   18;
   Score 577; DB 19;
Pred. No. 2.1e-53;
5; Mismatches 24;
  Score 523; DB 19;
Pred. No. 1.4e-47;
   Mismatches
   29;
   Å
   PEPTIDE SEQUENCES
   WELL
   Length 151;
   Length 151;
   Indels
   Indels
   AS
   ITS
   0
   0
   PREPARATION
   Gaps
   Gaps
   120
  60
  6
  120
   60
  120
   0
   0
```

```
EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1990-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1995-06-28
EARLIER FILING DATE: 1995-06-28
EARLIER FILING DATE: 1995-06-28
EARLIER FILING DATE: 1995-06-28
EARLIER FILING DATE: 1995-06-28
EARLIER FILING DATE: 1995-06-28
EARLIER FILING DATE: 1995-06-28

NUMBER OF SEO ID NOS: 10
SOFTWAREE: PAT 66.5%; SCOTE 520, DB 13; Length 151;
EARLIER FILING DATE: 1995-06-28

NUMBER OF SEO ID NOS: 10
SOFTWAREE: PAT 66.5%; SCOTE 520, DB 13; Length 151;
EARLIER FILING DATE: 1995-06-28

ORGANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Bacherichia coli
US-08-978-878-4

ONESANISM: Sacherichia coli
US-08
```

```
Result
No.
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  Title:
Perfect score:
   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
  Scoring table:
  Sequence:
  OM protein - protein search, using sw model
  Total number of hits satisfying chosen parameters:
                 22222111111111
2222211111111110
65432109
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
   81.5
78
                 520
442
87.5
83.5
  Match Length
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| _                   | σ                   | 0                   | ب                  | σ                | თ                   | 1                   | Φ                   | σ                  | ۲                  | μ                   | σ                  | 9               | σ               | σ                | σ                   | σ                  | ۲                   | μ                   |
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### ALIGNMENTS

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Preparation

RESULT 1 US-09-741-873C-4

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CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1997-11-26
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PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR PILING DATE: 1992-11-03
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PRIOR PILING DATE: 1994-10-05 밁 Ś 밁 밁 Ś US-09-741-873C-4 Sequence 4, Application US/09741873C GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
FILE REFERENCE: 012889-084 SEQ ID NO 4 Matches 103; Query Match Best Local & LENGTH: 151 TYPE: PRT ORGANISM: Escherichia 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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  CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
  APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
  APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
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CURRENT FILING DATE: 2002-03-19
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PRIOR FILING DATE: 1997-05-23
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  FILING DATE: 1997-04-11
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PRIOR FILING DATE: 2003-01-29
PRIOR FILING DATE: 2003-02-11
PRIOR PILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US60/447,358
PRIOR FILING DATE: 2003-02-11
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR PILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US60/479,650
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PRIOR PILING DATE: 2003-06-19
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LENGTH: 179
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LENGTH: 1327
   SEQUENCE 49, Application PC/TUS0402338
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TITLE OF INVENTION: MAPCAX8 AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS
TITLE OF INVENTION: USB
  APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OP INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
  CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
  APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
  SOFTWARE: PatentIn version 3.2
  NUMBER OF SEQ ID NOS: 54
  ORGANISM: Sorghum bicolor
   TYPE: PRT
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APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS900
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
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PRIOR FILING DATE: 1997-03-07
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LENGTH: 391
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   PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FLING DATE: 2003-09-30
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PRIOR FILING DATE: 2003-02-25
   APPLICANT:
   APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
   APPLICANT: Sherman, Bradley K
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  Pineda, Omaira
Repetti, Peter
Century, Karen
  Broun, Pierre E
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Yu, Guo-Liang
   Jiang, Cai-Zhong
  Riechmann,
   Keddie, James
Dubell III, Arnold N
  Reuber, T. Lynne
  Ratcliffe, Oliver
   Creelman,
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Haake, Volker
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  Jose Luis
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Pred. No.
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  Length 391
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  US-10-100-683-10327
   ; ORGANISM: Homo sapiens US-10-100-683-10326
  Sequence 10327, Appl
GENERAL INFORMATION
  Query Match
  SEQ ID NO 10326
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PRIOR APPLICATION NUMBER: US 60/043,314
PRIOR EILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,632
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,892
PRIOR FILING DATE: 1997-08-22
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PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,845
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PRIOR FILING DATE: 1997-05-23
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   TITLE OF INVENTION: Human Secreted Proteins
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   APPLICANT:
  Remaining Prior Application data
  NUMBER OF SEQ ID NOS: 13468
   PRIOR FILING DATE: 1997-08-22
   PRIOR
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   LENGTH: 386
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   FILING DATE: 1997-05-23
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Similarity 25.6%;
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  PRIOR APPLICATION NUMBER: JP 2000-372704
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: JP 2001-006144
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PRIOR APPLICATION NUMBER: JP 2001-026594
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: JP 2001-175175
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PRIOR FILING DATE: 2001-06-11
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LENGTH: 386
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   APPLICANT: ASAKO,
APPLICANT: MATSU
APPLICANT: SHIMI
  APPLICANT: WAKITA, RYUHEI
TITLE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE
TITLE OF INVENTION: 4-HALO-3-HYDROXYBUTANOATE
FILE REFERENCE: 7372-72249
  CURRENT APPLICATION NUMBER: US/10/004,115B
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   LENGTH: 38
TYPE: PRT
  ORGANISM: Corynebacterium sp
   TYPE: PRT
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   243 NSGGGSGSQSGSSGSGS-----NGDNNNGSSSGGSSGGSSGGSSGGSSGGSSGNSGGS
   51 GSANAALYDQLVTRVVTHEMAHAGYGNGADV-----GQGADNSTIELTQNGFRNNATIDQ 105
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   RGDSGSESS 305
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SHIMIZU, MASATOSHI
   Application US/10004115B
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Sequence 314, Application US/10451467A
GENERAL INFORMATION:
APPLICANT: CONTERRAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES

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   ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-314
   ; ORGANISM: Bankia gouldi
US-10-093-037A-63
   US-10-093-037A-63
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 314
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Best Local Similarity
   APPLICANT: Lam, David E.

TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
FILE REPERENCE: 564462001402
CURRENT APPLICATION NUMBER: US/10/093,037A
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US 09/910,579
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/134,078
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  SOFTWARE: FastSEQ for Windows Version 4.0
  APPLICANT: Jay M. Short
  PRIOR APPLICATION NUMBER: EP 00870318.3 PRIOR FILING DATE: 2000-12-22 PRIOR PPLICATION NUMBER: EP 01870002.1 PRIOR FILING DATE: 2001-01-04 PRIOR APPLICATION NUMBER: EP 01870003.9 PRIOR FILING DATE: 2001-01-09 PRIOR FILING DATE: 2001-01-09
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CURRENT FILING DATE: 2003-06-19
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  APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKWANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION
TITLE OF INVENTION: YEAST AND FUNGI
   TYPE: PRT
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   141 GFGNN 145
  195 DSYGSSNKKKSSYGSSNN---DSYGSNNDD----SYGSNNNDSYGSNNDDSYGSSNKKKS 247
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   Swanson, Ronald V. Mathur, Eric J.
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CURRENT FILING DATE: 2004-02-03
FRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 364
LENGTH: 878
   RESULT 14
US-10-771-241-364
   ; ORGANISM: E. US-10-771-241-364
  뭐
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   밁
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  RESULT 13
US-10-603-150-2
  닭
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  US-10-603-150-2
  Sequence 364, Application US/10771241
GENERAL INFORMATION:
APPLICANT: Syskind, Judith
APPLICANT: Forsyth, R. Allyn
   Sequence 2, Application US/10603150 GENERAL INFORMATION:
   SEQ ID NO 2
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   Query Match
   APPLICANT: Robert G. Wisotzkey
TITLE OF INVENTION: MAGED3-Like Gene Disruptions,
TITLE OF INVENTION: Compositions and Methods Related Thereto
FILE REFERENCE: R-1891
CURRENT APPLICATION NUMBER: US/10/603,150
CURRENT FILING DATE: 2003-06-24
  APPLICANT: FOrsyth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001C1
   PRIOR APPLICATION NUMBER: US 60/391,205
PRIOR FILING DATE: 2002-06-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Mus musculus
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  616 TSTNFGGALNNSAGFGGAMNTSASFGGVLNNSAGFGGAINTSAN
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   139 QVGFGNNA 146
  411 VFSGLDYNNGYLLSIEGDYWNIKDIEFKTGSKGIVLDNSNGSKLKNLVVHDIGEEAIHLR 470
   471 D-GSSNNS 477
   369 GNYNFQDKIQGAFNR-SVYLYGSANGNSTNPIILR--
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Best Local Similarity

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GENERAL INFORMATION:
APPLICANT: LEDBETTER, MARTHA
APPLICANT: HAYDEN LEDBETTER, MARTHA
APPLICANT: THOMPSON, PETER A.
ITITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
FILE REFERENCE 49076.000004.CIP2
CURRENT APPLICATION NUMBER: US/10/627,556
CURRENT FILING DATE: 2003-07-26
PRIOR APPLICATION NUMBER: 60/367,358
PRIOR FILING DATE: 2002-01-17
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PRIOR FILING DATE: 2002-01-17
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PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/385,691
PRIOR FILING DATE: 2001-06-03
NUMBER OF SEQ ID NOS: 699
SOFTWARE: Patentin version 3.2
SEQ ID NO 392
LENGTH: 273
TYPE: PRI
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: amino acid sequence
Search completed: March 11, 2004, 19:14:19 Job time : 5.3 secs
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  68 HEMAHAGYGNGADVGQGADNSTIELTONG 96
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  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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| 91.5             |                  | 92                | 92               |                   | 4.          | 95               | 95               | 95                | 95             | 95               | 95           | ທ                | ဂ<br>သ           | 102.5    | ຣ               | 60.           | m             | I I         | N             | <b>N3</b>     | 428           | a.              | m.             | an.         | an.            | to.           | Ò            | Ö            | 506          | Ò           | 0               | <b>a</b>      | n o             | 0               | 0               | 0               | C               | $\mathbf{L}$ | $\mathbf{L}$   | an.           | ü              | 683          | •••           | ٠         |
|------------------|------------------|-------------------|------------------|-------------------|-------------|------------------|------------------|-------------------|----------------|------------------|--------------|------------------|------------------|----------|-----------------|---------------|---------------|-------------|---------------|---------------|---------------|-----------------|----------------|-------------|----------------|---------------|--------------|--------------|--------------|-------------|-----------------|---------------|-----------------|-----------------|-----------------|-----------------|-----------------|--------------|----------------|---------------|----------------|--------------|---------------|-----------|
| 11.8             | •                | 11.9              |                  |                   |             |                  |                  | Ν                 | 2              |                  | 2            | ν.               | u<br>·           | 13.2     | إسا             |               | ω<br>·        | u           |               | 5             | 5             | 9               | 9.             | 9           | 9              | 4.            | 5            | ŗ            | <u>ა</u>     | 5           | 5               |               | σ.              | 7               | 7               | .7              | œ               | ٩.           | 9              | 5             | 7.             | 88.1         |               |           |
| 0                | 478              | 7                 | 598              | 644               |             | 1060             | _                | 400               | 400            | 400              | 0            | 0                | œ                | 186      | œ               | 70            | 48            | Φ           | 109           | w             | 131           | S               | ū              | 158         | 0              | N             | S            | S            | S            | S           | Çī I            | 5             | w               | UN I            | υ i             | S               | ū               | 151          | ĊΩ             | IJ            | ū              | 151          | տ             | U         |
|                  |                  |                   |                  |                   |             |                  |                  |                   |                |                  |              |                  |                  | 16       |                 |               | 19            | 19          | 19            | 21            | 13            | 30              | 16             | 16          | 19             | σ             | ű            | ω<br>ω       | 21           | <u>.</u>    | 19              | 19            | 19              | 19              | 19              |                 |                 | 19           |                | 9             |                | 19           | 9             | 19        |
| -09-791-537-2923 | -09-791-537-2388 | -10-282-122A-5061 | -09-791-537-1085 | -09-791-537-41783 | 9-543-407-6 | -09-816-660-1873 | -09-733-089-1873 | -10-438-246-17264 | 0-437-963-1864 | -10-155-881-2842 | 816-660-1873 | -09-733-089-1873 | -10-417-886-5833 | -09-252- | -09-252-691-583 | -09-543-407-3 | -09-543-407-3 | -543-407-3  | -09-543-407-3 | -09-741-873B- | -08-978-878-2 | -10-417-886-583 | -09-252-691C-5 | 691-583     | S-09-543-407-3 | 08-233-642A-5 | -60-444-371- | 60-352-946-2 | -09-741-873B | 08-978-878- | -09-543-407-7   | -09-543-407-1 | -09-543-407-    | -09-543-407-2   | 09-543-407-     | -09-543-407-1   | -09-543-407-1   | -09-543-407- | S-09-543-407-2 | S-09-543-407- | -08-233-642A-5 | 09-543-407-5 | S-09-543-407- | 43-407-2  |
| equence 2923     | ence             | equence 50        | equence 10       | equence 41783,    | quence 6,   | equence 18735,   | equence 18       | equence 17264,    | equence 18     | equence 284      | equence 187  | equence 187      | equence 583      | quenc    | equence 583     | equence 32,   | equence 39,   | equence 37, | equence 35,   | equence 2,    | equence 2,    | quence 583      | equence 583    | equence 583 | equence 34,    | quence 55,    | equence 2,   | equence 2,   | quence 4,    | equence 4,  | equence 7, Appl | equence 16,   | equence 31, App | equence 24. App | equence 18, App | equence 14, App | equence 12, App | equence 30,  | quence 26, App | ence 20,      | ce 57, Appl    | quence 5, A  | equence 22,   | equence 2 |

# ALIGNMENTS

```
RESULT 1
US-09-543-407-28
; Sequence 28, Application US/09543407
; Sequence 28, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.
; APPLICANT: COllinson, S. Karen
; APPLICANT: Kay, William W.
; APPLICANT: Kay, William W.
; TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
; FILE REFERENCE: 920043.406
; CURRENT FILING DATE: 2000-04-05
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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   RESULT 3
US-09-543-407-5
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  US-09-543-407-22
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  뮹
   US-09-543-407-28
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
   Sequence 22, Application US/09543407 GENERAL INFORMATION:
  Matches
   GENERAL INFORMATION:
  Matches
   Query Match
Best Local (
              APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   APPLICANT: White, Aaron P. APPLICANT: Doran, James I. APPLICANT: Collinson, S. APPLICANT: Kay, William W
CURRENT APPLICATION NUMBER: US/09/543,407
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial Sequence FEATURE:
   TYPE: PRT
   Local Similarity
   Local Similarity
  114
  121
   114
  121 NNAALVNOTASDSSVMVROVGFGNNATANOV 151
  151;
  144;
  61
  61
  61
  61
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  SDARKSETTITOSGYGNGADYDOLVTRVVTHEMAHAFRNNATIDOWNAKNSDITVGOYGG 120
  SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  Application US/09543407
  TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA-----DQWNAKNSDI 113
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
  SDARKSETTITQSGYGNGAD-----YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDI 113
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  100.0%;
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91.1%;
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Pred. No. 7.2e-68;
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   Score 775; DB 19;
Pred. No. 1.2e-74;
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   151
   PEPTIDE SEQUENCES
                                       PEPTIDE SEQUENCES
  Length 151;
  Indels 14;
   Length 151;
  Indels
  0
  Gaps
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  0
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; CURRENT FILING DATE: 2000-04-05; NUMBER OF SEQ ID NOS: 59; SOFTWARE: FASTSEQ for Windows Versic SEQ ID NO 5; LENGTH: 151; TYPE: PRT; ORGANISM: Salmonella enteritidis US-09-543-407-5
  á
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  밁
  RESULT 4
US-08-233-642A-57
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  밁
  S
  US-08-233-642A-57
   Sequence 57, Application:
   Matches 136; Conservative
   Query Match 88.1%;
Best Local Similarity 90.1%;
Query Match
Best Local Similarity
Matches 135; Conserv
  TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723936 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
   ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,642
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
COMPUTER: LEM PC compatible
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COMPUTER:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and
  NUMBER OF SEQUENCES:
   TITLE OF INVENTION: METHODS AND CO
  APPLICANT:
  APPLICANT:
   APPLICANT:
  MOLECULE TYPE:
  FILING DATE: 26-APR-1994
CLASSIFICATION: 424
   CITY: Seattle
STATE: Washington
  TOPOLOGY:
  COUNTRY:
   STREET:
  LENGTH:
   121
  121 NNAALVNOTASDSSVMVROVGFGNNATANOV 151
  61
  61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  98104-7092
   amino acid
   NNAALVNOTASDSSVMVROVGFGNNATANOY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  Application US/08233642A
   6300 Columbia Center,
  Kay, William W.
Collinson, S. Karen
Clouthier, Sharon C.
Doran, James L.
  151 amino acids
87.5%;
nilarity 89.4%;
Conservative
   U.S.A.
   linear
  protein
  Windows Version
  METHODS AND COMPOSITIONS FOR SALMONELLA-
   US/08/233,642A
   Berry
   Score 683; DB 19;
Pred. No. 9.5e-65;
      Score 678; DB 6;
Pred. No. 3.3e-64;
1; Mismatches 15
   920043.403C3
   Mismatches
  701 Fifth Avenue
   Version
  DB 19;
  14;
  Length 151;
  Indels
  Length 151;
  0
  Gaps
  120
   120
   60
  60
  0
```

Indels

0

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```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRSEISEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 151
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
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  US-09-543-407-26
   Sequence 26, Application US/09543407 GENERAL INFORMATION:
   Query Match
Best Local (
  Sequence 20, Applica GENERAL INFORMATION:
  09-543-407-20
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  TYPE: PRT ORGANISM: Artificial Sequence
  FEATURE:
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  106
  106 WNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   121
   13
   61
   61
   61
   ۳
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  -
   h 85.4%;
Similarity 81.9%;
  WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITOSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   SDARK------YDOLVTRVVTHEMAHAGOGADNSTIELTQNGFRNNATIDQ
   SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA------FRUNATIDQ 105
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  Application US/09543407
  Conservative
   0;
   Score 662; DB 19;
Pred. No. 1.7e-62;
  Mismatches
   PEPTIDE SEQUENCES
   PEPTIDE SEQUENCES
   Length 151;
  Indels
  30;
   Gaps
   120
   105
   60
   60
   120
   60
  60
```

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RESULT 8
US-09-543-407-12
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   RESULT 7
US-09-543-407-30
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   US-09-543-407-30
  US-09-543-407-26
  SEQ ID NO 30
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  Sequence 30, Application US/09543407 GENERAL INFORMATION:
   Query Match
Best Local Similarity
   Matches 129;
   Matches 128;
  Query Match
Best Local (
   TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
   CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   TYPE: PRT ORGANISM: Artificial Sequence
  FEATURE:
   119
  61
  98
  98 RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
  58
  99
  61 SDARKSETTITQSGYGNGAD-----
   61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA-----F
  \vdash
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  Similarity
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
  NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
   Conservative
   Conservative
  79.6%;
   79.1%; Score 613; DB 19; 74.6%; Pred. No. 3.2e-57; tive 0; Mismatches 0;
  ----YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGF
   0,
   Score 617; DB 19;
Pred. No. 1.2e-57;
0; Mismatches 0;
   GGNNAALVNQTASDSSVMVRQVGFGNNATANQY
  ----YDQLVTRVVTHEMAHAFR
  PEPTIDE SEQUENCES
  Length 151;
  Length 151;
   Indels
   46;
   44;
   Gaps
  151
   151
   Gaps
   60
  118
   98
  60
   97
  57
  97
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Sequence 12. Application US/09543407 GENERAL INFORMATION: APPLICANT: White, Aaron P. APPLICANT: Doran, James L.

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   S
   APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
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   밁
  US-09-543-407-14
   US-09-543-407-12
   US-09-543-407-14
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
  Sequence 14, Application US/09543407 GENERAL INFORMATION:
   Matches 121;
   Query Match
   Matches
  Query Match
Best Local 9
   APPLICANT: COllingon, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  APPLICANT: White, Aaron P. APPLICANT: Doran, James L
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   ORGANISM: Artificial Sequence
   FEATURE:
  ORGANISM: Artificial Sequence
  FEATURE:
   LENGTH: 151
  Local Similarity
  Local Similarity
  121
   121
   61
   61
  61
                                       61
   μ
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
   SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
   NNAALVNOTASDSSVMVROVGFGNNATANOY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                         SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
   Conservative
   Conservative
  78.1%;
80.1%;
  77.8%;
   4;
   <u>ن</u>
   Score 605; DB 19;
Pred. No. 2.3e-56;
5; Mismatches 25;
   Score 603; DB 19;
Pred. No. 3.8e-56;
4; Mismatches 25
   25;
  PEPTIDE SEQUENCES
   Length 151;
   Length 151;
   Indels
   Indels
   0,
   ٥,
   Gaps
   Gaps
  120
   60
   60
   0
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  US-09-543-407-18
   US-09-543-407-24
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   US-09-543-407-18
   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 18
   Sequence 18, Applica GENERAL INFORMATION:
  Sequence 24, Application US/09543407 GENERAL INFORMATION:
  Matches
  SEQ ID NO 24
   Query Match
   APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
   NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
  APPLICANT: White, Aaron P.
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmen OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
  FEATURE: FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmen OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   TYPE: PRT ORGANISM: Artificial Sequence
  LENGTH: 151
  LENGTH: 151
  Local
  121
  121 NNAALVNQTASDSSVMVRQVGFGNNATANQV
   121 NNAALVNOTASDSSVMVROVGFGNNATANOY 151
  122;
  61
   61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
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77.48;
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Score 600;
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  PEPTIDE SEQUENCES
   Length 151;
Length 151
   Indels
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  Gaps
   120
   60
  120
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  RESULT 12
US-09-543-407-31
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   US-09-543-407-16
   ; TYPB: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-31
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FABESEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 131
   Sequence 31, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
                                 CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
  Sequence 16, Application US/09543407 GENERAL INFORMATION:
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  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
ORGANISM: Artificial Sequence
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   121
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  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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  21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
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  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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  81.5%;
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    Mismatches

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  Score 596; DB 19;
Pred. No. 1.8e-55;
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   Gaps
   140
  120
  60
  120
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  80
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   RESULT 15
US-08-978-878-4
   밁
  US-09-543-407-16
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   US-09-543-407-7
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
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  Query Match
   Matches 103;
              TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN FILE REFERENCE: 012889-081 CURRENT PELLCATION NUMBER: US/08/978,878 CURRENT FILING DATE: 1997-11-26 EARLIER APPLICATION NUMBER: SE 8801723-1
   FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
  APPLICANT: NORMARK, Staffan APPLICANT: OLSEN, Arne
   APPLICANT: DOYAN, JAMES L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
   FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  ORGANISM: Escherichia coli
  TYPE: PRT
  LENGTH: 151
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Pred. No. 2.2e-52;
4; Mismatches 26;
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Pred. No. 5e-46;
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   26;
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  PEPTIDE SEQUENCES
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  WELL
  Length 151;
   Indels
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  STI
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EARLIER APPLICATION NUMBER: US 07/347,189

EARLIER FILING DATE: 1999-05-04

EARLIER APPLICATION NUMBER: US 07/789,437

EARLIER APPLICATION NUMBER: US 07/789,437

EARLIER APPLICATION NUMBER: US 07/970,846

EARLIER APPLICATION NUMBER: US 08/187,865

EARLIER APPLICATION NUMBER: US 08/187,865

EARLIER APPLICATION NUMBER: US 08/318,519

EARLIER APPLICATION NUMBER: US 08/318,519

EARLIER APPLICATION NUMBER: US 08/318,519

EARLIER APPLICATION NUMBER: US 08/318,519

EARLIER FILING DATE: 1994-10-05

EARLIER FILING DATE: 1994-10-05

EARLIER FILING DATE: 1994-10-05

EARLIER FILING DATE: 1995-06-28

NUMBER OF SEQ ID NO 4

SEQ ID NO 4

EARLIER FILING DATE: 1995-06-28

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PAT

ORGANISM: Eacherichia coli

US 08/495,959

EARLIER FILING DATE: 1995-06-28

ORGANISM: Eacherichia coli

US 08/495,959

EARLIER FILING DATE: 1994-10-05

ORGANISM: Eacherichia coli

US 08/495,959

EARLIER FILING DATE: 1994-10-05

ORGANISM: Eacherichia coli

US 08/495,959

EARLIER FILING DATE: 1994-10-05

ORGANISM: Eacherichia coli

US 08/495,959

EARLIER FILING DATE: 1994-10-05

ORGANISM: Eacherichia coli

US 08/495,959

EARLIER FILING DATE: 1994-10-05

ORGANISM: Eacherichia coli

US 08/495,959

EARLIER FILING DATE: 1994-10-05

ORGANISM: Eacherichia coli

US 08/495,959

EARLIER FILING DATE: 1994-10-05

ORGANISM: Eacherichia coli

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
  OM protein -
   Database
  Searched:
   Scoring table:
  Total number of hits satisfying chosen parameters:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
  428
84.5
77
  protein search, using sw model
   Match Length
   Gapop 10.0 , Gapext 0.5
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   BLOSUM62
  1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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775
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  125546 seqs, 13197846 residues
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen
   B
   US-10-603-150-2
US-10-045-674A-591
US-10-045-674A-527
US-10-767-701-45219
  US-09-741-873C-4
US-09-741-873C-2
US-10-767-701-45603
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   Description
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| 45                | 44                | 43                  | 42                  | 41                  | 40                  | 39              | 38                  | 37                 | 36               | 35               | ω<br>4              | 33                 | 32                 | 31              | 30                  | 29                | 28               | 27               |  |
|-------------------|-------------------|---------------------|---------------------|---------------------|---------------------|-----------------|---------------------|--------------------|------------------|------------------|---------------------|--------------------|--------------------|-----------------|---------------------|-------------------|------------------|------------------|--|
| 69                | 69                | 69                  | 69                  | 69                  | 69.5                | 69.5            | 69.5                | 70                 | 70               | 70               | 70                  | 71                 | 71                 | 71              | 71                  | 71.5              | 71.5             | 72               |  |
| 8.9               | 8.9               | 8.9                 | 8.9                 | 8.9                 | 9.0                 | 9.0             | 9.0                 | 9.0                | 9.0              | 9.0              | 9.0                 | 9.2                | 9.2                | 9.2             | 9.2                 | 9.2               | 9.2              | 9.3              |  |
| 1574              | 904               | 414                 | 351                 | 182                 | 624                 | 577             | 310                 | 321                | 246              | 245              | 194                 | 541                | 514                | 250             | . 179               | 878               | 463              | 1532             |  |
| σ                 | თ                 | σ                   | -                   | σ                   | μ                   | σ               | -                   | _                  | σ                | σ                | σ                   | ഗ                  | ຫ                  | Q               | Q                   | σ                 | 0                | 9                |  |
| US-10-695-499-179 | US-10-786-892-158 | US-10-767-701-45857 | PCT-US04-05654-1755 | US-10-767-701-44940 | PCT-US04-05654-1466 | US-10-775-337-3 | PCT-US04-05654-1593 | PCT-US04-05654-590 | US-10-779-461-41 | US-10-779-461-59 | US-10-767-701-43391 | US-09-830-230A-429 | US-09-830-230A-430 | US-10-779-461-6 | US-10-767-701-42696 | US-10-771-241-364 | US-10-641-678-71 | US-10-695-499-62 |  |
| Sequence          | Sequence          | Sequence            | Sequence            | Sequence            | Sequence            | Sequence        | Sequence            | Sequence           | Sequence         | Sequence         | Sequence            | Sequence           | Sequence           | Sequence        | Sequence            | Sequence          | Seguence         | Sequence         |  |
| 179, App          | 158, App          | 45857, A            | 1755, Ap            | 44940, A            | 1466, Ap            | 3, Appli        | 1593, Ap            | 590, App           | 41, Appl         | 59, Appl         | 43391, A            | 429, App           | 430, App           | 6, Appli        | 42696, A            | 364, App          | 71, Appl         | 62, Appl         |  |

## ALIGNMENTS

RESULT 1
US-09-741-873C-4
Sequence 4, Application US/09741873C
GENERAL INFORMATION:

CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1997-11-26
PRIOR PELING DATE: 1989-05-04
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR PILING DATE: 1994-01-28
PRIOR PILING DATE: 1994-01-05
PRIOR PILING DATE: 1994-10-05
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PRIOR PILING DATE: 1994-11-06
PRIOR PILING ð δ 밁 밁 S US-09-741-873C-4 Query Match Best Local ( Matches 102; APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As
FILE REFERENCE: 012889-084 LENGTH: 151
TYPE: PRT
ORGANISM: Escherichia coli 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 61 TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG 61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG Similarity Conservative 67.5%; Score 506; DB 5 16; Mismatches DB 5; Length 151; 33, Well Indels ΑB Its Preparation Gaps 120 60 60 120

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72.5 72.5 72.5 72.5 72.7 72 72 72 72 72 72 72

US-10-767-701-56903
US-10-779-461-1
US-09-596-774-2
US-10-045-674A-594
US-09-596-774-7
US-09-596-774-6
US-10-695-499-178
US-10-695-499-178
US-10-695-499-178
US-10-296-085A-19
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73.5 73 73 73 73

US-10-771-241-299 US-10-620-246-6

75.5 75.5 74

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   ; ORGANISM: Escherichia coli
US-09-741-873C-2
OTHER INFORMATION: Clone ID: US-10-767-701-45603
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   US-09-741-873C-2
  Sequence 2, Applicat GENERAL INFORMATION:
  NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45603
LENGTH: 234
TYPE: PRT
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APPLICANT:
  APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
  PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 08/187,865
   PRIOR FILING DATE: 1989-05-04
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
   CURRENT APPLICATION NUMBER: US/09/741,873C CURRENT FILING DATE: 2000-12-22
   APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne
   CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
  NUMBER OF SEQ ID NOS: 11
   PRIOR APPLICATION NUMBER: US 08/978,878 PRIOR FILING DATE: 1997-11-26
  PRIOR APPLICATION NUMBER: SE 8801723-1 PRIOR FILING DATE: 1998-05-06
  APPLICANT: Kovalic, David K.
  PRIOR FILING DATE: 1994-10-05
   PRIOR
   PRIOR APPLICATION NUMBER: US 07/347,189
  FILE REFERENCE: 012889-084
  TITLE OF INVENTION: Fibronectin Binding Protein As Well As
  PEATURE:
NAME/KON: unsure
LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
  ORGANISM: Sorghum bicolor
   LENGTH:
   FEATURE:
  Match 55.2%;
Local Similarity 64.1%;
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   FILING DATE: 1994-01-28
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   Olsen, Arne
   Conservative
   Application US/10767701
   2000-12-2
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Pred. No. 5.3e-32;
   Mismatches
  Length 131;
   Indels
  Its Preparation
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   Gaps
   60
  80
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   RESULT 4
US-10-603-150-2
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  US-10-045-674A-591
  RESULT 5
  US-10-603-150-2
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   SEQ ID NO 2
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   FILE REFERENCE: R-1891
CURRENT APPLICATION NUMBER: US/10/603,150
CURRENT FILING DATE: 2003-06-24
   PRIOR APPLICATION NUMBER: US 60/391,205
PRIOR FILING DATE: 2002-06-24
NUMBER OF SEQ ID NOS: 4
   APPLICANT: Robert G. Wisotzkey
TITLE OF INVENTION: MAGED3-Like Gene Disruptions,
TITLE OF INVENTION: Compositions and Methods Related Thereto
                                  APPLICANT: HOOGÉNBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
TITLE OF INVENTION: OF PERTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
   SOFTWARE: FastSEQ for Windows Version 4.0
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
  APPLICANT:
  APPLICANT:
  APPLICANT:
  APPLICANT: LADNER,
  LENGTH: 1160
TYPE: PRT
ORGANISM: Mus musculus
  515
  566 GRAGFGGALNTNATFGGVLNGSAGFGGAMNTNATFG--GALNSNAGFGGAISTSTNFGGA
  624 LNNSAGFGGAMNTSÅSFGGVLNNSAGFGGAINTSAN
  121 -NNAA----LVNQTASDSSVMVRQVGFGN--NATAN
  11 AIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI 70
   61
   46
  71 TQSGYGNGADYDQLVTRVVTHE--MAHAFRNNATIDQWNAKNSDITVG-----QYGG-
   83 QLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNA
   39;
  43;
   1 MKLLKVAAFAAIVV--SGSALAGVVPQW---GGGGNHNGGGN-----SGGPDSTL 45
   Similarity
  LADNER, ROBERT C.
COHEN, EDWARD H.
NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
  AISTSFSGVLNSSASFGGAIN---
   GXYGEAGGSGXAYAQGGGQGGGGGGGQYGGSG-----
   SIY----
   MATTKLAALCFIVLLGIGGANAARVARYVSAGGGGGGGGGGGGRWRGGASRWGSGSGSGC
  Application US/10045674A
  Conservative
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   -AGGSGSNGGAYAQGGAQGGGGGGGGQYGGSGS 134
   10.9%;
  ; Score 77; DB 6; ; Pred. No. 32; 19; Mismatches 6
   11; Mismatches
   Score 84.5; DB Pred. No. 0.93;
  ---TSAGFGSTLN----SSASFGSALSTSASFGGVLN 565
   -QYGSANAALALQSDARKSETTITQSGYGNGADYD 82
   DB 6;
   46;
  66;
  659
  149
  Length 1160;
   Length 234;
   Indels
  Indels
  28;
   65;
   SGYGSGSGYG
   Gaps
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  623
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   6
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PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR PRIOR PRICE PRIOR NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 527
LENGTH: 533
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  RESULT 6
US-10-045-674A-527
  S
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  ई
  US-10-045-674A-591
   Sequence 527, Application US/10045674A GENERAL INFORMATION:
   SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 591
   Query Match
  Matches
   Query Match
  APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
  CURRENT APPLICATION NUMBER: US/10/045,674A CURRENT FILING DATE: 2001-10-25
   TITLE OF INVENTION: LIBRARIES FILE REFERENCE: DYAX/002 CIP2
   TITLE OF INVENTION:
  PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
  PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
  OTHER INFORMATION:
OTHER INFORMATION:
  TYPE: PRT
ORGANISM: Artificial Sequence
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  OTHER INFORMATION: Description of Unknown Organism: M13 protein OTHER INFORMATION: sequence
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ORGANISM: Unknown Organism
   FEATURE:
   ENGTH:
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   Local Similarity
  123 AALVNQTASDSSVMVRQVGFGNNA 146
   303
   243
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  64 R-KSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNN 122
  15 SGSALAGVVPQWGG--GGNHNGGGNSSGPDSTLSIYQ-YGSANAAL-----
   Similarity
   LADNER, ROBERT C.
COHEN, EDWARD H.
NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
   SGGGSEGGGSEGGGSEGGGSGGGSGSGDFDYEKMANANKGAMTENADENALQSDA
  SGSALAGVVPOWGG--GGNHNGGGNSSGPDSTLSIYQ-YGSANAAL-
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   9.7%; Score 75.5;
25.7%; Pred. No. 13;
  9.7%; Score 75.5; 1
25.7%; Pred. No. 17;
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  15;
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  47;
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   Length 424;
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  45;
   -GDFAGSN 341
   -ALQSDA 63
  Gaps
  ALOSDA 63
  Gaps
   302
                    122
   411
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  ; ORGANISM: E. US-10-771-241-299
   US-10-771-241-299
   RESULT 8
  ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C9039_1.pep US-10-767-701-45219
   RESULT 7
US-10-767-701-45219
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   SEQ ID NO 299
LENGTH: 382
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   Sequence 299, Application US/10771241 GENERAL INFORMATION:
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Matches 40; Conserv
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   CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
   APPLICANT: FORSYth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001C1
   CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
  APPLICANT: Zyskind, Judith APPLICANT: Forsyth, R. Al
   APPLICANT: Kovalic, Dav
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwe
  SOFTWARE:
  NUMBER OF SEQ ID NOS:
  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
  FILE REFERENCE: 38-21 (53535) B
   TYPE: PRT
   TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
  LENGTH: 447
   117 TPNPYEQAISIIGRTLSAFDEDNLIPCFGFGDASTHDQ 154
  122 N-----AALVNOTAS--DSSVMVROVGFGNNATANO 150
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   123 AALVNOTASDSSVMVROVGFGNNA 146
  65 GDDYRSL--SQVTEALAQAGLESSNLIVGIDFTKSNEWTGKISFNRRCLHDI-----GN 116
   78 GADYDQLVTRVVTHEMAHAFRNNATI------DQWNAKNS-----DITVGQYGGN 121
  24 POWGGGGNHNGGGNSSGPDS----TLSIYQYGSANAALALQSDARKSETTITQSGYGN- 77
  FastSEQ for Windows Version 3.0
   Zhou, Yihua
Cao, Yongwei
   PSYGYGYSYDYGSTSSGYNSRNTGNTSSGY---SARYAPSSENNVQPETTARLQRKYSRI 64
  Coli
  Conservative
   Conservative
  Application US/10767701
  David
                   25.2%;
   9.5%; Score 74; DB 25.3%; Pred. No. 18;
  ---- QVGDGDNS
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  35,
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Gaps
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GNHNGGGNSSGPDSTLSI-YQ--YGSANAALALQSDARKSETTITQSGYGNGADYDQLVT 86

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   RESULT
   US-10-620-246-6
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  US-10-620-246-6
  RESULT 10
US-10-767-701-56903
  Sequence 6, Application GENERAL INFORMATION
   SOFTWARE: 1
SEQ ID NO 6
   Sequence 56903, Appl: GENERAL INFORMATION: APPLICANT: Kovalic,
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  PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
   CURRENT FILING DATE: US/10/620,246
CURRENT FILING DATE: 2003-07-15
  TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1A
   APPLICANT: ANDERSEN, Peter
  PRIOR APPLICATION NUMBER: 1277/97 PRIOR FILING DATE: 1997-11-10
   NUMBER OF SEQ ID NOS: 173
  PRIOR APPLICATION NUMBER: 60/044,624
  PRIOR FILING DATE: 1998-10-08
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
  ORGANISM: Mycobacterium tuberculosis
  TYPE: PRT
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  APPLICATION NUMBER: 6 FILING DATE: 1999-01-
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   FILING DATE: 2001-02-20
   APPLICATION NUMBER: 60/070,488
   APPLICATION NUMBER:
  APPLICATION NUMBER: 1281/98
   158
   87
   107
   LING DATE: 1999-10-08
  98 HAEFRLENNEFNVVDVGSLNGTYVNREPVDSAVLANGDEVQIG 140
  49
   162
   24;
   Similarity
   PatentIn Ver.
  Application US/10620246
  GMSGGIIAHA---
  RVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
  NA----KNSDITVGQYGGNNAALVNQTASDSSVMVR----QVG 141
   OAGTESAVSGVEGLPPGSALLVVKRGPNAGSRFLLDQAITSAGRHPDSDIFLDDVTVSRR 97
   QYGSANAALALQSDARKSETTITQSGYGNGADY--DQLVTRVVTHEMAHAFRNNATIDQW 106
  CATION NUMBER:
   WELDINGH, Karin
FLORIO, Walter
   RASMUSSEN, Peter Birk
  ROSENKRANDS,
   Conservative
  Application US/10767701
   1998-01-05
  1997-04-18
   2002-05-02
  Rikke
  David K.
  9.4%;
  09/791,171
   60/116,673
  09/415,884
   22;
   Score 73; DB 6; Length 162, Pred. No. 6.4;
  -DGITFGOPLGDTMVLVKAPGADNVKIENOTG 240
   Mismatches
     and
   47;
       Other Molecules Associated With
   Indels
  -GYSRSGDSSQIYY
   10;
   Gaps
  199
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   밁
   , OTHER INFORMATION: Clone ID: 30950641.pep US-10-767-701-56903
  S
  밁
  RESULT 11
US-10-779-461-1
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   RESULT 12
   밁
   US-10-779-461-1
  CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 56903
LENGTH: 174
  US-09-596-774-2
  SEQ ID NO 1
LENGTH: 238
TYPE: PRT
  Sequence 1, Application US/10779461 GENERAL INFORMATION:
  Matches
   Query Match
  Sequence 2, Applicat GENERAL INFORMATION:
   Query Match
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  CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
  TITLE OF INVENTION:
   Matches
   FILE REFERENCE: 38-21 (53535) B
   FILE REFERENCE: 00980/1
  APPLICANT: Morton, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
APPLICANT: GRONER, BERND
APPLICANT: MORITZ, DIRK
TITLE OF INVENTION: BIFUNCTIONAL PROTEIN,
FILE REFERENCE: 24741-1521
CURRENT APPLICATION NUMBER: US/09/596,774
  SOFTWARE: PatentIn version 3.2
   ORGANISM: Sorghum bicolor
  TYPE: PRT
  FEATURE:
   FEATURE: OTHER INFORMATION: phage display generated human antibody
   ORGANISM: artificial
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Local Similarity 24.5%;
  113
  111
   99
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  25 QWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD---ARKSETTITQ 72
  6
  3 LIKVAAFAAIVVSGSALAGVVPQWGGGGNHNG--GGNSSGPDSTLSIYQYGSANAALALQ 60
   73 SGYGN--GADYD 82
   24;
  Similarity
  PATSITAVTVGNEVLSGTNAAML 135
  ----SDITVGQ--YGGNNAALV 126
  MLAAAAAFAVLAPPAASSGPTPAPPALGINYGQVADNLPPPQAALLLLRALNATRVKLYD
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   Application US/09596774
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  Plants and Uses Thereof For Plant Improvement
  33.38;
  159
   22;
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Pred. No. 7
   Score 73; DB Pred. No. 10; 5; Mismatches
  ហ
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  6
  6
  54.
   -GSAQAVLTQPSSVSGAPGQRVTISC
  19;
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US-09-596-774-2
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CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR FILING DATE: 2000-04-17
  APPLICANT: LADNER, ROBERT C. APPLICANT: COHEN, EDWARD H.
  NUMBER OF SEQ ID NOS: 635
  NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 3.2
  PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 08/793,048
PRIOR FILING DATE: 1996-11-01
PRIOR APPLICATION NUMBER: PCT/EP95/01494
PRIOR FILING DATE: 1995-04-20
PRIOR APPLICATION NUMBER: EP 94810244.7
PRIOR PRIOR DATE: 1994-05-02
  FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: M13-III
OTHER INFORMATION: protein sequence
  TITLE OF INVENTION: OF PEPTIDITITLE OF INVENTION: LIBRARIES FILE REFERENCE: DYAX/002 CIP2
   APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

FITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING

FITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI

FITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
   ORGANISM: Artificial Sequence
   PRIOR APPLICATION NUMBER: 09/159,027
   CURRENT FILING DATE:
   ORGANISM: Artificial Sequence
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  104 GYVPYWGQGTTVTVSSGGGGSGGGGGGGGGTQLTQSHKFLSTSVGDRVSITCKASQDV 163
                                       28 GGGNHNGG--GNSSGPDSTLSIYQY---GSANAAL-----ALQSDAR-KSETTITQS 73
  25;
   34;
   21 GVVPQWG------GGGNHNGGGNSSGPDSTLSI------
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GGGSEGGGSEGGGSGSGSGDFDYEKMANANKGAMTENADENALQSDAKGKLDSVAT-- 321
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   HOET, RENE
  Application US/10045674A
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   HORACIO G.
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   9.4%; Score 72.5; D
21.2%; Pred. No. 12;
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Pred. No. 24;
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  38;
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   47
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  문
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   S
  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TOTHER INFORMATION: chimeric amino acid sequence US-09-596-774-7
   CURRENT APPLICATION NUMBER: US/09/596,774
CURRENT FILING DATE: 2000-06-19
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PRIOR FILLY DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 08/793,048
PRIOR FILLY DATE: 1996-11-01
PRIOR APPLICATION NUMBER: PCT/EP95/01494
PRIOR FILLY DATE: 1995-04-20
PRIOR APPLICATION NUMBER: EP 94810244.7
PRIOR FILLY DATE: 1994-05-02
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   밁
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   Sequence 7, Applicat GENERAL INFORMATION:
  -09-596-774-6
              SOFTWARE: Patentin
                                     NUMBER OF SEQ ID NOS: 16
  APPLICANT: GRONER, BERND
APPLICANT: MORITZ, DIRK
TITLE OF INVENTION: BIFUNCTIONAL PROTEIN, PREPARATION AND USE
FILE REFERENCE: 24741-1521
  PRIOR APPLICATION NUMBER: EP 94810244.7
PRIOR FILING DATE: 1994-05-02
NUMBER OF SEQ ID NOS: 16
   PRIOR APPLICATION NUMBER: 08/793,048
PRIOR FILING DATE: 1996-11-01
PRIOR APPLICATION NUMBER: PCT/EP95/01494
PRIOR FILING DATE: 1995-04-20
  FILE REFERENCE: 24741-1521
CURRENT APPLICATION NUMBER: US/09/596,774
CURRENT FILING DATE: 2000-06-19
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PRIOR FILING DATE: 1998-09-23
  LENGTH: 443
TYPE: PRT
ORGANISM: Artificial Sequence
  APPLICANT: MORITZ, DIRK
TITLE OF INVENTION: BIFUNCTIONAL PROTEIN, PREPARATION AND USE
  APPLICANT: GRONER, BERND
  FEATURE:
ID NO 6
  Local Similarity
  164 YNAVAWYQQKPGQSPKLLIYSASSRYTGVPSRFTGSGSGPDFTFTISSVQAEDLAVYF 221
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  134 SVMVROVGFGNNA 146
  48 -----YQY--GSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAF
   21 GVVPQWG-----GGGNHNGGGNSSGPDSTLSI----
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  74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
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  14; Mismatches
  Score 72.5;
Pred. No. 25;
   DB 5;
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   Gaps
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|-------------------------------------------------------------------|-----------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Search completed: March 11, 2004, 19:14:20<br>Job time : 6.3 secs | 21 GVVPQWGGGNHNGGGNSSGPDSTL1      | ctificial Sequence  AATION: Description of Artificial Sequence: Synthetic  AATION: chimeric amino acid sequence  9.4%; Score 72.5; DB 5; Length 461;  milarity 21.2%; Pred. No. 26;  Conservative 14; Mismatches 38; Indels 41; Gaps |
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Maximum Match 100%
Listing first 45 summaries
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  Perfect score:
  Title:
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Query
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m2_6/ptodate/2/paa/US101_COMB.pep:*
m2_6/ptodate/2/paa/US101_COMB.pep:*
m2_6/ptodate/2/paa/US102_COMB.pep:*
m2_6/ptodate/2/paa/US103_COMB.pep:*
m2_6/ptodate/2/paa/US104_COMB.pep:*
m2_6/ptodate/2/paa/US104_COMB.pep:*
m2_6/ptodate/2/paa/US106_COMB.pep:*
m2_6/ptodate/2/paa/US106_COMB.pep:*
m2_6/ptodate/2/paa/US106_COMB.pep:*
  _6/ptodata/2/paa/US06
   6/ptodata/2/paa/PCTUS_COMB.pep:*
6/ptodata/2/paa/US06_COMB.pep:*
  6/ptodata/2/paa/US097A_COMB.pep:*
  SUMMARIES
   6019581
   Description
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| U             | 1 14            | ٠ (              | ۸ ۱             | J I              | . د              | 0               | 9               | œ               | 7              | σ                 | л           | 4              | w            | N               | _            | 0               | ø          | œ             | 7             | ð             | ທ           | 4.          | ũ              | N              | ŭ               | Ö               | φ.            | œ           | 7             | ð            | ĊΠ          | 4.            | w          | N             | Ъ             | 0            | φ             | œ          | 7             | σ             | u             | 4.                | w            | Ν              | μ.           |
|---------------|-----------------|------------------|-----------------|------------------|------------------|-----------------|-----------------|-----------------|----------------|-------------------|-------------|----------------|--------------|-----------------|--------------|-----------------|------------|---------------|---------------|---------------|-------------|-------------|----------------|----------------|-----------------|-----------------|---------------|-------------|---------------|--------------|-------------|---------------|------------|---------------|---------------|--------------|---------------|------------|---------------|---------------|---------------|-------------------|--------------|----------------|--------------|
| 6             | 90.             | •                | 0 0             | 0 1              | 9 9              | 90              | 98              | 98              | 9              | 101.5             | 10          | 103            | 104.5        | 114.5           | 4.           |                 | 17.        | 237           | $\mathbf{r}$  | 332           | 436         | 436         | 462            | 475            | 475             | 475             | 496           | 512         | 512           | 514          | 514         | 517           | 566        | 594           | 597           | 599          | 600           | 603        | 613           | 657           | 659           | 676               | 681          | 700            | 768          |
| 12.6          | 12.0            | 12.0             | ٥,              | ا د              | 9                | 2               | N               | ٧.              | Ψ              | 13.2              | ·           | 13.4           | 13.6         |                 | 14.9         | 4               | 28.3       | 30.9          | ٠             | 43.2          | •           | 56.8        | ٠              | ٠              | •               | •               |               | ٠           | ٠             |              | •           | 67.3          | •          | •             |               | 8            | 8             | 78.5       |               |               | Ġ             | 8                 | 8            |                | 0            |
| 1249          |                 | ى د              | א ני<br>ה       | л (<br>С )       | 175              | 775             | 145             | 145             | 151            | 520               | 445         | 445            | 151          | 186             | 186          | 186             | 70         | 48            | 68            | 109           | 131         | 131         | 109            | 158            | 158             | 158             | 120           | 151         | 151           | 151          | 151         | S             | 151        | w             | S             | 151          | S             | 151        | ū             | ū             | S             |                   | σ            | 151            |              |
|               | 1               |                  | ) t             | ا د              |                  |                 |                 | 21              |                | <b>p.</b> a       |             |                | 19           |                 | 16           | 16              | 19         | 19            | 19            | 19            | 21          | 13          | 19             | 30             | 16              | 16              | δ             | ü           | ω<br>ω        | 21           | 13          | 19            |            | 19            | 19            | 19           | 19            | 19         | 19            | 19            | 19            | σ                 |              |                |              |
| 10-455-719-35 | -09-/08-42/-912 | -09-308-437-8138 | -09-755-660-335 | -09-737-090-7352 | -09-818-60-22-20 | -09-737-080-727 | -09-803-110-885 | -09-739-449-885 | -09-543-407-   | PCT-US02-18256-21 | 60-039-2063 | -10-369-493-   | -09-543-407- | -10-417-886-583 | -09-252-691C | -09-252-691-583 | -543-407-3 | -09-543-407-3 | -09-543-407-3 | -09-543-407-3 | 9-741-873B- | -08-978-878 | -09-543-407-34 | -10-417-886-58 | -09-252-691C-58 | S-09-252-691-58 | 08-233-642A-5 | 60-444-371- | -60-352-946-2 | -09-741-873B | 08-978-878- | -09-543-407-7 | 09-543-407 | -09-543-407-3 | -09-543-407-2 | 09-543-407-1 | -09-543-407-2 | 9-543-40   | -09-543-407-2 | -09-543-407-2 | S-09-543-407- | US-08-233-642A-57 | -09-543-407- | -09-543-407-   | -09-543-407- |
| equence       | equence 9129,   | equence 2333,    | )<br>(          | omionae aleas    | 202020           | בנכ פחופותם     | equence 8854    | equence 8854, A | equence 6, App | 21, Ap            | equence 206 | equence 20638, | е<br>е       | equence 5833,   | 583          | 583             | 32,        | 39,           | 37,           | 35,           | 2           | Ν           | 34, Ap         | 834,           | 5834, A         | e 5834,         | 55, Appl      | N           | 2, Appl       | e 4, Appl    | 0           | 7             | 16         | u ا           | 20.           | equence 1    | equence 26,   | equence 12 | equence 28,   | equence 22    | equence 14,   | quence 5          | equence 5,   | quence 24, App | equence 30,  |

## ALIGNMENTS

```
RESULT 1

(S-09-543-407-30)

Sequence 30, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 151

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE
FORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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   RESULT 2
   US-09-543-407-30
  US-09-543-407-5
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  RESULT 3
  US-09-543-407-24
  NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
Type: nom
            Sequence 5, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   Sequence 24, Application US/09543407 GENERAL INFORMATION:
   Matches 151;
   Query Match
  Query Match
  Matches
   APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   APPLICANT: White, Aaron P. APPLICANT: Doran, James L
CURRENT APPLICATION NUMBER: US/09/543,407
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major
  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
   Local
  Local Similarity
   121
   121
  121
  113
  143;
   19
  61
   61
  61
   H
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   Similarity
   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
  HEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT-----YDQLVTRVVT 112
   NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
  HEMAHA-----NQTASDSSVMVRQVGFGNNATANQY 151
  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   Doran, James L
   Conservative
  Conservative
  91.1%;
   100.0%; Score 768; DB 1 100.0%; Pred. No. 7e-73;
   0
  Score 700; DB 19;
Pred. No. 1.2e-65;
0; Mismatches 0;
   Mismatches
   DB 19;
   <u>,</u>
  0
                                      PEPTIDE SEQUENCES
   PEPTIDE SEQUENCES
  Length 151;
   Length 151;
   Indels
  Indels
  16;
   0,
   120
   120
   60
   0
```

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; ORGANISM: Salmonella US-09-543-407-5
   RESULT 4
US-08-233-642A-57
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   CURRENT FILING DATE: 2
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for W
SEQ ID NO 5
LENGTH: 151
  US-08-233-642A-57
Query Match
Best Local Sim
Matches 136;
  Sequence 57, Application US/08233642A GENERAL INFORMATION:
  Matches
  Query Match
Best Local Similarity
   APPLICATION NUMBER: US/08/233
APPLICATION NUMBER: US/08/233
EILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION UNMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V6
CURRENT APPLICATION DATA:
   TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
   TYPE: PRT
   APPLICANT:
APPLICANT:
APPLICANT:
  NUMBER OF SEQUENCES: 5
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS:
   TITLE OF INVENTION:
  MOLECULE TYPE:
   CITY:
STATE:
  STREET:
   COUNTRY:
  ADDRESSEE:
  LENGTH:
  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  137;
  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
   61 SDARKGETTITOSGYGNGADVGOGADNSTIELTONGFRNNATYDQLVTRVVTHEMAHAGG 120
   : Seattle
E: Washington
TRY: U.S.A.
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                   Similarity
  amino acid
GY: linear
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  6300 Columbia Center,
   151 amino acids
   Kay, William W.
Collinson, S. Karen
Clouthier, Sharon C.
Doran, James L.
DOVAN, JAMES L.
VENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
  Conservative
 Conservative
  Seed and Berry
  protein
   enteritidis
  Windows Version
  88.7%;
  2000-04-05
   BASED VACCINES
                   88.0%;
90.1%;
  US/08/233,642A
   Score 676; DB 6; Length 151;
Pred. No. 4.2e-63;
2; Mismatches 13; Indels
  920043.403C3
  Score 681; DB 19;
Pred. No. 1.2e-63;
  Mismatches
  701 Fifth Avenue
  151
   Length 151;
  Indels
  0
        0
  60
   120
  60
        0;
```

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
FULCREBY APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
  RESULT
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   В
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   RESULT 5
US-09-543-407-14
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  US-09-543-407-22
   밁
   ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-14
   Query Match
Best Local Similarity 81.9
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
  Sequence 14, Application US/09543407 GENERAL INFORMATION:
   Sequence 22, Application US/09543407 GENERAL INFORMATION:
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   ORGANISM: Artificial Sequence FEATURE:
  TYPE: PRT
   121
  106
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   121
   61
  5
   61
  5
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  LVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
   LVTRVVTHEMAHA-
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT---------
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSI YQYGSANAALALQ
   NNPALVNOTASDSSVMVRQVGFGNNATANQY
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  85.8%;
   0
   Score 659; DB 19;
Pred. No. 2.7e-61;
0; Mismatches 0
   SVMVRQVGFGNNATANQY 151
  DB 19;
  PEPTIDE SEQUENCES
  PEPTIDE SEQUENCES
  Length 151;
   Indels
   30;
   Gaps
  ğ
  105
   60
  60
  120
   60
```

```
RESULT 8
US-09-543-407-12
; Sequence 12, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.
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  US-09-543-407-28
   US-09-543-407-28
  US-09-543-407-22
  Query Match
Best Local Similarity
Matches 129; Conserv
  Sequence 28, Application US/09543407 GENERAL INFORMATION:
   SEQ ID NO 28
LENGTH: 151
  Query Match
Best Local Similarity
  Matches 136;
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
   TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmen OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  TYPE: PRT ORGANISM: Artificial Sequence
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   FEATURE:
   ORGANISM: Artificial Sequence FEATURE:
  119
   106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
   99
   61
   13
  61
   13
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
   -----GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
   NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  SDARKSETTITQSGYGNGADVGQGADN----
  MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
  Conservative
  Conservative
  79.8%;
74.6%;
  85.5%;
  <u>,,</u>
  0
  Score 613; DB 1:
Pred. No. 2e-56;
0; Mismatches
  Score 657; DB 19;
Pred. No. 4.3e-61;
   GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
  Mismatches
   DB 19;
  0
  0
  PEPTIDE SEQUENCES
   Length 151;
  ---YDQLVTRVVTHEMAHADQ 105
   Length 151;
  Indels
  Indels
   TDQLVTRVVTHEMAHAFR
  44;
  30;
   151
  Gaps
  Gaps
   98
  60
   60
  60
   60
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  RESULT 9
US-09-543-407-26
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   US-09-543-407-26
   US-09-543-407-12
   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
  Sequence 26, Application US/09543407 GENERAL INFORMATION:
  Query Match
Best Local Similarity
  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
TYPE: PRT
   Matches
  Query Match
Best Local Similarity
   Matches
  APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
  APPLICANT: White, Aaron P. APPLICANT: Doran, James I
  FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 59
   NUMBER OF SEQ ID NOS: 59
   APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  FEATURE:
   ORGANISM: Artificial Sequence
  TYPE: PRT
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  ORGANISM: Artificial Sequence FEATURE:
   123;
   121
  122;
   121
  61
   61
61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
  61
  <u>بـــ</u>
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
  Н
   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
   NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
   Conservative
   Conservative
  78.1%;
81.5%;
  78.5%;
   4;
  6,
  Score 600; DB 19;
Pred. No. 4.9e-55;
4; Mismatches 24;
  Score 603; DB 19;
Pred. No. 2.4e-55;
6; Mismatches 23;
  23;
   PEPTIDE SEQUENCES
   Length 151;
   Length 151;
   Indels
  Indels
  0;
  0;
  Gaps
   Gaps
  60
  120
   0
  0
```

```
; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragmen; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major US-09-543-407-20
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  US-09-543-407-20
  RESULT 11
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  US-09-543-407-18
   RESULT 10
US-09-543-407-18
  밁
   S
  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 151
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
  Sequence 20, Application US/09543407 GENERAL INFORMATION:
  Sequence 18, Application US/09543407 GENERAL INFORMATION:
   Matches
  Query Match
Best Local :
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
  TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
  APPLICANT: White, Aaron P. APPLICANT: Doran, James L
   ORGANISM: Artificial Sequence FEATURE:
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  LENGTH: 151
TYPE: PRT
  TYPE: PRT
  ORGANISM: Artificial FEATURE:
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   61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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   Conservative
   Sequence
   78.0%;
81.5%;
   ა
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  Score 599; DB 19;
Pred. No. 6.3e-55;
   Mismatches
   151
  PEPTIDE SEQUENCES
   PEPTIDE SEQUENCES
  Length 151;
   Indels
   fragment
   0
   Gaps
  60
   120
  60
```

Query Match

77.7%;

Score 597;

В

19;

Length 151;

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PETLE REFERENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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   В
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  US-09-543-407-16
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   ; SOPTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
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; ORGANISM: Salmonella enteritidis
US-09-543-407-31
  밁
  S
  ; Sequence 31, Application U
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P
; APPLICANT: Doran, James
; APPLICANT: Collinson, S.;
; APPLICANT: Kay, William
  US-09-543-407-31
   Sequence 16, Application US/09543407 GENERAL INFORMATION:
   Matches 117;
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
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   ORGANISM: Artificial
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   Doran, James L.
Collinson, S. K.
Kay, William W.
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  PEPTIDE SEQUENCES
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  0
   Gaps
   120
  60
  80
   120
  120
  60
   60
   0
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US-08-978-878-4
  ; TYPE: PRT ; ORGANISM: Escherichia US-09-543-407-7
   US-09-543-407-7
   US-09-543-407-16
Sequence 4, Application US/08978878
GENERAL INFORMATION:
APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN
FILE REFERENCE: 012889-081
CURRENT APPLICATION UNMERR: US/08/978,878
CURRENT FILLING DATE: 1997-11-26
EARLIER APPLICATION UNMERR: SE 8801723-1
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  APPLICANT: White, Aaron P
   FEATURE: FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   LENGTH: 151
   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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  Score 517; DB 19;
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Pred. No. 2e-51;
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   24;
  AS
  WELL
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  Length 151;
   Length 151;
  Indels
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EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1991-11-03
EARLIER FILING DATE: 1992-11-03
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER APPLICATION NUMBER: US 08/318,519
EARLIER APPLICATION NUMBER: US 08/318,519
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 151
TYPE: PAT
ORGANISM: Escherichia coli
US-08-978-878-4
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Search completed: March 11, 2004, 19:13:14
Job time: 171.3 secs
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   Query Match 66.9%; Score 514; DB 13; Best Local Similarity 68.9%; Pred. No. 6.7e-46; Matches 104; Conservative 18; Mismatches 29;
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Result
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  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   Total number of hits satisfying chosen parameters:
   Scoring table:
  Title:
Perfect score:
   OM protein -
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
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74
73.5
73.5
73.5
71.5
71.5
71.5
71.5
70.5
70.5
  77.5
76.5
76.5
75.5
  protein search, using sw model
   March 11, 2004, 18:35:05; Search time 5.3 Seconds (without alignments) 376.014 Million cell updates/sec
  Match Length DB
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   768
   125546 segs, 13197846 residues
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  US-09-543-407-30
  Pending Patents AA New:*
  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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/cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*
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 PCT-US04-05654-1755
US-10-603-150-2
US-10-100-683-10327
US-10-100-683-10327
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US-10-045-674A-591
US-10-767-701-4466
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US-10-627-556-396
US-10-627-556-396
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   US-10-100-683-7608
  US-09-741-873C-4
US-09-741-873C-2
  SUMMARIES
  Sequence 4, Appli
Sequence 2, Appli
Sequence 49, Appl
Sequence 590, App
Sequence 1768, Ap
Sequence 1755, Ap
Sequence 2, Appli
Sequence 10326, A
Sequence 10326, A
Sequence 40, Appl
Sequence 527, App
Sequence 527, App
Sequence 591, App
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42697, A
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572417, A
572417, A
392, App
392, App
400, App
400, App
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## ALIGNMENTS

RESULT 1 US-09-741-873C-4

Sequence 4, Applicat GENERAL INFORMATION:

Application US/09741873C

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TYPE: PRT
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US-09-741-873C-4
   FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR PTLING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR PTLING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1989-05-04
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/18,519
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-00-05
PRIOR FILING DATE: 1994-00-05
PRIOR FILING DATE: 1994-00-05
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PRIOR PRIOR PRIOR DATE: 1994-00-05
PRIOR PRIOR PRIOR DATE: 1994-00-05
                                 S
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   Query Match
Best Local Similarity
Matches 104; Conserv
   SEQ ID NO 4
  APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
   SOFTWARE: Patentin
  121
  61
  19
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHNNGGGNSSGPDSTLSIYQYGSANAALALQ
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  Conservative
   version 3.0
  66.9%; Score 514; DB 5; 68.9%; Pred. No. 2.1e-38;
   18;
  Mismatches
   Αg
  Length 151;
  Well
  Indels
  Αg
   Its Preparation
  0;
  Gaps
   120
   60
  6
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  ; ORGANISM: Escherichia coli
US-09-741-873C-2
  US-09-741-873C-2
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   Sequence 49, Application PC/TUS0402338
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE
TITLE OF INVENTION: USE
                  SOFTWARE: POSEQ ID NO 49
  Matches
   Query Match
Best Local :
   Sequence 2, Application US/09741873C GENERAL INFORMATION:
   PRIOR APPLICATION NUMBER: US50/461,789
PRIOR FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US50/470,684
PRIOR FILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US50/479,650
PRIOR FILING DATE: 2003-06-19
  CURRENT APPLICATION NUMBER: PCT/US04/02338
CURRENT FILING DATE: 2004-01-28
  NUMBER OF SEQ ID NOS: 54
  PRIOR APPLICATION NUMBER: US60/447,358 PRIOR FILING DATE: 2003-02-11
  PRIOR APPLICATION NUMBER: US60/443,484
PRIOR FILING DATE: 2003-01-29
  -US04-02338-49
  PRIOR FILING DATE: 1994-01-28
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
  APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
   PRIOR
   CURRENT APPLICATION NUMBER: US/09/741,873C CURRENT FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: SE 8801723-1 PRIOR FILING DATE: 1998-05-06
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APPLICATION NUMBER: US 07/789,437
  APPLICATION NUMBER: US 08/978,878 FILING DATE: 1997-11-26
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   141
   121
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   GFGNNATAHQY 131
  Conservative
  56.8%; Score 436; DB 5; Length 131; 65.6%; Pred. No. 1.2e-31; Vative 17; Mismatches 28; Indels
  Ās
  APC AND AXIN PATHWAYS AND METHODS
  Well As
  Its
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  Preparation
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  RESULT 4
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   Matches
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CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
   APPLICANT:
   APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: MBI-0047 PCT
  APPLICANT: Sherman, Bradley K
   APPLICANT:
  TYPE: PRT
ORGANISM: Oryza sativa
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Century, Karen
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   Riechmann,
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  Gutterson, Neal
   Pineda, Omaira
   Reuber, T. Lynne
  Ratcliffe, Oliver
   Creelman, Robert A
   Jiang, Cai-Zhong
  Geddie, James
Subell III, Arnold N
   Application PC/TUS0405654
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US-10-100-683-7608

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Sequence 1755, Applications
GENERAL INFORMATION:
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Bradley K
APPLICANT: Shermann, Jose Luis
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  PRIOR APPLICATION NUMBER: US 60/040,162 PRIOR FILING DATE: 1997-03-07
  CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
  TITLE OF INVENTION: Human Secreted Proteins FILE REFERENCE: PS900
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  APPLICANT:
   LENGTH: 443
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  FILING DATE:
  APPLICATION NUMBER: US 60/056,892
  APPLICATION NUMBER: US 60/047,632
  APPLICATION NUMBER: US 60/043,314
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  FILING DATE: 1997-05-23
  FILING DATE: 1997-04-11
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   287 SS 288
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  21 GVVPQ---WGGGGNHNGGGNSSGPDSTLSIYQ--YGSANAALALQSDARKSETTITQSGY 75
  33;
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  Riechmann, Jose Luis
Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
Reuber, T. Lyn
Keddie, James
Dubell III, Ar
                                    Ratcliffe, Oliver
Adam, Luc J
Reuber, T. Lynne
  Creelman, Robert A
  Conservative
   Application PC/TUS0405654
  et al.
  1997-05-23
   1997-08-22
   1997-05-23
  1997-08-22
   1997-04-11
  1997-08-22
  2002-03-
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  46;
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  26;
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995 GSNTS 999

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  US-10-603-150-2
  US-10-603-150-2
   SEQ ID NO 2
   Sequence 2, Applicat
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CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: PatentIn version 3.2
  PRIOR FILING DATE: 2002-06-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows
  CURRENT APPLICATION NUMBER: US/10/603,150
CURRENT FILING DATE: 2003-06-24
  PRIOR APPLICATION NUMBER: US 60/391,205
  FILE REFERENCE: R-1891
  TITLE OF INVENTION: MAGED3-Like Gene Disruptions, TITLE OF INVENTION: Compositions and Methods Re-
  APPLICANT: Robert G. Wisotzkey
   APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: MBI-0047 PCT
   APPLICANT:
   ORGANISM: Mus musculus
  ORGANISM: Oryza sativa FEATURE:
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  Similarity
   Application US/10603150
   AGYACGGAPSPEFAGSEQSSDTQSA--SAATMDE-----HHSPVGGGGNA 120
   Broun, Pierre E
Kumimoto, Roderick W
   Yu, Guo-Liang
  Gutterson, Neal
  Century, Karen
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  10.1%;
   Peter
   10.3%; Score 79; 30.4%; Pred. No.
  12;
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  Score 77.5;
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  46;
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  994
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Sequence 10326, Appl GENERAL INFORMATION

Application US/10100683

-10-100-683-10326

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   US-10-100-683-10327; Application US/10100683
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   ; ORGANISM: Homo sapiens 
US-10-100-683-10326
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Best Local Similarity
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   GENERAL INFORMATION:
                                    PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,845
PRIOR APPLICATION NUMBER: US 60/043,580
   CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
  Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 13468
   PRIOR APPLICATION NUMBER: US 60/043,576 PRIOR FILING DATE: 1997-04-11
  CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
   SOFTWARE:
  PRIOR FILING DATE: 1997-08-22
  PRIOR
  PRIOR FILING DATE: 1997-03-07
  FILE REFERENCE: PS900
  TITLE OF INVENTION: Human Secreted Proteins
   PRIOR FILING DATE: 1997-03-07
   PRIOR APPLICATION NUMBER: US 60/040,162
   TITLE OF INVENTION: Human Secreted Proteins
  FILE REFERENCE: PS900
  FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
  APPLICATION NUMBER: US 60/043,314
   FILING DATE: 1997-08-22
   APPLICATION NUMBER: US 60/056,664
  FILING DATE: 1997-05-23
   FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,599
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  FILING DATE: 1997-08-22
   APPLICATION NUMBER:
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  APPLICATION NUMBER: US 60/047,601
   APPLICATION NUMBER: US 60/056,892
  FILING DATE: 1997-05-23
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   76 GNGAD----VGQGADNSTIELTQNGFRNNAT 102
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  GGGSSNSGGGSGSQSGSSGSGSNGDNNNGS 267
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US 60/047,599
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Sequence 299, Application US, GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: FORSYTH, R. All)
TITLE OF INVENTION: GENES II
TITLE OF INVENTION: ESCHER)
   Ş
   밁
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   RESULT 11
US-10-771-241-299
   밁
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   US-10-779-461-40
  US-10-779-461-40
  RESULT 10
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  ; ORGANISM: Homo sapiens US-10-100-683-10327
  Sequence 40, Application US/10779461
GENERAL INFORMATION:
APPLICANT: Morton, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
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  FILE REFERENCE: 00980/1
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CURRENT FILING DATE: 2004-02-13
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  PRIOR APPLICATION NUMBER: US 60/047,632
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,892
PRIOR FILING DATE: 1997-08-22
   SOFTWARE: PatentIn version 3.2
  SOFTWARE: PatentIn Ver. 2.0
   OTHER INFORMATION: phage display generated human antibody
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TYPE: PRT
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  95 YCAISPLRGLTADVFDVWGQGTLVTVSSGGGGGGGGGGGGG
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Similarity 31.1%;
28; Conservative 1
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   Application US/10771241
  Conservative
 . R. Allyn
GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
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Pred. No. 12;
13; Mismatches
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Pred. No. 7
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   Length 386;
   Indels
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   237
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  S
  ; OTHER INFORMATION: Description of Artificial Sequence: Vector pCES5
; OTHER INFORMATION: protein sequence
US-10-045-674A-527
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US-10-045-674A-527
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  GENERAL INFORMATION:
   NUMBER OF SEQ ID NOS: 485
SOFTWARE: FRETSEQ for Windows Version 3.0
SEQ ID NO 299
LENGTH: 382
  Sequence 527,
  Matches 38;
  Query Match
  APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
   CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
  PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
  FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
  NUMBER OF SEQ ID NOS: 635
  APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
   PRIOR FILING DATE: 1999-01-27
   FILE REFERENCE: ELITRA.001C1
  PRIOR FILING DATE:
  TITLE OF INVENTION:
  APPLICANT:
  TYPE: PRT
ORGANISM: Artificial Sequence
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   ORGANISM: E. Coli
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  352
  104 DQLVTRVV-THEMAHAGGNNAALVNQTASDSSVMVRQVGFG 143
  158
  83
   APPLICATION NUMBER: US/10/771,241 FILING DATE: 2004-02-03
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R-KSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG-GN 121
  DETVVTVIPTHGAIARATFNAQIGGKVLMTLKYGNKSVPFG 316
  QPLGDTMVLVKAPGADNVKIENQTGIHTDWRGYAILPFATEYRENRVALNANSLADNVEL
  GNTHGGNTSSGTSGYSSLNYRGAYGNTNVGYSRSGDS--SQIYYGMSGGIIAHADGITFG
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  US-10-045-674A-591
  US-10-045-674A-591
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LENGTH: 424
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
SEQ ID NO 45603
LENGTH: 234
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   Sequence 45603,
   Matches
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   APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof Fo
FILE REFERENCE: 38-21(53535)B
   PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
   NUMBER OF SEQ ID
  CURRENT
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   TITLE OF INVENTION: NOVEL MET
TITLE OF INVENTION: DISPLAYE
TITLE OF INVENTION: OF PEPTI
TITLE OF INVENTION: LIBRARIE
FILE REFERENCE: DYAX/002 CIP2
  APPLICANT: LADNER, ROBERT C. APPLICANT: COHEN, EDWARD H.
   PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
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  CURRENT
   APPLICANT:
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  359 FR 360
   303 KGKLDSVATDYGAAIDGFIGDVSGLANGNGATGDFAGSNSQMAQVGDG-DNSPL---MNN
   243 SGGGSEGGGSEGGGSEGGGSEGGGSGSGDFDYEKMANANKGAMTENADENALQSDA
  461 NSPLMNNFRQYLPSLPQSVECRPYVFG 487
  122 NAALVNQ----TASDSSVMVRQVGFG 143
   412 KGKLDSVATDYGAAIDGFIGD-----VSGLANG--NGATGDFAGS---NSQMAQVGDGD
  FILING DATE:
  97 FR 98
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  15 SGSALAGVVPQWGG--GGNHNGGGNSSGPDSTLSIYQ-YGSANAAL-----ALQSDA
  APPLICATION NUMBER: US/10/045,674A FILING DATE: 2001-10-25
   T: HOOGENBOOM, HENDRICUS R. J. M.
INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM.
INVENTION: OF ENTINESS, POLYPEPTIDES OR PROTEINS AND THE NOVEL
   Similarity
  ROOKEY,
  Application US/10045674A
   Conservative
   Application US/10767701
                                     ATE: 2004-01-29
NOS: 63128
   RENE
  HORACIO G.
KRISTIN L.
  Description sequence
   LIBRARIES
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Pred. No.
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   302
   8
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ORGANISM: Sorghum bicolor

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Query Match
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Watches 41; Conserva
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   ; LENGTH: 624
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Orthologous to G1196
PCT-US04-05654-1466
   ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82834_1.pep
US-10-767-701-45603
  PCT-US04-05654-1466
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SEQ ID NO 1466
  APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYUUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
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   PRIOR APPLICATION NUMBER: 10/675,852
   NUMBER OF SEQ ID NOS: 2950
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  NAME/KEY: unsure
LOCATION: (1)..(234)
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   1 MATTKLAALCFIVLLGIGGANAARVARYVSAGGGGGGGGGGGGRGRWRGGASRWGSGSGSGC 60
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Riechmann, Jose Luis
Jiang, Cai-Zhong
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Gutterson, Neal
Yu, Guo-Liang
Broun, Pierre E
  Pineda, Omaira
   Reuber, T. Lynne
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  bell III, Arnold N
  tcliffe, Oliver
   ie, James
  Luc J
   Volker
   Jacqueline E
   2003-09-30
   Robert A
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26.1%;
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 86 SDADV-----
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Search completed: March 11, 2004, 19:14:20 Job time : 5.3 secs